

SEQUENCE LISTING

<110> Dumas Milne Edwards, Jean Baptiste
Bougueleret, Lydie
Jobert, Severin

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<151> 1999-12-08

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<151> 2000-03-06

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Ser	Arg	Pro	Ala	Gln	Pro	Pro	Arg	Leu	Leu	His	Thr	Ala	Asp	Thr	Cys	
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Gln	Leu	Glu	Val	Ala	Leu	Ile	Gly	Ala	Ser	Pro	Arg	Gly	Asn	Arg	Ser	
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Leu	Phe	Gly	Leu	Glu	Val	Ala	Thr	Leu	Gly	Gln	Gly	Pro	Asp	Cys	Pro	
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Ser	Met	Gln	Glu	Gln	His	Ser	Ile	Asp	Asp	Glu	Tyr	Ala	Pro	Ala	Val	
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Phe	Gln	Leu	Asp	Gln	Leu	Leu	Trp	Gly	Ser	Leu	Pro	Ser	Gly	Phe	Ala	
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Gln	Trp	Arg	Pro	Val	Ala	Tyr	Ser	Gln	Lys	Pro	Gly	Gly	Arg	Glu	Ser	
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gcc	ctg	ccc	tgc	caa	gct	tcc	cct	ctt	cat	cct	gcc	tta	gca	tac	tct	966
Ala	Leu	Pro	Cys	Gln	Ala	Ser	Pro	Leu	His	Pro	Ala	Leu	Ala	Tyr	Ser	
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Leu	Pro	Gln	Ser	Pro	Ile	Val	Arg	Ala	Phe	Phe	Gly	Ser	Gln	Asn	Asn	
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Phe	Cys	Ala	Phe	Asn	Leu	Thr	Phe	Gly	Ala	Ser	Thr	Gly	Pro	Gly	Tyr	
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Trp	Asp	Gln	His	Tyr	Leu	Ser	Trp	Ser	Met	Leu	Leu	Gly	Val	Gly	Phe	

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Pro Pro Val Asp Gly Leu Ser Pro Leu Val Leu Gly Ile Met Ala Val				
330	335	340		
gcc ctg ggt gcc cca ggg ctc atg ctg cta ggg ggc ggc ttg gtt ctg				1206
Ala Leu Gly Ala Pro Gly Leu Met Leu Leu Gly Gly Gly Leu Val Leu				
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Leu Leu His His Lys Lys Tyr Ser Glu Tyr Gln Ser Ile Asn				
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Met Ala Pro Leu Gly Met Leu Leu Gly Leu Met Ala	
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gcc tgc aca cct tct gcc tca gtc atc aga acc tgaaggagtt tgccctgacc	163
Ala Cys Thr Pro Ser Ala Ser Val Ile Arg Thr	
1 5	
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gggcaggctg tccctgcagg atcccacgta cggctgaatc ttcagactgg ggaaagagag	343
gcaaaaactcc aatatgagga caagttccga aataatttga aaggcaaaag gctggatatc	403
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cgccccattg aggaactgaa gaaagacttt gatgagctga atgttgtcat tgagactgac	583
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ccgctcactg caaaggaggg tgctcaccgt gcgctgggtc acactgctct acgacctggt	943
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seq LLGPLMAACFTFC/LS

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Met Ala
ccc cag agc ctg cct tca tct agg atg gct cct ctg ggc atg ctg ctt 164
Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro Leu Gly Met Leu Leu
-25 -20 -15
ggg ccg ctg atg gcc gcc tgc ttc acc ttc tgc ctc agt cat cag aac 212
Gly Pro Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser His Gln Asn
-10 -5 1 5
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Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr Lys Glu
10 15 20
aca gag aga aaa gaa acc aaa gcc gag gag gag ctg gat gcc gaa gtc 308
Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp Ala Glu Val
25 30 35
ctg gag gtg ttc cac ccg acg cat gag tgg cag gcc ctt cag cca ggg 356
Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln Pro Gly
40 45 50
cag gct gtc cct gca gga tcc cac gta cgg ctg aat ctt cag act ggg 404
Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln Thr Gly
55 60 65
gaa aga gag gca aaa ctc caa tat gag gac aag ttc cga aat aat ttg 452
Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn Asn Leu
70 75 80 85
aaa ggc aaa agg ctg gat atc aac acc aac acc tac aca tct cag gat 500
Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser Gln Asp
90 95 100
ctc aag agt gca ctg gca aaa ttc aag gag ggg gca gag atg gag agt 548
Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met Glu Ser
105 110 115
tca aag gaa gac aag gca agg cag gct gag gta aag cgg ctc ttc cgc 596
Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg Leu Phe Arg
120 125 130
ccc att gag gaa ctg aag aaa gac ttt gat gag ctg aat gtt gtc att 644

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Glu	Thr	Asp	Met	Gln	Ile	Met	Val	Arg	Leu	Ile	Asn	Lys	Phe	Asn	Ser	
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Ser	Ser	Ser	Ser	Leu	Glu	Glu	Lys	Ile	Ala	Ala	Leu	Phe	Asp	Leu	Glu	
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Tyr	Tyr	Val	His	Gln	Met	Asp	Asn	Ala	Gln	Asp	Leu	Leu	Ser	Phe	Gly	
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Gly	Leu	Gln	Val	Val	Ile	Asn	Gly	Leu	Asn	Ser	Thr	Glu	Pro	Leu	Val	
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Lys	Glu	Tyr	Ala	Ala	Phe	Val	Leu	Gly	Ala	Ala	Phe	Ser	Ser	Asn	Pro	
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Lys	Val	Gln	Val	Glu	Ala	Ile	Glu	Gly	Gly	Ala	Leu	Gln	Lys	Leu	Leu	
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Val	Ile	Leu	Ala	Thr	Glu	Gln	Pro	Leu	Thr	Ala	Lys	Lys	Lys	Val	Leu	
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Phe	Ala	Leu	Cys	Ser	Leu	Leu	Arg	His	Phe	Pro	Tyr	Ala	Gln	Arg	Gln	
			265				270					275				
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Phe	Leu	Lys	Leu	Gly	Gly	Leu	Val	Leu	Arg	Thr	Leu	Val	Gln	Glu		
		280				285					290					
aag	ggc	acg	gag	gtg	ctc	gcc	gtg	cgc	gtg	gtc	aca	ctg	ctc	tac	gac	1124
Lys	Gly	Thr	Glu	Val	Leu	Ala	Val	Arg	Val	Val	Thr	Leu	Leu	Tyr	Asp	
		295				300				305						
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Leu	Val	Thr	Glu	Lys	Met	Phe	Ala	Glu	Glu							
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<222> 66..1256

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score 4.89555877630516

seq LLLLRLNDAALRA/LQ

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        -35                -30                -25
    ttc acg caa gct gcc cgg act agc ctc tta ctg ctc agg ctc aac gac      158
    Phe Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp
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    gct gcc ctg cgg gcg ctg caa gag tgt cag cgg caa cag gta cgg ccg      206
    Ala Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro
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    gtg att gct ttc caa ggc cac cga ggg tat ctg aga ctc cca ggc cct      254
    Val Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro
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    Gly Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu
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    ggc gct ggt ggt agc ttg gac ctt gtg tgc caa cgc ttc ctc agg tct      350
    Gly Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser
        45                50                55
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    Gly Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile
        60                65                70                75
    att tgg gca gcc atg gat tct atc cca gcc cca tca tca gtt cag gga      446
    Ile Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly
        80                85                90
    cac aac ctg act gaa gat gcc aga cat cct gag agt tgg cag aac aca      494
    His Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr
        95                100                105
    gga ggc tat tct gaa gga gat gca gta tca cag cca cag atg gca cta      542
    Gly Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu
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    gag gag gtg tca gtg tca gat cca ctg gca agc aac caa gga cag tca      590
    Glu Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser
        125                130                135
    ctc cca gga tcc tca agg gag cac atg gca cag tgg gaa gtg aga agc      638
    Leu Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser
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    cag acc cat gtt cca aac aga gaa cct gtt cag gca ctg cct tcc tct      686
    Gln Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser
        160                165                170
    gcc agc cgg aaa cgt ctg gac aag aaa cgt tca gtg cct gta gcc act      734
    Ala Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr
        175                180                185
    gta gaa ctg gaa gaa aag agg ttc aga act ctg cct tta gtg cca agc      782
    Val Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Ser
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    Glu Gln Glu Asp Glu Asp Met Asp Pro Arg Leu Glu His Ser Ser Ser
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    Val Gln Glu Asp Ser Glu Ser Pro Ser Pro Glu Asp Ile Pro Asp Tyr
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Glu Gln Asp Phe Glu Thr Asp Tyr Ala Glu Tyr Arg Ile Leu His Ala
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Arg Val Gly Thr Ala Ser Gln Arg Phe Ile Glu Leu Gly Ala Glu Ile
      285      290      295
aaa aga gtt cgg cga gga act cca gaa tac aag gtc ctg gaa gac aag      1118
Lys Arg Val Arg Arg Gly Thr Pro Glu Tyr Lys Val Leu Glu Asp Lys
      300      305      310      315
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Ile Ile Gln Glu Tyr Lys Lys Phe Arg Lys Gln Tyr Pro Ser Tyr Arg
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Glu Glu Lys Arg Arg Cys Glu Tyr Leu His Gln Lys Leu Ser His Ile
      335      340      345
aaa ggt ctc atc ctg gag ttt gag gaa aag aac agg ggc agc      1256
Lys Gly Leu Ile Leu Glu Phe Glu Glu Lys Asn Arg Gly Ser
      350      355      360
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ctcccggcc atg gtc aac gac cct cca gta cct gcc tta ctg tgg gcc cag      231
      Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln
      -20      -15      -10
gag gtg ggc caa gtc ttg gca ggc cgt gcc cgc agg ctg ctg ctg cag      279
Glu Val Gly Gln Val Leu Ala Gly Arg Ala Arg Leu Leu Leu Gln
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Leu	Ser	Pro	Val	His	Phe	Tyr	Tyr	Arg	Thr	Asp	Cys	Asp	Ser	Ser	Thr	
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Thr	Ser	Leu	Cys	Ser	Phe	Pro	Val	Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly	
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Gly	Arg	Asp	Arg	Val	Leu	Met	Tyr	Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu	
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gag	ctt	gag	ctg	cca	gag	tcc	cct	gtg	aat	caa	gat	ttg	ggc	atg	ttc	567
Glu	Leu	Glu	Leu	Pro	Glu	Ser	Pro	Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	
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Ser	Ser	Arg	Ser	Val	Met	Leu	His	Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	
				125				130					135			
ctg	gac	aca	ctg	gtc	ttc	tct	agc	ctc	ctg	cta	ttt	ggc	ttt	gca	gag	711
Leu	Asp	Thr	Leu	Val	Phe	Ser	Ser	Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	
		140					145					150				
cag	aag	cag	ctg	ctg	gag	gtg	gaa	ctc	tac	gca	gac	tat	aga	gag	aac	759
Gln	Lys	Gln	Leu	Leu	Glu	Val	Glu	Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	
	155				160					165						
tgc	gtg	agt	gag	tac	gtg	ccg	acc	act	gga	gcg	atc	att	gag	atc	cac	807
Ser	Val	Ser	Glu	Tyr	Val	Pro	Thr	Thr	Gly	Ala	Ile	Ile	Glu	Ile	His	
	170				175					180					185	
agc	aag	cgc	atc	cag	ctg	tat	gga	gcc	tac	ctc	cgc	atc	cac	gcg	cac	855
Ser	Lys	Arg	Ile	Gln	Leu	Tyr	Gly	Ala	Tyr	Leu	Arg	Ile	His	Ala	His	
				190				195						200		
ttc	act	ggg	ctc	aga	tac	ctg	cta	tac	aac	ttc	ccg	atg	acc	tgc	gcc	903
Phe	Thr	Gly	Leu	Arg	Tyr	Leu	Leu	Tyr	Asn	Phe	Pro	Met	Thr	Cys	Ala	
			205					210					215			
ttc	ata	ggg	gtt	gcc	agc	aac	ttc	acc	ttc	ctc	agc	gtc	atc	gtg	ctc	951
Phe	Ile	Gly	Val	Ala	Ser	Asn	Phe	Thr	Phe	Leu	Ser	Val	Ile	Val	Leu	
		220					225					230				
ttc	agc	tac	atg	cag	tgg	gtg	tgg	ggg	ggc	atc	tgg	ccc	cga	cac	cgc	999
Phe	Ser	Tyr	Met	Gln	Trp	Val	Trp	Gly	Gly	Ile	Trp	Pro	Arg	His	Arg	
	235				240						245					
ttc	tct	ttg	cag	gtt	aac	atc	cga	aaa	aga	gac	aat	tcc	cgg	aag	gaa	1047
Phe	Ser	Leu	Gln	Val	Asn	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Arg	Lys	Glu	
				255						260					265	
gtc	caa	cga	agg	atc	tct	gct	cat	cag	cca	ggg	gca	ggg	cct	gaa	ggc	1095
Val	Gln	Arg	Arg	Ile	Ser	Ala	His	Gln	Pro	Gly	Ala	Gly	Pro	Glu	Gly	
				270				275						280		
cag	gag	gag	tca	act	ccg	caa	tca	gat	gtt	aca	gag	gat	ggg	gag	agc	1143
Gln	Glu	Glu	Ser	Thr	Pro	Gln	Ser	Asp	Val	Thr	Glu	Asp	Gly	Glu	Ser	
			285					290					295			
cct	gaa	gat	ccc	tca	ggg	aca	gag	ggg	cag	ctg	tcc	gag	gag	gag	aaa	1191
Pro	Glu	Asp	Pro	Ser	Gly	Thr	Glu	Gly	Gln	Leu	Ser	Glu	Glu	Glu	Lys	
			300				305					310				
cca	gat	cag	cag	ccc	ctg	agc	gga	gaa	gag	gag	cta	gag	cct	gag	gcc	1239
Pro	Asp	Gln	Gln	Pro	Leu	Ser	Gly	Glu	Glu	Glu	Leu	Glu	Pro	Glu	Ala	

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      315              320              325
    agt gat ggt tca ggc tcc tgg gaa gat gca gct ttg ctg acg gag gcc      1287
    Ser Asp Gly Ser Gly Ser Trp Glu Asp Ala Ala Leu Leu Thr Glu Ala
    330              335              340              345
    aac ctg cct gct cct gct cct gct tct gct tct gcc cct gtc cta gag      1335
    Asn Leu Pro Ala Pro Ala Pro Ala Ser Ala Ser Ala Pro Val Leu Glu
      350              355              360
    act ctg ggc agc tct gaa cct gct ggg ggt gct ctc cga cag cgc ccc      1383
    Thr Leu Gly Ser Ser Glu Pro Ala Gly Gly Ala Leu Arg Gln Arg Pro
      365              370              375
    acc tgc tct agt tcc tgaagaaaag gggcagactc ctcacattcc agcactttcc      1438
    Thr Cys Ser Ser Ser
      380
    cacctgactc ctctccctc gtttttcctt caataaacta ttttgtgtca gtcctcaaaaa      1498
    aaaaaaaaaa aa      1510

<210> 9
<211> 882
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 78..410

<220>
<221> sig_peptide
<222> 78..155
<223> Von Heijne matrix
      score 10.0731536331164
      seq LWLALVSCILTQA/SA

<400> 9
    atggctggcc agaggaggaa cgctttgtgt tctcatcgga gctgcatggg aagtctgcat      60
    acagcaaagt gacctgc atg cct cac ctt atg gaa agg atg gtg ggc tct      110
              Met Pro His Leu Met Glu Arg Met Val Gly Ser
              -25              -20
    ggc ctc ctg tgg ctg gcc ttg gtc tcc tgc att ctg acc cag gca tct      158
    Gly Leu Leu Trp Leu Ala Leu Val Ser Cys Ile Leu Thr Gln Ala Ser
    -15              -10              -5              1
    gca gtg cag cga ggt tat gga aac ccc att gaa gcc agt tcg tat ggg      206
    Ala Val Gln Arg Gly Tyr Gly Asn Pro Ile Glu Ala Ser Ser Tyr Gly
      5              10              15
    ctg gac ctg gac tgc gga gct cct ggc acc cca gag gct cat gtc tgt      254
    Leu Asp Leu Asp Cys Gly Ala Pro Gly Thr Pro Glu Ala His Val Cys
      20              25              30
    ttt gac ccc tgt cag aat tac acc ctc cta gat ttg ggg ccc atc act      302
    Phe Asp Pro Cys Gln Asn Tyr Thr Leu Leu Asp Leu Gly Pro Ile Thr
      35              40              45
    cgg aga ggt gca cag tct ccc ggt gtc atg aat gga acc cct agc act      350
    Arg Arg Gly Ala Gln Ser Pro Gly Val Met Asn Gly Thr Pro Ser Thr
      50              55              60              65
    gca ggg ttc ctg gtg gcc tgg cct atg gtc ctc ctg act gtc ctc ctg      398
    Ala Gly Phe Leu Val Ala Trp Pro Met Val Leu Leu Thr Val Leu Leu
      70              75              80
    gct tgg ctg ttc tgagagctcc gctgagcatc tggccttgaa gtttgtgttc      450
    Ala Trp Leu Phe
      85

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ttccctctg	caatggctcc	cttcagcact	tctgctttcc	actccaattc	acacaggctt	510
ggтатаaaca	gaatcaaggc	caggctaggt	taggaaaagg	gaagagcttt	caccttcttt	570
aaaactctcg	gctgggcgca	gtggctcatg	cctgtaatcc	cagcattttg	ggaggctgag	630
gcagggtggat	cacctgaggt	cagcagttca	aaatcagcct	ggccaaaatg	ctgaaactcc	690
gtctctacta	aaaatacaaa	aattagccag	gcatggtgac	aggcgctgt	aatcccagct	750
actcgggagg	ccaaggcagg	agaattgctc	gaactcaggg	ggtggagggt	gcagtgagtt	810
gagattgtgc	cattgcactc	cagcctgggc	aacagagcaa	gactctgtct	caggcaaaaa	870
aaaaaaaaaa	aa					882

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<220>  
<221> CDS  
<222> 84..299
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[illegible]

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gttgtgtaag ggtaggcttt gttgaaaaag aaagaaagat tgaactacag gtgcatagca 1319
agcactcttt ctgggtaact aggctgctgg ttttaattac cctcagattt caccataaaa 1379
aacgcacaat tgtattattt tacagagatg tgtccagcgc cccctgtggt gtgtgagaga 1439
aagcagctgc aactcaagtg actagggtggg cccagctggc ttcgtgcagg agggcacggg 1499
gggtgagcca ttctcgccat tctcatgtca gactgaaagg agggcctggg ccagctttga 1559
aaaggcagga tgaaatggaa aggtcaccac acttagggat tttagacctt gactaacaag 1619
ctccaggtgt agaaaaattc aaaacaaaat gtcaggaatc tagcagtgtt gtctgccctg 1679
gagcaaacia acagtatgtg attttgcttc gcctattttt tttttctttt ttgggggaag 1739
ataattaaag gcagaatgac tgcgtttgta aaagaaggac caccaactat actgacattt 1799
ataaatgaac ctttattaaa gacacttcaa tgcaaaaaaa aaaaaaaaaa 1849

```

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<210> 11
<211> 565
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 55..468

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<220>
<221> sig_peptide
<222> 55..99
<223> Von Heijne matrix
      score 8.96936032049195
      seq FTTLLFLAAVAGA/LV

```

```

<400> 11
attccccaga ccttctgcag attctgtggt tatactcact cctcatccca aaga atg      57
                                         Met
                                         -15
aaa ttt acc act ctc ctc ttc ttg gca gct gta gca ggg gcc ctg gtc      105
Lys Phe Thr Thr Leu Leu Phe Leu Ala Ala Val Ala Gly Ala Leu Val
                                         -10
                                         -5
                                         1
tat gct gaa gat gcc tcc tct gac tcg acg ggt gct gat cct gcc cag      153
Tyr Ala Glu Asp Ala Ser Ser Asp Ser Thr Gly Ala Asp Pro Ala Gln
      5
      10
      15
gaa gct ggg acc tct aag cct aat gaa gag atc tca ggt cca gca gaa      201
Glu Ala Gly Thr Ser Lys Pro Asn Glu Glu Ile Ser Gly Pro Ala Glu
      20
      25
      30
cca gct tca ccc cca gag aca acc aca aca gcc cag gag act tcg gcg      249
Pro Ala Ser Pro Pro Glu Thr Thr Thr Thr Ala Gln Glu Thr Ser Ala
      35
      40
      45
      50
gca gca gtt cag ggg aca gcc aag gtc acc tca agc agg cag gaa cta      297
Ala Ala Val Gln Gly Thr Ala Lys Val Thr Ser Ser Arg Gln Glu Leu
      55
      60
      65
aac ccc ctg aaa tcc ata gtg gag aaa agt atc tta cta aca gaa caa      345
Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu Gln
      70
      75
      80
gcc ctt gca aaa gca gga aaa gga atg cac gga ggc gtg cca ggt gga      393
Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly Gly
      85
      90
      95
aaa caa ttc atc gaa aat gga agt gaa ttt gca caa aaa tta ctg aag      441
Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu Lys
      100
      105
      110
aaa ttc agt cta tta aaa cca tgg gca tgagaagctg aataatggga      488
Lys Phe Ser Leu Leu Lys Pro Trp Ala
115
      120

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tcattggact taaagcctta aatacccttg tagcccagag ctattaaaac gaaagcatcc 548
 aaaaaaaaaa aaaaaaa 565

<210> 12
 <211> 1663
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 152..475

<220>
 <221> sig_peptide
 <222> 152..244
 <223> Von Heijne matrix
 score 10.0910253445132
 seq LVLLLVTRSPVNA/CL

<400> 12
 atgtgtctgc tgccgccatt gtgcggcgct ggtccctca gagggttcct gctgctgccg 60
 gtgccttgga cctccccct cgcttctcgt tctactgccc caggagcccg gcgggtccgg 120
 gactcccgtc cgtgccggtg cgggcgcggg c atg tgg ctg tgg gag gac cag 172
 Met Trp Leu Trp Glu Asp Gln
 -30 -25
 ggc ggc ctc ctg ggc cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg 220
 Gly Gly Leu Leu Gly Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu
 -20 -15 -10
 gtg acg cgg agc ccg gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc 268
 Val Thr Arg Ser Pro Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe
 -5 1 5
 gtt cta ctg cgc gtc ttc agc ttt gag ccg gtg ccc tct tgc agg gcc 316
 Val Leu Leu Arg Val Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala
 10 15 20
 ctg cag gtg ctc aag ccc cgg gac cgc att tct gcc atc gcc cac cgt 364
 Leu Gln Val Leu Lys Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg
 25 30 35 40
 ggc ggc agc aam sag gcg ccc gag aac acg ctg gcg gcc att cgg cag 412
 Gly Gly Ser Xaa Xaa Ala Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln
 45 50 55
 cta aga atg gag caa cag gcg tgg agt tgg aca ttg agt tta ctt ctg 460
 Leu Arg Met Glu Gln Gln Ala Trp Ser Trp Thr Leu Ser Leu Leu Leu
 60 65 70
 acg gga ttc ctg tct taatgcacga taacacagta gataggacga ctgatgggac 515
 Thr Gly Phe Leu Ser
 75
 tgggcgattg tgtgatttga catttgaaca aattaggaag ctgaatcctg cagcaaacca 575
 cagactcagg aatgatttcc ctgatgaaaa gatccctacc ctaagggaag ctgttgcaga 635
 gtgcctaaac cataacctca caatcttctt tgatgtcaaa ggccatgcac acaaggctac 695
 tgaggctcta aagaaaatgt atatggaatt tcctcaactg tataataata gtgtgggtctg 755
 ttctttcttg ccagaagtta tctacaaggt aacattcggg atttttcttg tacatattag 815
 atgagacaaa cagatcggga tgtaataaca gcattaactc acagaccttg gagcctaagc 875
 catacaggag atgggaaacc acgctatgat actttctgga aacattttat atttgttatg 935
 atggacattt tgctcgattg gagcatgcat aatatcttgt ggtacctgtg tgggaatttca 995
 gctttcctca tgcaaaagga ttttgtatcc ccggcctact tgaagaagtg gtcagctaaa 1055
 ggaatccagg ttgttggttg gactgttaac acctttgatg aaaagagtta ctacgaatcc 1115
 catcttgggt ccagctatat cactgacagc atggtagaag actgcgaacc tcacttctag 1175
 actttcacgg tgggacgaaa cgggttcaga aactgccagg ggccatcac agggatatca 1235

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aaataccctt tgtgctagcc caggccctgg ggaatcaggt gactcacaca aatgcaatag 1295
ttggtcactg catttttacc tgaaccaaag ctaaaccagg tgttgccacc atgcaccatg 1355
gcatgccaga gttcaacact gttgctcttg aaaatctggg tctgaaaaaa cgcacaagag 1415
cccctgccct gccctagctg aggcacacag ggagacccag tgaggataag cacagattga 1475
attgtacaat ttgcagatgc agatgtaaat gcatgggaca tgcataataa ctcagagttg 1535
acattttaaa acttgccaca cttatttcaa atatttgtac tcagctatgt taacatgtac 1595
tgtagacatc aaacttgtgg ccatactaata aaaattatta aaaggagcac taaaaaaaaa 1655
aaaaaaaaa 1663

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<210> 13
<211> 744
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 112..552

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<220>
<221> sig_peptide
<222> 112..183
<223> Von Heijne matrix
      score 11.7298925418815
      seq FVLGLGLTPPTLA/QD

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```

<400> 13
tcacaactgg aacccatctc caggaacaaa cagctggaac ccatctcccg ttgaagggaa 60
actgccagat ttttgtaaga ttcttctctc tgggagcctg tggttgaaga g atg gtg 117
                                     Met Val
atg ggc ctg ggc gtt ttg ttg ttg gtc ttc gtg ctg ggt ctg ggt ctg 165
Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu Gly Leu
      -20                                -15                                -10
acc cca ccg acc ctg gct cag gat aac tcc agg tac aca cac ttc ctg 213
Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His Phe Leu
      -5                                1                                5                                10
acc cag cac tat gat gcc aaa cca cag ggc cgg gat gac aga tac tgt 261
Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg Tyr Cys
      15                                20                                25
gaa agc atc atg agg aga cgg ggc ctg acc tca ccc tgc aaa gac atc 309
Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys Asp Ile
      30                                35                                40
aac aca ttt att cat ggc aac aag cgc acg atc aag gcc atc tgt gaa 357
Asn Thr Phe Ile His Gly Asn Lys Arg Thr Ile Lys Ala Ile Cys Glu
      45                                50                                55
aac aag aat gga aac cct cac aga gaa aac cta aga ata agc aag tct 405
Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser Lys Ser
      60                                65                                70
tct ttc cag gtc acc act tgc aag cta cat gga ggt tcc ccc tgg cct 453
Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro Trp Pro
      75                                80                                85                                90
cca tgc cag tac cga gcc aca gcg ggg ttc aga aac gtt gtt gtt gct 501
Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val Val Ala
      95                                100                                105
tgt gaa aat ggc tta cct gtc cac ttg gat cag tca att ttc cgt cgt 549
Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe Arg Arg
      110                                115                                120
ccg taaccagcgg gccctgggtc aagtgtggc tctgctgtcc ttgccttcca 602
Pro

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tttccctctt gcaccagaa cagtgggtggc aacattcatt gccaaaggcc caaagaaaga 662
gctacctgga ccttttgttt tctgtttgac aacatgttta ataaataaaa atgtcttgat 722
atcagcaaaa aaaaaaaaaa aa 744

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<210> 14
<211> 1759
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 101..1243

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<220>
<221> sig_peptide
<222> 101..199
<223> Von Heijne matrix
      score 3.57142340200611
      seq FLCLGMALCPRQA/TR

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<400> 14
gtagagtgtc gaaggtcctg ccaacggctc tcttggcgtc tcaacgttcg gatcagcagc 60
ttttttccat tctctctctc cacttcttca gtgagcagcc atg agt tgg act gtg 115
                               Met Ser Trp Thr Val
                               -30
cct gtt gtg cgg gcc agc cag aga gtg agc tcg gtg gga gcg aat ttc 163
Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser Val Gly Ala Asn Phe
                               -25                               -20                               -15
cta tgc ctg ggg atg gcc ctg tgt ccg cgt caa gca acg cgc atc ccg 211
Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln Ala Thr Arg Ile Pro
                               -10                               -5                               1
ctc aac ggc acc tgg ctc ttc acc ccc gtg agc aag atg gcg act gtg 259
Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser Lys Met Ala Thr Val
5                               10                               15                               20
aag agt gag ctt att gag cgt ttc act tcc gag aag ccc gtt cat cac 307
Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu Lys Pro Val His His
                               25                               30                               35
agt aag gtc tcc atc ata gga act gga tcg gtg ggc atg gcc tgc gct 355
Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val Gly Met Ala Cys Ala
                               40                               45                               50
atc agc atc tta tta aaa ggc ttg agt gat gaa ctt gcc ctt gtg gat 403
Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu Leu Ala Leu Val Asp
                               55                               60                               65
ctt gat gaa gac aaa ctg aag ggt gag acg atg gat ctt caa cat ggc 451
Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met Asp Leu Gln His Gly
70                               75                               80
agc cct ttc acg aaa atg cca aat att gtt tgt agc aaa gat tac ttt 499
Ser Pro Phe Thr Lys Met Pro Asn Ile Val Cys Ser Lys Asp Tyr Phe
85                               90                               95                               100
gtc aca gca aac tcc aac cta gtg att atc aca gca ggt gca cgc caa 547
Val Thr Ala Asn Ser Asn Leu Val Ile Ile Thr Ala Gly Ala Arg Gln
                               105                               110                               115
gaa aag gga gaa acg cgc ctt aat tta gtc cag cga aat gtg gcc atc 595
Glu Lys Gly Glu Thr Arg Leu Asn Leu Val Gln Arg Asn Val Ala Ile
120                               125                               130
ttc aag tta atg att tcc agt att gtc cag tac agc ccc cac tgc aaa 643
Phe Lys Leu Met Ile Ser Ser Ile Val Gln Tyr Ser Pro His Cys Lys
135                               140                               145

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ctg att att gtt tcc aat cca gtg gat atc tta act tat gta gct tgg	691
Leu Ile Ile Val Ser Asn Pro Val Asp Ile Leu Thr Tyr Val Ala Trp	
150 155 160	
aag ttg agt gca ttt ccc aaa aac cgt att att gga agc ggc tgt aat	739
Lys Leu Ser Ala Phe Pro Lys Asn Arg Ile Ile Gly Ser Gly Cys Asn	
165 170 175 180	
ctg gat act gct cgt ttt cgt ttc ttg att gga caa aag ctt ggt atc	787
Leu Asp Thr Ala Arg Phe Arg Phe Leu Ile Gly Gln Lys Leu Gly Ile	
185 190 195	
cat tct gaa agc tgc cat gga tgg atc ctc gga gag cat gga gac tca	835
His Ser Glu Ser Cys His Gly Trp Ile Leu Gly Glu His Gly Asp Ser	
200 205 210	
agt gtt cct gtg tgg agt gga gtg aac ata gct ggt gtc cct ttg aag	883
Ser Val Pro Val Trp Ser Gly Val Asn Ile Ala Gly Val Pro Leu Lys	
215 220 225	
gat ctg aac tct gat ata gga act gat aaa gat cct gag caa tgg aaa	931
Asp Leu Asn Ser Asp Ile Gly Thr Asp Lys Asp Pro Glu Gln Trp Lys	
230 235 240	
aat gtc cac aaa gaa gtg act gca act gcc tat gag att att aaa atg	979
Asn Val His Lys Glu Val Thr Ala Thr Ala Tyr Glu Ile Ile Lys Met	
245 250 255 260	
aaa ggt tat act tct tgg gcc att ggc cta tct gtg gcc gat tta aca	1027
Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser Val Ala Asp Leu Thr	
265 270 275	
gaa agt att ttg aag aat ctt agg aga ata cat cca gtt tcc acc ata	1075
Glu Ser Ile Leu Lys Asn Leu Arg Arg Ile His Pro Val Ser Thr Ile	
280 285 290	
att aag ggc ctc tat gga ata gat gaa gaa gta ttc ctc agt att cct	1123
Ile Lys Gly Leu Tyr Gly Ile Asp Glu Glu Val Phe Leu Ser Ile Pro	
295 300 305	
tgt atc ctg gga gag aac ggt att acc aac ctt ata aag ata aag ctg	1171
Cys Ile Leu Gly Glu Asn Gly Ile Thr Asn Leu Ile Lys Ile Lys Leu	
310 315 320	
acc cct gaa gaa gag gcc cat ctg aaa aaa agt gca aaa aca ctc tgg	1219
Thr Pro Glu Glu Glu Ala His Leu Lys Lys Ser Ala Lys Thr Leu Trp	
325 330 335 340	
gaa att cag aat aag ctt aag ctt taaagttgcc taaaactacc attccgaaat	1273
Glu Ile Gln Asn Lys Leu Lys Leu	
345	
tattgaagag atcatagata caggattata taacgaaatt ttgaataaac ttgaattcct	1333
aaaagatgga aacaggaaag taggtagagt gattttccta tttatttagt cctccagctc	1393
ttttattgag catccacgtg ctggacgata cttattttaca attcctaagt attttttggt	1453
cctctgatgt agcagcactt gccatgttat atatattgtag ttggcatttg gttcccaaaa	1513
agtaggatgt aggtatttat tgtgttctag aaattccgac tcttttcatt agatatatgc	1573
tattttctttc atttctgtctg gttttatacct atgttcattt atatgctgta aaaaagtagt	1633
agcttcttct acaatgtaaa aataaatgta catacaaaaa aatgcagtag tatatacaat	1693
cttttgtttt gcttcctttg atagttaata aattccgttt gttgaatcaa taataaaaaa	1753
aaaaaa	1759

<210> 15

<211> 1755

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 101..517


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<220>
<221> sig_peptide
<222> 101..199
<223> Von Heijne matrix
      score 3.57613483592743
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                                         Met Ser Trp Thr Val
                                         -30
cct gtt gtg cgg gcc agc cag aga atg agc tcg gtg gga gcg aat ttc 163
Pro Val Val Arg Ala Ser Gln Arg Met Ser Ser Val Gly Ala Asn Phe
      -25      -20      -15
cta tgc ctg ggg atg gcc ctg tgt ctg cgt caa gca acg cgc atc ccg 211
Leu Cys Leu Gly Met Ala Leu Cys Leu Arg Gln Ala Thr Arg Ile Pro
      -10      -5      1
ctc aac ggc acc tgg ctc ttc aca ccc gtg agc aag atg gcg act gtg 259
Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser Lys Met Ala Thr Val
5      10      15      20
aag agt gag ctt att gag cgt ttc act tcc gag aag ccc gtt cat cac 307
Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu Lys Pro Val His His
      25      30      35
agt aag gtc tcc atc ata gga act gga tcg gtg ggc atg gcc tgc gct 355
Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val Gly Met Ala Cys Ala
      40      45      50
atc agc atc ttg tta aaa ggc ttg agt gat gaa ctt gcc ctt gtg gat 403
Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu Leu Ala Leu Val Asp
      55      60      65
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Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met Asp Leu Gln His Gly
      70      75      80
agc cct ttc acg aaa atg cca ata ttg ttt gta gca aag att act ttg 499
Ser Pro Phe Thr Lys Met Pro Ile Leu Phe Val Ala Lys Ile Thr Leu
85      90      95      100
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Ser Gln Gln Thr Pro Thr
      105
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ttccagtatt gtccagtaca gccccactg caaactgatt attgtttcca atccagtgga 667
tatcttaact tatgtagctt ggaagttgag tgcatttccc aaaaaccgta ttattggaag 727
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gtagcttctt ctacaatgta aaaataaatg tacatacaaa aaaatgcagt agtatatata 1687

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 Ser Ser Thr Leu Lys Pro Thr Ile Glu Ala Leu Pro Asn Val Leu Pro
 5 10 15
 tta aat gaa gat gtt aat aag cag gaa gaa aag aat gaa gat cat act 202
 Leu Asn Glu Asp Val Asn Lys Gln Glu Glu Lys Asn Glu Asp His Thr
 20 25 30
 ccc aat tat gct cct gct aat gag aaa aat ggc aat tat tat aaa gat 250
 Pro Asn Tyr Ala Pro Ala Asn Glu Lys Asn Gly Asn Tyr Tyr Lys Asp
 35 40 45 50
 ata aaa caa tat gtg ttc aca aca caa aat cca aat ggc act gag tct 298
 Ile Lys Gln Tyr Val Phe Thr Thr Gln Asn Pro Asn Gly Thr Glu Ser
 55 60 65
 gaa ata tct gtg aga gcc aca act gac ctg aat ttt gct cta aaa aac 346
 Glu Ile Ser Val Arg Ala Thr Thr Asp Leu Asn Phe Ala Leu Lys Asn
 70 75 80
 gga tca acc cca aac gtg cct gca ttt tgg aca atg tta gct aaa gct 394
 Gly Ser Thr Pro Asn Val Pro Ala Phe Trp Thr Met Leu Ala Lys Ala
 85 90 95
 ata aat gga aca gca gtg gtc atg gat gat aaa gat caa tta ttt cac 442
 Ile Asn Gly Thr Ala Val Val Met Asp Asp Lys Asp Gln Leu Phe His
 100 105 110
 cca att cca gag tct gat gtg aat gct aca cag gga gaa aat cag cca 490
 Pro Ile Pro Glu Ser Asp Val Asn Ala Thr Gln Gly Glu Asn Gln Pro
 115 120 125 130
 gat cta gag gat ctg aag atc aaa ata atg ctg gga atc tcg ttg atg 538
 Asp Leu Glu Asp Leu Lys Ile Lys Ile Met Leu Gly Ile Ser Leu Met
 135 140 145
 acc ctc ctc ctc ttt gtg gtc ctc ttg gca ttc tgt agt gct aca ctg 586
 Thr Leu Leu Leu Phe Val Val Leu Leu Ala Phe Cys Ser Ala Thr Leu
 150 155 160
 tac aaa ctg agg cat ctg agt tat aaa agt tgt gag agt cag tac tct 634
 Tyr Lys Leu Arg His Leu Ser Tyr Lys Ser Cys Glu Ser Gln Tyr Ser
 165 170 175
 gtc aac cca gag ctg gcc acg atg tct tac ttt cat cca tca gaa ggt 682

Val	Asn	Pro	Glu	Leu	Ala	Thr	Met	Ser	Tyr	Phe	His	Pro	Ser	Glu	Gly		
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Val	Ser	Asp	Thr	Ser	Phe	Ser	Lys	Ser	Ala	Glu	Ser	Ser	Thr	Phe	Leu		
195					200					205					210		
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Gly	Thr	Thr	Ser	Ser	Asp	Met	Arg	Arg	Ser	Gly	Thr	Arg	Thr	Ser	Glu		
				215					220					225			
tct	aag	ata	atg	acg	gat	atc	att	tcc	ata	ggc	tca	gat	aat	gag	atg	826	
Ser	Lys	Ile	Met	Thr	Asp	Ile	Ile	Ser	Ile	Gly	Ser	Asp	Asn	Glu	Met		
			230					235					240				
cat	gaa	aac	gat	gag	tcg	ggt	acc	cgg	tgaagaaatc	aaggaacccg						873	
His	Glu	Asn	Asp	Glu	Ser	Val	Thr	Arg									
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	Met Asp Ser Ser	Thr Ala His	Ser Pro Val	Phe Leu Val													
	-20		-15		-10												
ttt cct cca	gaa atc act	gct tca	gaa tat	gag tcc	aca gaa	ctt tca										159	
Phe Pro Pro	Glu Ile Thr	Ala Ser	Glu Tyr	Glu Ser	Thr Glu	Leu Ser											
	-5		1		5												
gcc acg acc	ttt tca act	caa agc	ccc ttg	caa aaa	tta ttt	gct aga										207	
Ala Thr Thr	Phe Ser Thr	Gln Ser	Pro Leu	Gln Lys	Leu Phe	Ala Arg											
10		15		20		25											
aaa atg aaa	atc tta ggg	act atc	cag atc	ctg ttt	gga att	atg acc										255	
Lys Met Lys	Ile Leu Gly	Thr Ile	Gln Ile	Leu Phe	Gly Ile	Met Thr											
	30		35		40												
ttt tct ttt	gga gtt atc	ttc ctt	ttc act	ttg tta	aaa cca	tat cca										303	
Phe Ser Phe	Gly Val Ile	Phe Leu	Phe Thr	Leu Leu	Lys Pro	Tyr Pro											
	45		50		55												
agg ttt ccc	ttt ata ttt	ctt tca	gga tat	cca ttc	tgg ggc	tct gtt										351	
Arg Phe Pro	Phe Ile Phe	Leu Ser	Gly Tyr	Pro Phe	Trp Gly	Ser Val											
	60		65		70												
ttg ttc att	aat tct gga	gcc ttc	cta att	gca gtg	aaa aga	aaa acc										399	
Leu Phe Ile	Asn Ser Gly	Ala Phe	Leu Ile	Ala Val	Lys Arg	Lys Thr											
	75		80		85												
aca gaa act	ctg ata ata	ttg agc	cga ata	atg aat	ttt ctt	agt gcc										447	
Thr Glu Thr	Leu Ile Ile	Leu Ser	Arg Ile	Met Asn	Phe Leu	Ser Ala											

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90          95          100          105
ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta      495
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          110          115          120
gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag      543
Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys

          125          130          135
gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc      591
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe

          140          145          150
agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc      639
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys

          155          160          165
cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata      692
His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys

170          175          180
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                        Met Ala Thr Ala Gln Leu Gln
                        -35
agg act ccc atg agt gca ctg gta ttt ccc aat aag ata tca act gaa      162
Arg Thr Pro Met Ser Ala Leu Val Phe Pro Asn Lys Ile Ser Thr Glu
      -30          -25          -20
cac cag tct ttg gtg tta gtg aag agg ctt cta gca gtt tca gta tcc      210
His Gln Ser Leu Val Leu Val Lys Arg Leu Leu Ala Val Ser Val Ser
      -15          -10          -5
tgt atc acg tat ttg agg gga ata ttc cca gaa tgc gct tat gga aca      258
Cys Ile Thr Tyr Leu Arg Gly Ile Phe Pro Glu Cys Ala Tyr Gly Thr
1          5          10          15
aga tat cta gat gat ctt tgt gtc aaa ata ctg aga gaa gat aaa aat      306
Arg Tyr Leu Asp Asp Leu Cys Val Lys Ile Leu Arg Glu Asp Lys Asn
      20          25          30
tgc cca gga tct aca cag tta gtg aaa tgg att cta gga tgt tat gat      354
Cys Pro Gly Ser Thr Gln Leu Val Lys Trp Ile Leu Gly Cys Tyr Asp
      35          40          45
gct tta cag aaa aaa tat cta agg atg gtt gtt cta gct gta tac aca      402
Ala Leu Gln Lys Lys Tyr Leu Arg Met Val Val Leu Ala Val Tyr Thr
      50          55          60
aac cca gaa gat cct cag aca att tca gaa tgt tac caa ttc aaa ttc      450

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Lys	Tyr	Thr	Asn	Asn	Gly	Pro	Leu	Met	Asp	Phe	Ile	Ser	Lys	Asn	Gln	
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Ser	Asn	Glu	Ser	Ser	Met	Leu	Ser	Thr	Asp	Thr	Lys	Lys	Ala	Ser	Ile	
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ctc	ctc	att	cgc	aag	att	tat	atc	cta	atg	caa	aat	ctg	ggg	cct	tta	594
Leu	Leu	Ile	Arg	Lys	Ile	Tyr	Ile	Leu	Met	Gln	Asn	Leu	Gly	Pro	Leu	
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Pro	Asn	Asp	Val	Cys	Leu	Thr	Met	Lys	Leu	Phe	Tyr	Tyr	Asp	Glu	Val	
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Thr	Pro	Pro	Asp	Tyr	Gln	Pro	Pro	Gly	Phe	Lys	Asp	Gly	Asp	Cys	Glu	
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Gly	Val	Ile	Phe	Glu	Gly	Glu	Pro	Met	Tyr	Leu	Asn	Val	Gly	Glu	Val	
				165				170						175		
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Ser	Thr	Pro	Phe	His	Ile	Phe	Lys	Val	Lys	Val	Thr	Thr	Glu	Arg	Glu	
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Thr	Pro	Phe	Gln	Lys	Ile	Leu	Arg	Asp	Lys	Asp	Val	Glu	Asp	Glu	Gln	
				210		215					220					
gag	cat	tat	aca	agt	gat	gat	ttg	gac	att	gaa	act	aaa	atg	gaa	gaa	930
Glu	His	Tyr	Thr	Ser	Asp	Asp	Leu	Asp	Ile	Glu	Thr	Lys	Met	Glu	Glu	
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cag	gaa	aaa	aac	cct	gca	tct	tct	gaa	ctt	gaa	gaa	cca	agt	tta	gtt	978
Gln	Glu	Lys	Asn	Pro	Ala	Ser	Ser	Glu	Leu	Glu	Glu	Pro	Ser	Leu	Val	
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tgt	gag	gaa	gat	gaa	att	atg	agg	tct	aaa	gaa	agt	cca	gat	ctt	tct	1026
Cys	Glu	Glu	Asp	Glu	Ile	Met	Arg	Ser	Lys	Glu	Ser	Pro	Asp	Leu	Ser	
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Ile	Ser	His	Ser	Gln	Val	Glu	Gln	Leu	Val	Asn	Lys	Thr	Ser	Glu	Leu	
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Asp	Met	Ser	Glu	Ser	Lys	Thr	Arg	Ser	Gly	Lys	Val	Phe	Gln	Asn	Lys	
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Met	Ala	Asn	Gly	Asn	Gln	Pro	Val	Lys	Ser	Ser	Lys	Glu	Asn	Arg	Lys	
305					310					315				320		
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Arg	Ser	Gln	His	Glu	Ser	Gly	Arg	Ile	Val	Leu	His	His	Phe	Asp	Ser	
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Ser	Ser	Gln	Glu	Ser	Val	Pro	Lys	Arg	Arg	Lys	Phe	Ser	Glu	Pro	Lys	
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Glu	His	Ile														
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Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly Ala Glu Asn Leu His
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gtg aaa ata agt tgc tct ctg gac tgg ttg atg gtc tca gtt atc cca 152
Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met Val Ser Val Ile Pro
5      10      15      20
ggt gca gaa agc aga aat ctg tat ata ttt gcg gat gaa tta cat ctg 200
Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala Asp Glu Leu His Leu
      25      30      35
gga atg ggc tgc cct gca aat cgg ata cat aca tat gta tat gag ttt 248
Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr Tyr Val Tyr Glu Phe
      40      45      50
ata tat ctt gtt cgt gat tgt ggc atc agg aca agg gta gtt tct gag 296
Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr Arg Val Val Ser Glu
      55      60      65
gaa act ctc ctt ttt caa acc gag ctg tac ttt acc cca agg aat ata 344
Glu Thr Leu Leu Phe Gln Thr Glu Leu Tyr Phe Thr Pro Arg Asn Ile
      70      75      80
gat cat gac cct cag gaa atc cat ttg gag tgt tcc acc tct agg aaa 392
Asp His Asp Pro Gln Glu Ile His Leu Glu Cys Ser Thr Ser Arg Lys
85      90      95      100
tca gtg tgg ctt aca cca gtt tct act gag aat gaa ata aaa ttg gat 440
Ser Val Trp Leu Thr Pro Val Ser Thr Glu Asn Glu Ile Lys Leu Asp
      105      110      115
cct agt cct ttt att gct gac ttt cag aca aca gca gaa gag tta gga 488
Pro Ser Pro Phe Ile Ala Asp Phe Gln Thr Thr Ala Glu Glu Leu Gly
      120      125      130
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Leu Leu Ser Ser Ser Pro Asn Leu Leu

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ggggcaagcc tgcaagcacg catcactggg gatctgacat gacaatggcc gcctgcccc	180
tctgagggtt acaggactta cccagtgagg aagcagctaa gcagggtctga ccagccgacc	240
tggacctggc caagggctct gtcacccctc atg gcc acc ccg cca ttc cgg ctg	294
	Met Ala Thr Pro Pro Phe Arg Leu
	-30 -25
ata agg aag atg ttt tcc ttc aag gtg agc aga tgg atg ggg ctt gcc	342
Ile Arg Lys Met Phe Ser Phe Lys Val Ser Arg Trp Met Gly Leu Ala	
	-20 -15 -10
tgc ttc cgg tcc ctg gcg gca tcc tct ccc agt att cgc cag aag aaa	390
Cys Phe Arg Ser Leu Ala Ala Ser Ser Pro Ser Ile Arg Gln Lys Lys	
	-5 1 5
cta atg cac aag ctg cag gag gaa aag gct ttt cgc gaa gag atg aaa	438
Leu Met His Lys Leu Gln Glu Glu Lys Ala Phe Arg Glu Glu Met Lys	
	10 15 20
att ttt cgt gaa aaa ata gag gac ttc agg gaa gag atg tgg act ttc	486
Ile Phe Arg Glu Lys Ile Glu Asp Phe Arg Glu Glu Met Trp Thr Phe	
	25 30 35 40
cga ggc aag atc cat gct ttc cgg ggc cag atc ctg ggt ttt tgg gaa	534
Arg Gly Lys Ile His Ala Phe Arg Gly Gln Ile Leu Gly Phe Trp Glu	
	45 50 55
gag gag aga cct ttc tgg gaa gag gag aaa acc ttc tgg aaa gag gaa	582
Glu Glu Arg Pro Phe Trp Glu Glu Lys Thr Phe Trp Lys Glu Glu	
	60 65 70
aaa tcc ttc tgg gaa atg gaa aag tct ttc agg gag gaa gag aaa act	630
Lys Ser Phe Trp Glu Met Glu Lys Ser Phe Arg Glu Glu Glu Lys Thr	
	75 80 85
ttc tgg aaa aag tac cgc act ttc tgg aag gag gat aag gcc ttc tgg	678
Phe Trp Lys Lys Tyr Arg Thr Phe Trp Lys Glu Asp Lys Ala Phe Trp	
	90 95 100

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aaa gag gac aat gcc tta tgg gaa aga gac cgg aac ctt ctt cag gag      726
Lys Glu Asp Asn Ala Leu Trp Glu Arg Asp Arg Asn Leu Leu Gln Glu
105                      110                      115                      120
gac aag gcc ctg tgg gag gaa gaa aag gcc ctg tgg gta gag gaa aga      774
Asp Lys Ala Leu Trp Glu Glu Glu Lys Ala Leu Trp Val Glu Glu Arg
                      125                      130                      135
gcc ctc ctt gag ggg gag aaa gcc ctg tgg gaa gat aaa acg tcc ctc      822
Ala Leu Leu Glu Gly Glu Lys Ala Leu Trp Glu Asp Lys Thr Ser Leu
                      140                      145                      150
tgg gag gaa gag aat gcc ctc tgg gag gaa gag agg gcc ttc tgg atg      870
Trp Glu Glu Glu Asn Ala Leu Trp Glu Glu Glu Arg Ala Phe Trp Met
                      155                      160                      165
gag aac aat ggc cac att gcc gga gag cag atg ctc gaa gat ggg ccc      918
Glu Asn Asn Gly His Ile Ala Gly Glu Gln Met Leu Glu Asp Gly Pro
                      170                      175                      180
cac aac gcc aac aga ggg cag cgc ttg ctg gcc ttc tcc cga ggc agg      966
His Asn Ala Asn Arg Gly Gln Arg Leu Leu Ala Phe Ser Arg Gly Arg
185                      190                      195                      200
gcg tagccagcat gcaggtgcan gggccctgtg gtccagactc ccctggggtg      1019
Ala
ggattcaagt ccaggggtgag cccatgtgct ggagaaaata cacactcatt ggtctccttg      1079
ctttgaaaga tccaataaag tcttgaggca aggtttggaa aaccaaaaaa aaaaaaaa      1138

<210> 21
<211> 468
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 76..276

<220>
<221> sig_peptide
<222> 76..135
<223> Von Heijne matrix
      score 5.21332530399231
      seq SPVFLVFPPEITA/SE

<400> 21
agcacaagaa aagaacatgg tctagactga agtaccaact aaatcatctc ctttcaaatt      60
atcaccgaca ccatac atg gat tca agc acc gca cac agt ccg gtg ttt ctg      111
                      Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu
                      -20                      -15                      -10
gta ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt      159
Val Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu
                      -5                      1                      5
tca gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct      207
Ser Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala
10                      15                      20
aga aaa atg aaa atc tta ggg gat atc cat tct ggg gct ctg ttt tgt      255
Arg Lys Met Lys Ile Leu Gly Asp Ile His Ser Gly Ala Leu Phe Cys
25                      30                      35                      40
tca tta att ctg gag cct tcc taattgcagt gaaaagaaaa accacagaaa      306
Ser Leu Ile Leu Glu Pro Ser
                      45
ctctgggaat tttgattaca ttgatgactt tcagcattat tgaattattc atttctctgc      366
ctttctcaat tttggggtgc cactcagagg attgtgattg tgaacaatgt tgttgactag      426

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cactgtgaga ataaagatgt gttaaaataa aaaaaaaaaa aa 468

<210> 22
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 6..287

<220>
<221> sig_peptide
<222> 6..80
<223> Von Heijne matrix
score 4.17710408129886
seq ISLSHLFLDLSRS/LW

<400> 22
atttg atg tgc ttc tta gtc tcg ttt aac ttg ccg att cat ata tcc ctg 50
Met Cys Phe Leu Val Ser Phe Asn Leu Pro Ile His Ile Ser Leu
-25 -20 -15
tct cat ttg ttc tta gat ttg tca cga agc ctc tgg ttt ttg gct tgt 98
Ser His Leu Phe Leu Asp Leu Ser Arg Ser Leu Trp Phe Leu Ala Cys
-10 -5 1 5
cct ggt ttg aac ttg gtg tat ctg gct ctt gac tca ttt tct gac ctc 146
Pro Gly Leu Asn Leu Val Tyr Leu Ala Leu Asp Ser Phe Ser Asp Leu
10 15 20
aga cca tcc tta aat ctg ctt ttc tac ttt gta cca ggc ttt ggc gtc 194
Arg Pro Ser Leu Asn Leu Leu Phe Tyr Phe Val Pro Gly Phe Gly Val
25 30 35
tcc aag tac ctg acc tca gct caa cct gtc ttg ggt ttt ctt ctc ctc 242
Ser Lys Tyr Leu Thr Ser Ala Gln Pro Val Leu Gly Phe Leu Leu Leu
40 45 50
cct gac att gac aac cca gcc ctc cta ggc aca gag aga tgg agc 287
Pro Asp Ile Asp Asn Pro Ala Leu Leu Gly Thr Glu Arg Trp Ser
55 60 65
tgagtgtggt tttcctgaaa taaagcttgc attatgagag ggaataaaca gaagaaaaaa 347
atagtaagta aaatcttgct tgccctctcag taaaataaag ctctattttt cgtttttttt 407
ttttccaact tcctgtacaa aaaagggaaa acttttagctt ttgggggaaa tttggagcta 467
gcctgttggt actgttgagc ttagtgtatc tataactata tattattcca caatatctta 527
aatactttat aaagatattt tcataaatta cagcaatcct ggcttttagat gattgatggc 587
cattttttaa caattaaagc taatttctag ctttttatga gtttggtatt aagcacagta 647
gtttcttaga aagtctccag ggaatgcatt ttgcaaaata aaaatcagct aatgacccaa 707
aaaaaaaaaa aaa 720

<210> 23
<211> 727
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 171..692

<220>
<221> sig_peptide
<222> 171..227

<223> Von Heijne matrix
 score 4.17573075349936
 seq LLLGQRCSLKVSG/QE

<400> 23
 attgtgacat caccgtgcac tagccaatgg ctgcctgcct aagctgggtc cctgggtctcc 60
 tgggactact agccctttgt tgatagggag aagccaacat ctcccgcagg accccctaata 120
 cttcagggca gctcccagag catggatccc tcttgattcc actcagcccg atg ttc 176
 Met Phe
 ctc aca gtc aag ctg ctc ctg ggc cag aga tgc agt ctg aag gtg tca 224
 Leu Thr Val Lys Leu Leu Leu Gly Gln Arg Cys Ser Leu Lys Val Ser
 -15 -10 -5
 ggg caa gag agt gta gcc acg ctg aag aga ctg gtg tcc agg cgg ctg 272
 Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg Arg Leu
 1 5 10 15
 aag gtg cct gag gag cag cag cac ctg ctt ttc cgt ggc cag ctc ctg 320
 Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln Leu Leu
 20 25 30
 gag gat gac aag cac ctc tct gac tac tgc att ggg ccc aat gcc tct 368
 Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn Ala Ser
 35 40 45
 atc aat gtc atc atg cag ccc ttg gag aag atg gcg cta aag gag gcc 416
 Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys Glu Ala
 50 55 60
 cac cag ccg cag acc cag ccc ctg tgg cac cag ctg gga ctg gtc cta 464
 His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu Val Leu
 65 70 75
 gct aaa cac ttt gaa cca cag gat gcc aag gcc gtg ctg cag ctg cta 512
 Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln Leu Leu
 80 85 90 95
 agg cag gag cac gag gag cgc ctg cag aag ata agc ctg gag cac ctg 560
 Arg Gln Glu His Glu Glu Arg Leu Gln Lys Ile Ser Leu Glu His Leu
 100 105 110
 gag cag ctg gcc cag tac ctc ctg gca gag gag cct cac gtg gag cca 608
 Glu Gln Leu Ala Gln Tyr Leu Leu Ala Glu Glu Pro His Val Glu Pro
 115 120 125
 gct gga gag agg gag ctt gag gcg aag gca cgg cct cag agc tcc tgt 656
 Ala Gly Glu Arg Glu Leu Glu Ala Lys Ala Arg Pro Gln Ser Ser Cys
 130 135 140
 gac atg gag gag aag gag gag gca gca gct gat cag taaacggggcc 702
 Asp Met Glu Glu Lys Glu Glu Ala Ala Ala Asp Gln
 145 150 155
 atcctaccg aaaaaaaaaa aaaaa 727

<210> 24
 <211> 470
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 137..454

<220>
 <221> sig_peptide
 <222> 137..187
 <223> Von Heijne matrix
 score 10.7019149919754

seq VLMLLAVLIWTGA/EN

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<400> 24
atcctgtgaa ctacccaaaa ggaggaaaac gaacgcagct gagcatggga tgccatataa    60
aaatcactta aaccagtcgc cactccttgt ttcctgagtt gtcctgtgct ggaggtctgc    120
tcagacgaag gtctcc atg gcg tta gaa gtc ttg atg ctc ctc gct gtc ttg    172
               Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu
               -15                               -10
att tgg acc ggt gct gag aac ctc cat gtg aaa ata agt tgc tct ctg    220
Ile Trp Thr Gly Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu
-5                               1                               5                               10
gac tgg ttg atg gtc tca gtt atc cca gtt gca gaa agc aga aat ctg    268
Asp Trp Leu Met Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu
               15                               20                               25
tat ata ttt gcg gat gaa tta cat ctg gga atg ggc tgc cct gca aat    316
Tyr Ile Phe Ala Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn
               30                               35                               40
cgg ata cat aca tat gta tat gag ttt ata tat ctt gtt cgt gat tgt    364
Arg Ile His Thr Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys
               45                               50                               55
ggc atc agg aca agg gta aga aca gtg att gtc tgt aaa aaa tac tgc    412
Gly Ile Arg Thr Arg Val Arg Thr Val Ile Val Cys Lys Lys Tyr Cys
60                               65                               70                               75
atg ttt tgt cag act ttt atg cct agt att aaa att gtc ttt    454
Met Phe Cys Gln Thr Phe Met Pro Ser Ile Lys Ile Val Phe
               80                               85
taaaaaaaaa aaaaaa    470

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<210> 25
<211> 987
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 238..609

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<220>
<221> sig_peptide
<222> 238..291
<223> Von Heijne matrix
      score 10.0374888212272
      seq LLLLVMA LPPGTT/GV

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<400> 25
attccattca cagactcttg ttgggcagca gccacccgct cacctccatc cccaggactt    60
agagggacgc agggcggttg gaacagagga cactccaggc gctgaccctg ggaggccagg    120
accagggcca aagtcccggt ggcaagagga gtcctcagag gtccttcatt cagcggttcc    180
gggaggtctg ggaagcccac ggctggctg gggcagggtc aacgccgcca ggccgcc    237
atg gtc ctg tgc tgg ctg ctg ctt ctg gtg atg gct ctg ccc cca ggc    285
Met Val Leu Cys Trp Leu Leu Leu Leu Val Met Ala Leu Pro Pro Gly
               -15                               -10                               -5
acg acg ggc gtc aag gac tgc gtc ttc tgt gag ctc acc gac tcc atg    333
Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met
               1                               5                               10
cag tgt cct ggt acc tac atg cac tgt ggc gat gag gag gac tgc ttc    381
Gln Cys Pro Gly Thr Tyr Met His Cys Gly Asp Asp Glu Asp Cys Phe
15                               20                               25                               30

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aca ggc cac ggg gtc gcc ccg ggc act ggt ccg gtc atc aac aaa ggc      429
Thr Gly His Gly Val Ala Pro Gly Thr Gly Pro Val Ile Asn Lys Gly
          35          40          45
tgc ctg cga gcc acc agc tgc ggc ctt gag gaa ccc gtc agc tac agg      477
Cys Leu Arg Ala Thr Ser Cys Gly Leu Glu Glu Pro Val Ser Tyr Arg
          50          55          60
ggc gtc acc tac agc ctc acc acc aac tgc tgc acc ggc cgc ctg tgt      525
Gly Val Thr Tyr Ser Leu Thr Thr Asn Cys Cys Thr Gly Arg Leu Cys
          65          70          75
aac aga gcc ccg agc agc cag aca gtg ggg gcc acc acc agc ctg gca      573
Asn Arg Ala Pro Ser Ser Gln Thr Val Gly Ala Thr Thr Ser Leu Ala
          80          85          90
ctg ggg ctg ggt atg ctg ctt cct cca cgt ttg ctg tgaccaacag      619
Leu Gly Leu Gly Met Leu Leu Pro Pro Arg Leu Leu
          95          100          105
ggaggacagg gcctgggact gttctcccag atccgccact ccccatgtcc ccatgtcctt      679
ccccactaa atggccagag aggcctctga caacctcttg cggccctggc ttcacccctt      739
ctaaggctgt ccaccaggag cccggtgcta ggggaagcat cccagggcct gactgagcgg      799
caggggagca cggcccgtgg gtttgattgt attactctgt tccactgggt ctaagacgca      859
gagcttctca catctcaatc aggatgcttc tctccattgg tagcacttta gagtccatga      919
aatatggtaa aaaatatata tatatcataa taaatgacag ctgatgttca tggaaaaaaa      979
aaaaaaa      987

<210> 26
<211> 908
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..862

<220>
<221> sig_peptide
<222> 80..127
<223> Von Heijne matrix
      score 3.66725851505537
      seq FSLLSISGPPISS/SA

<400> 26
gaatgtttat cctctggaca aaccagccag cctctccaga gcaggcgtgt gatctctgta      60
ccccgcagtg ggtcagaat atg gag aac ttc tca ctc ctc agc atc tct gga      112
          Met Glu Asn Phe Ser Leu Leu Ser Ile Ser Gly
          -15          -10
cct cca atc tct tcc tcc gcc ctg agt gct ttt ccc gac att atg ttc      160
Pro Pro Ile Ser Ser Ser Ala Leu Ser Ala Phe Pro Asp Ile Met Phe
-5          1          5          10
tct cgt gcc acc agc ctg cca gac att gca aag aca gca gta ccc act      208
Ser Arg Ala Thr Ser Leu Pro Asp Ile Ala Lys Thr Ala Val Pro Thr
          15          20          25
gag gca tcc agc cca gct cag gcc ctg cca ccc cag tac caa agc atc      256
Glu Ala Ser Ser Pro Ala Gln Ala Leu Pro Pro Gln Tyr Gln Ser Ile
          30          35          40
att gtc agg caa ggg ata cag aac aca gtg ctc tca cca gac tgc agc      304
Ile Val Arg Gln Gly Ile Gln Asn Thr Val Leu Ser Pro Asp Cys Ser
          45          50          55
ttg ggg gac acc cag cac gga gag aag ctg agg cgg aac tgc act atc      352
Leu Gly Asp Thr Gln His Gly Glu Lys Leu Arg Arg Asn Cys Thr Ile

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Cys Cys Leu Cys Ala Leu Leu Ser Asn Phe Cys Pro Ser Thr Thr Val
-15          -10          -5          1
aaa gga gac gtc gtg act tcc ttc ttt cgt gct gac tat gac tta gcc      208
Lys Gly Asp Val Val Thr Ser Phe Phe Arg Ala Asp Tyr Asp Leu Ala
5          10          15
agt agg tct gca gat cag tcc tcc cag aaa gtg aag ttg cgc atg ttc      256
Ser Arg Ser Ala Asp Gln Ser Ser Gln Lys Val Lys Leu Arg Met Phe
20          25          30
act ggg cgt ctt ccc atc ggc ccc ttc gcc agt gtg ggg aac gcg gcg      304
Thr Gly Arg Leu Pro Ile Gly Pro Phe Ala Ser Val Gly Asn Ala Ala
35          40          45
gag ctg tgagccggcg actcgggtcc ctgaggtctg gattctttct ccgctactga      360
Glu Leu
50
gacacggcgg acacacacaa acacagaacc acacagccag tcccaggagc ccagtaatgg      420
agagcccca aaagaagaac cagcagctga aagtcgggat cctacacctg ggcagcagac      480
agaagaagat caggatacag ctgagatccc agtgcgcgac atggaagggtg atctgcaaga      540
gctgcatcag tcaaacaccg gggataaatc tggatttggg ttcgggcgtc aagggtgaaga      600
taatacctaa agaggaacac tgtaaaatgc cagaagcagg tgaagagcaa ccacaagttt      660
aaatgaagac aagctgaaac aacgcaagct ggttttatat tagatatttg acttaaaacta      720
tctcaataaa gttttgcagc tttcaccaaa aaaaaaaaaa aa      762

<210> 28
<211> 1102
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 310..906

<220>
<221> sig_peptide
<222> 310..357
<223> Von Heijne matrix
      score 11.0931109030915
      seq FPLLLLSLGLVLA/EA

<400> 28
atacagtgac ctagagcagg catgggtggg tcacaggctt tggagagcac tctctgtcct      60
gatcttttca gttgagagac ttcagctgtt cattgctcat ttggacttag ttcaagggtca      120
tgtcaaagaa gaagggtgcac ttacgctagt tgtagctct gtcttttgta accatcaagt      180
tccatgcatg tgatcagatt taggaggggg cggtggggga taatcaattt tgggtgtcac      240
caggtaaaca gagccctcag catctgaata gaaactgaac aggaacagaa gagattcact      300
acatctgag atg gag acc ttt cct ctg ctg ctg ctc agc ctg ggc ctg gtt      351
      Met Glu Thr Phe Pro Leu Leu Leu Leu Ser Leu Gly Leu Val
          -15          -10          -5
ctt gca gaa gca tca gaa agc aca atg aag ata att aaa gaa gaa ttt      399
Leu Ala Glu Ala Ser Glu Ser Thr Met Lys Ile Ile Lys Glu Glu Phe
1          5          10
aca gac gaa gag atg caa tat gac atg gca aaa agt ggc caa gaa aaa      447
Thr Asp Glu Glu Met Gln Tyr Asp Met Ala Lys Ser Gly Gln Glu Lys
15          20          25          30
cag acc att gag ata tta atg aac ccg atc ctg tta gtt aaa aat acc      495
Gln Thr Ile Glu Ile Leu Met Asn Pro Ile Leu Leu Val Lys Asn Thr
35          40          45
agc ctc agc atg tcc aag gat gat atg tct tcc aca tta ctg aca ttc      543
Ser Leu Ser Met Ser Lys Asp Asp Met Ser Ser Thr Leu Leu Thr Phe

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	50		55		60	
aga agt tta cat tat aat gac ccc aag gga aac agt tcg ggt aat gac						591
Arg Ser Leu His Tyr Asn Asp Pro Lys Gly Asn Ser Ser Gly Asn Asp						
65	70	75				
aaa gag tgt tgc aat gac atg aca gtc tgg aga aaa gtt tca gaa gca						639
Lys Glu Cys Cys Asn Asp Met Thr Val Trp Arg Lys Val Ser Glu Ala						
80	85	90				
aac gga tcg tgc aag tgg agc aat aac ttc atc cgc agc tcc aca gaa						687
Asn Gly Ser Cys Lys Trp Ser Asn Asn Phe Ile Arg Ser Ser Thr Glu						
95	100	105			110	
gtg atg cgc agg gtc cac agg gcc ccc agc tgc aag ttt gta cag aat						735
Val Met Arg Arg Val His Arg Ala Pro Ser Cys Lys Phe Val Gln Asn						
115	120	125				
cct ggc ata agc tgc tgt gag agc cta gaa ctg gaa aat aca gtg tgc						783
Pro Gly Ile Ser Cys Cys Glu Ser Leu Glu Leu Glu Asn Thr Val Cys						
130	135	140				
cag ttc act aca ggc aaa caa ttc ccc agg tgc caa tac cat agt gtt						831
Gln Phe Thr Thr Gly Lys Gln Phe Pro Arg Cys Gln Tyr His Ser Val						
145	150	155				
acc tca tta gag aag ata ttg aca gtg ctg aca ggt cat tct ctg atg						879
Thr Ser Leu Glu Lys Ile Leu Thr Val Leu Thr Gly His Ser Leu Met						
160	165	170				
agc tgg tta gtt tgt ggc tct aag ttg taaatccac agagctttag						926
Ser Trp Leu Val Cys Gly Ser Lys Leu						
175	180					
gactaggggtc ttactaaaga aggacctctt cttgttcatt cttgtttaaa cctttcctta						986
atatctactc ttttagcacta tagtgaactc ctgattattt attctaactg gaggagtga						1046
aaatccaaaa ttgtggataa ttcaattaaa agttatgact gaaaaaaaaa aaaaaa						1102

<210> 29

<211> 436

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 24..287

<220>

<221> sig_peptide

<222> 24..131

<223> Von Heijne matrix

score 3.79790641648006

seq ILMRDFSPSGIFG/AF

<400> 29

acagcggaca ccaggactcc aaa atg gcg tca gtt gta cca gtg aag gac aag	53
Met Ala Ser Val Val Pro Val Lys Asp Lys	

-35

-30

aaa ctt ctg gag gtc aaa ctg ggg gag ctg cca agc tgg atc ttg atg	101
Lys Leu Leu Glu Val Lys Leu Gly Glu Leu Pro Ser Trp Ile Leu Met	

-25

-20

-15

cgg gac ttc agt cct agt ggc att ttc gga gcg ttt caa aga ggt tac	149
Arg Asp Phe Ser Pro Ser Gly Ile Phe Gly Ala Phe Gln Arg Gly Tyr	

-10

-5

1

5

tac cgg tac tac aac aag tac atc aat gtg aag aag ggg agc atc tcg	197
Tyr Arg Tyr Tyr Asn Lys Tyr Ile Asn Val Lys Lys Gly Ser Ile Ser	

10

15

20

```

ggg att acc atg gtg ctg gca tgc tac gtg ctc ttt agc tac tcc ttt      245
Gly Ile Thr Met Val Leu Ala Cys Tyr Val Leu Phe Ser Tyr Ser Phe
      25              30              35
tcc tac aag cat ctc aag cac gag cgg ctc cgc aaa tac cac      287
Ser Tyr Lys His Leu Lys His Glu Arg Leu Arg Lys Tyr His
      40              45              50
tgaagaggac acactctgca cccccccacc ccacgacctt ggccccgagcc cctccgtgag      347
gaacacaatc tcaatcggtg ctgaatcctt tcatatccta ataggaatta acctccaaat      407
aaaacatgac tggtaaaaaa aaaaaaaaaa      436

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<210> 30
<211> 1938
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 132..1574

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<220>
<221> sig_peptide
<222> 132..206
<223> Von Heijne matrix
      score 11.1130239236827
      seq LALLLTSTPEALG/AN

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<400> 30
ctcccccttcc cgctcccagg aaccccatcca gcctcaggaa ctgccccccag ccatcgagcc      60
ttggctacttt aagggaacctg ggcccaatcc acagctggga cagtcctggc ccaactgcact      120
gggaatctag g atg ggg gcc ttg gcc aga gcc ctg ccg tcc ata ctg ctg      170
      Met Gly Ala Leu Ala Arg Ala Leu Pro Ser Ile Leu Leu
      -25              -20              -15
gca ttg ctg ctt acg tcc acc cca gag gct ctg ggt gcc aac ccc ggc      218
Ala Leu Leu Leu Thr Ser Thr Pro Glu Ala Leu Gly Ala Asn Pro Gly
      -10              -5              1
ttg gtc gcc agg atc acc gac aag gga ctg cag tat gcg gcc cag gag      266
Leu Val Ala Arg Ile Thr Asp Lys Gly Leu Gln Tyr Ala Ala Gln Glu
      5              10              15              20
ggg cta ttg gct ctg cag agt gag ctg ctc agg atc acg ctg cct gac      314
Gly Leu Leu Ala Leu Gln Ser Glu Leu Leu Arg Ile Thr Leu Pro Asp
      25              30              35
ttc acc ggg gac ttg agg atc ccc cac gtc ggc cgt ggg cgc tat gag      362
Phe Thr Gly Asp Leu Arg Ile Pro His Val Gly Arg Gly Arg Tyr Glu
      40              45              50
ttc cac agc ctg aac atc cac agc tgt gag ctg ctt cac tct gcg ctg      410
Phe His Ser Leu Asn Ile His Ser Cys Glu Leu Leu His Ser Ala Leu
      55              60              65
agg cct gtc cct ggc cag ggc ctg agt ctc agc atc tcc gac tcc tcc      458
Arg Pro Val Pro Gly Gln Gly Leu Ser Leu Ser Ile Ser Asp Ser Ser
      70              75              80
atc cgg gtc cag ggc agg tgg aag gtg cgc aag tca ttc ttc aaa cta      506
Ile Arg Val Gln Gly Arg Trp Lys Val Arg Lys Ser Phe Phe Lys Leu
      85              90              95              100
cag ggc tcc ttt gat gtc agt gtc aag ggc atc agc att tcg gtc aac      554
Gln Gly Ser Phe Asp Val Ser Val Lys Gly Ile Ser Ile Ser Val Asn
      105              110              115
ctc ctg ttg ggc agc gat tcc tcc ggg agg ccc aca gtt act gcc tcc      602
Leu Leu Leu Gly Ser Asp Ser Ser Gly Arg Pro Thr Val Thr Ala Ser

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Arg	Gln	Thr	Arg	His	Gly	His	Ile	Ala	Leu	Ser	Arg	Thr	Ala	
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cagtatttgg	tgaagatgat	cagtctcagg	atgttctgag	attgcatcag	gatattaatg									665
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gaaaccccat	ctctagaaaa	aacaccaaaa	aattggacaa	gagtgttggc	acatgcctgt									965
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					Met									
					1									
gcc aaa tat	caa ggt	gaa gtt	caa agt	ttg aaa	ctg gat	gat gat	tca							167
Ala Lys Tyr	Gln Gly	Glu Val	Gln Ser	Leu Lys	Leu Asp	Asp Asp	Ser							
	5		10		15									
ggt ata gaa	gga gta	agc gac	caa gta	ctt gtg	gca gtt	gtg gtc	agt							215
Val Ile Glu	Gly Val	Ser Asp	Gln Val	Leu Val	Ala Val	Val Val	Ser							
	20		25		30									
ttc gct ttg	att gct	acc ctg	gta tat	gca ctt	ttc aga	aat gta	cat							263
Phe Ala Leu	Ile Ala	Thr Leu	Val Tyr	Ala Leu	Phe Arg	Asn Val	His							
	35		40		45									
caa aac att	cac cca	gaa aac	cag gag	cta gta	agg gta	ctt cga	gaa							311
Gln Asn Ile	His Pro	Glu Asn	Gln Glu	Leu Val	Arg Val	Leu Arg	Glu							
	50		55		60		65							
cag ctt caa	aca gaa	cag gat	gca cct	gct gac	tcg aca	gca gtt	cta							359
Gln Leu Gln	Thr Glu	Gln Asp	Ala Pro	Ala Asp	Ser Thr	Ala Val	Leu							
	70		75		80									
cac tgacatgtac	tgtcccatct	gcctgcacca	agcctccttc	ccggtggaga										412
His														
ccaactgtgg	acatcttttt	tgtggtgcct	gcattattgc	ttactggcga	tatggttcat									472
ggcttggggc	aatcagttgt	ccaatctgta	gacaaacgag	acatggccac	attgcattgt									532
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cacatgcctg	tagtccctgc	ttcttgggag	gctgaaatgg	gaggatcacc	tgagcccagg									1012
aggttgaggc	tatagtgagc	catgatcgca	ctattgcact	cccacctggg	tggcagttag									1072
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 acgtctcttc ggagagcgcg cac atg gcg act cag gcg cac tcc ctc agc tac 173
 Met Ala Thr Gln Ala His Ser Leu Ser Tyr
 -25 -20
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 Ala Gly Cys Asn Phe Leu Cys Gln Arg Leu Val Leu Ser Thr Leu Ser
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 Gly Arg Pro Val Lys Ile Arg Lys Ile Arg Ala Arg Asp Asp Asn Pro
 1 5 10 15
 ggc ctc cga gat ttt gaa gcc agc ttc ata agg cta ttg gac aaa ata 317
 Gly Leu Arg Asp Phe Glu Ala Ser Phe Ile Arg Leu Leu Asp Lys Ile
 20 30
 acg aat ggt tct cga att gaa ata aac caa aca gga aca acc tta tat 365
 Thr Asn Gly Ser Arg Ile Glu Ile Asn Gln Thr Gly Thr Thr Leu Tyr
 35 40 45
 tat cag cct ggc ctc ctg tat ggt gga tct gtg gaa cat gac tgt agc 413
 Tyr Gln Pro Gly Leu Leu Tyr Gly Gly Ser Val Glu His Asp Cys Ser
 50 55 60
 gtc ctt cgt ggc att ggg tat tac ctg gag agt ctt ctt tgc ttg gct 461
 Val Leu Arg Gly Ile Gly Tyr Leu Glu Ser Leu Leu Cys Leu Ala
 65 70 75
 cca ttt atg aag cac ccg tta aaa ata gtt cta cga gga gtg acc aat 509
 Pro Phe Met Lys His Pro Leu Lys Ile Val Leu Arg Gly Val Thr Asn
 80 85 90 95
 gat cag att gac cct tca gtt gat gtt ctt aag gca aca gca ctc cct 557
 Asp Gln Ile Asp Pro Ser Val Asp Val Leu Lys Ala Thr Ala Leu Pro
 100 105 110
 ttg ttg aaa caa ttt ggg att gat ggt gaa tca ttt gaa ctg aag att 605
 Leu Leu Lys Gln Phe Gly Ile Asp Gly Glu Ser Phe Glu Leu Lys Ile
 115 120 125
 gtg cga cgg gga atg cct ccc gga gga gga ggc gaa gtg gtt ttc tca 653
 Val Arg Arg Gly Met Pro Pro Gly Gly Gly Gly Glu Val Val Phe Ser
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 Cys Pro Val Arg Lys Val Leu Lys Pro Ile Gln Leu Thr Asp Pro Gly
 145 150 155
 aaa atc aaa cgt att aga gga atg gcg tac tct gta cgt gtg tca cct 749
 Lys Ile Lys Arg Ile Arg Gly Met Ala Tyr Ser Val Arg Val Ser Pro
 160 165 170 175
 cag atg gcg aac cgg att gtg gat tct gca agg agc atc ctc aac aag 797

Gln Met Ala Asn Arg Ile Val Asp Ser Ala Arg Ser Ile Leu Asn Lys	
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Phe Ile Pro Asp Ile Tyr Ile Tyr Thr Asp His Ile Lys Gly Val Asn	
195 200 205	
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Ser Gly Lys Ser Pro Gly Phe Gly Leu Ser Leu Val Ala Glu Thr Thr	
210 215 220	
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Ser Gly Thr Phe Leu Ser Ala Glu Leu Ala Ser Asn Pro Gln Gly Gln	
225 230 235	
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Gly Ala Ala Val Leu Pro Glu Asp Leu Gly Arg Asn Cys Ala Arg Leu	
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Leu Leu Glu Glu Ile Tyr Arg Gly Gly Cys Val Asp Ser Thr Asn Gln	
260 265 270	
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Ser Leu Ala Leu Leu Leu Met Thr Leu Gly Gln Gln Asp Val Ser Lys	
275 280 285	
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Val Leu Leu Gly Pro Leu Ser Pro Tyr Thr Ile Glu Phe Leu Arg His	
290 295 300	
ttg aag agc ttt ttc cag att atg ttt aaa att gaa acc aag cca tgt	1181
Leu Lys Ser Phe Phe Gln Ile Met Phe Lys Ile Glu Thr Lys Pro Cys	
305 310 315	
ggt gaa gaa ctc aag ggt ggg gat aaa gtg ctg atg acc tgt gtt ggc	1229
Gly Glu Glu Leu Lys Gly Gly Asp Lys Val Leu Met Thr Cys Val Gly	
320 325 330 335	
att ggt ttc tcc aac ctt agc agg acc ctc aag tgataaccat cacaagataa	1282
Ile Gly Phe Ser Asn Leu Ser Arg Thr Leu Lys	
340 345	
ggccccagtg cctacagaca aagcagaagc tgccacggac accaatggga ccaagtccaa	1342
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<222> 35..109

<223> Von Heijne matrix

score 5.38058532480537

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ctg agg acc cgg aca gcc gtt aca tcc ttg cta agc ccc act ccg gct      103
Leu Arg Thr Arg Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala
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aca gct ctt gct gtc aga tac gca tcc aag aag tcg ggt ggt agc tcc      151
Thr Ala Leu Ala Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser
               1                               5                               10
aaa aac ctc ggt gga aag tca tca ggc aga cgc caa ggc att aag aaa      199
Lys Asn Leu Gly Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys
               15                               20                               25                               30
atg gaa ggt cac tat gtt cat gct ggg aac atc att gca aca cag cgc      247
Met Glu Gly His Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg
               35                               40                               45
cat ttc cgc tgg cac cca ggt gcc cat gtg agt tgc tcc gtt gct gcc      295
His Phe Arg Trp His Pro Gly Ala His Val Ser Cys Ser Val Ala Ala
               50                               55                               60
ccc ctt ttt cct ttt cta ggt tgacctctcc ttgccctaa gcatggtaat      346
Pro Leu Phe Pro Phe Leu Gly
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aacagttgca tgtattgagt gcttaccaaa tggcaagcat tgtgccaaaa aaaaaaaaaa      406
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<222> 177..236

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score 6.51720597568932

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ctctctgaca aagaaatcca gatgatgcga gacctgatga agacaataca tggaaa atg      179
                                   Met
                                   -20
aca gtc ttg gaa ata act ttg gct gtc atc ctg act cta ctg gga ctt      227
Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly Leu
               -15                               -10                               -5
gcc atc ctg gct att ttg tta aca aga tgg gca cga cgt aag caa agt      275
Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln Ser
               1                               5                               10
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Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu Leu	
15 20 25	
gac tat gag gat ggt aga gga tcc cga cat gca tat tca aca caa agt	371
Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln Ser	
30 35 40 45	
gag aga tcc aaa aga gat tac aca cca tca acc aac tct cta gca ctg	419
Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala Leu	
50 55 60	
tct cga tca agt att gct tta cct caa gga tcc atg agt agt ata aaa	467
Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile Lys	
65 70 75	
tgt tta caa aca act gaa gaa cct cct tcc aga act gca gga gcc atg	515
Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met	
80 85 90	
atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc	563
Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu	
95 100 105	
tct caa aaa acc att gtg caa act cta gga cct att gta caa tat cct	611
Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro	
110 115 120 125	
gga tcc aat ggg agg ata aac ata agc cag ctc acc tca gag gat ctc	659
Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp Leu	
130 135 140	
act ggg gct aaa gga agg gtc aca tct ggt cca cag ttc cct aat agc	707
Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser	
145 150 155	
cac cat gtg cca gag aat cta cat gga tac atg aat tcc ctt tcc ctt	755
His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu	
160 165 170	
ttc tcc cct gct tgactccctc tcccttatgt gtaaacaatt taaaaaatatg	807
Phe Ser Pro Ala	
175	
atagtgtata aatgaaaaaa aaaaaaaaaa	836

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<222> 208..1239

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<223> Von Heijne matrix

score 5.73027134157378

seq GLVLICVCSKTHS/LK

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gctgctgttt gaattatctg tgaatgttg gaagaggaat gccagagctg ccggctgaaa	180
attaccaaac caagagaaat ctgcagg atg gac ttt ctg gtc ctc ttc ttg ttc	234
Met Asp Phe Leu Val Leu Phe Leu Phe	

-25

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Tyr	Leu	Ala	Ser	Val	Leu	Met	Gly	Leu	Val	Leu	Ile	Cys	Val	Cys	Ser	
-20					-15					-10					-5	
aaa	acc	cat	agc	ttg	aaa	ggc	ctg	gcc	agg	gga	gga	gca	cag	ata	ttt	330
Lys	Thr	His	Ser	Leu	Lys	Gly	Leu	Ala	Arg	Gly	Gly	Ala	Gln	Ile	Phe	
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Ser	Cys	Ile	Ile	Pro	Glu	Cys	Leu	Gln	Arg	Ala	Val	His	Gly	Leu	Leu	
		15					20					25				
cat	tac	ctt	ttc	cat	acg	aga	aac	cac	acc	ttc	att	gtc	ctg	cac	ctg	426
His	Tyr	Leu	Phe	His	Thr	Arg	Asn	His	Thr	Phe	Ile	Val	Leu	His	Leu	
	30					35				40						
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Val	Leu	Gln	Gly	Met	Val	Tyr	Thr	Glu	Tyr	Thr	Trp	Glu	Val	Phe	Gly	
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tac	tgt	cag	gag	ctg	gag	ttg	tcc	ttg	cat	tac	ctt	ctt	ctg	ccc	tat	522
Tyr	Cys	Gln	Glu	Leu	Glu	Leu	Ser	Leu	His	Tyr	Leu	Leu	Leu	Pro	Tyr	
			65						70					75		
ctg	ctg	cta	ggc	gta	aac	ctg	ttt	ttt	ttc	acc	ctg	act	tgt	gga	acc	570
Leu	Leu	Leu	Gly	Val	Asn	Leu	Phe	Phe	Phe	Thr	Leu	Thr	Cys	Gly	Thr	
			80					85					90			
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Asn	Pro	Gly	Ile	Ile	Thr	Lys	Ala	Asn	Glu	Leu	Leu	Phe	Leu	His	Val	
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Tyr	Glu	Phe	Asp	Glu	Val	Met	Phe	Pro	Lys	Asn	Val	Arg	Cys	Ser	Thr	
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Cys	Asp	Leu	Arg	Lys	Pro	Ala	Arg	Ser	Lys	His	Cys	Ser	Val	Cys	Asn	
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tgg	tgt	gtg	cac	cgt	ttc	gac	cat	cac	tgt	gtt	tgg	gtg	aac	aac	tgc	762
Trp	Cys	Val	His	Arg	Phe	Asp	His	His	Cys	Val	Trp	Val	Asn	Asn	Cys	
				145					150					155		
atc	ggg	gcc	tgg	aac	atc	agg	tac	ttc	ctc	atc	tac	gtc	ttg	acc	ttg	810
Ile	Gly	Ala	Trp	Asn	Ile	Arg	Tyr	Phe	Leu	Ile	Tyr	Val	Leu	Thr	Leu	
			160					165					170			
acg	gcc	tcg	gct	gcc	acc	gtc	gcc	att	gtg	agc	acc	act	ttt	ctg	gtc	858
Thr	Ala	Ser	Ala	Ala	Thr	Val	Ala	Ile	Val	Ser	Thr	Thr	Phe	Leu	Val	
		175					180					185				
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His	Leu	Val	Val	Met	Ser	Asp	Leu	Tyr	Gln	Glu	Thr	Tyr	Ile	Asp	Asp	
	190				195					200						
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Leu	Gly	His	Leu	His	Val	Met	Asp	Thr	Val	Phe	Leu	Ile	Gln	Tyr	Leu	
205					210					215					220	
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Phe	Leu	Thr	Phe	Pro	Arg	Ile	Val	Phe	Met	Leu	Gly	Phe	Val	Val	Val	
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ctg	agc	ttc	ctc	ctg	ggc	ggc	tac	ctg	ttg	ttt	gtc	ctg	tat	ctg	gcg	1050
Leu	Ser	Phe	Leu	Leu	Gly	Gly	Tyr	Leu	Leu	Phe	Val	Leu	Tyr	Leu	Ala	
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gcc	acc	aac	cag	act	act	aac	gag	tgg	tac	aga	ggc	gac	tgg	gcc	tgg	1098
Ala	Thr	Asn	Gln	Thr	Thr	Asn	Glu	Trp	Tyr	Arg	Gly	Asp	Trp	Ala	Trp	
		255				260						265				
tgc	cag	cgt	tgt	ccc	ctt	gtg	gcc	tgg	cct	ccg	tca	gca	gag	ccc	caa	1146
Cys	Gln	Arg	Cys	Pro	Leu	Val	Ala	Trp	Pro	Pro	Ser	Ala	Glu	Pro	Gln	
	270				275					280						
gtc	cac	cgg	aac	att	cac	tcc	cat	ggg	ctt	cgg	agc	aac	ctt	caa	gag	1194

Val His Arg Asn Ile His Ser His Gly Leu Arg Ser Asn Leu Gln Glu
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 Ile Phe Leu Pro Ala Phe Pro Cys His Glu Arg Lys Lys Gln Glu
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 <223> Von Heijne matrix
 score 3.75144398608723
 seq SGLLLQVLFRLIT/FV

<400> 37
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 atg ggc agc cag gag gtg ctg ggc cac gcg gcc cgg ctg tcc tcc tcc 107
 Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ser Ser Ser
 -25 -20 -15
 ggt ctc ctc ctg cag gtg ttg ttt cgg ttg atc acc ttt gtc ttg aat 155
 Gly Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn
 -10 -5 1
 gca ttt att ctt cgc ttc ctg tca aag gaa atc gtt ggc gta gta aat 203
 Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn
 5 10 15 20
 gta aga cta acg ctg ctt tac tca acc acc ctc ttc ctg gcc aga gag 251
 Val Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu
 25 30 35
 gcc ttc cgc aga gca tgt ctc agt ggg ggc acc cag cga gac tgg agc 299
 Ala Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser
 40 45 50
 cag acc ctc aac ctg ctg tgg cta aca gtc ccc ctg ggt gtg ttt tgg 347
 Gln Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp
 55 60 65
 tcc tta ttc ctg ggc tgg atc tgg ttg cag ctg ctt gaa gtg cct gat 395
 Ser Leu Phe Leu Gly Trp Ile Trp Leu Gln Leu Leu Glu Val Pro Asp
 70 75 80
 cct aat gtt gtc cct cac tat gca act gga gtg gtg ctg ttt ggt ctc 443
 Pro Asn Val Val Pro His Tyr Ala Thr Gly Val Val Leu Phe Gly Leu
 85 90 95 100
 tcg gca gtg gtg gag ctt cta gga gag ccc ttt tgg gtc ttg gca caa 491
 Ser Ala Val Val Glu Leu Leu Gly Glu Pro Phe Trp Val Leu Ala Gln
 105 110 115
 gca cat atg ttt gtg aag ctc aag gtg att gca gag agc ctg tcg gta 539
 Ala His Met Phe Val Lys Leu Lys Val Ile Ala Glu Ser Leu Ser Val
 120 125 130
 att ctt aag acc gtt ctg aca gct ttt ctc gtg ctg tgg ttg cct cac 587
 Ile Leu Lys Thr Val Leu Thr Ala Phe Leu Val Leu Trp Leu Pro His

	135						140				145						
tgg	gga	ttg	tac	att	ttc	tct	ttg	gcc	cag	ctt	ttc	tat	acc	aca	gtt	635	
Trp	Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val		
	150						155				160						
ctg	gtg	ctc	tgc	tat	gtt	att	tat	ttc	aca	aag	tta	ctg	ggt	tcc	cca	683	
Leu	Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro		
165						170				175					180		
gaa	tca	acc	aag	ctt	caa	act	ctt	cct	gtc	tcc	aga	ata	aca	gat	ctg	731	
Glu	Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu		
				185					190						195		
tta	ccc	aat	att	aca	aga	aat	gga	gcg	ttt	ata	aac	tgg	aaa	gag	gct	779	
Leu	Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala		
			200					205					210				
aaa	ctg	act	tgg	agt	ttt	ttc	aaa	cag	tct	ttc	ttg	aaa	cag	att	ttg	827	
Lys	Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu		
			215				220						225				
aca	gaa	ggc	gag	cga	tat	gtg	atg	aca	ttt	ttg	aat	gta	ttg	aac	ttt	875	
Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe		
			230			235					240						
ggt	gat	cag	ggt	gtg	tat	gat	ata	gtg	aat	aat	ctt	ggc	tcc	ctt	gtg	923	
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val		
245					250					255					260		
gcc	aga	tta	att	ttc	cag	cca	ata	gag	gaa	agt	ttt	tat	ata	ttt	ttt	971	
Ala	Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe		
				265					270						275		
gct	aag	gtg	ctg	gag	agg	gga	aag	gat	gcc	aca	ctt	cag	aag	cag	gag	1019	
Ala	Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu		
			280					285					290				
gac	gtt	gct	gtg	gct	gct	gca	gtc	gag	tcc	ctg	ctc	aag	ctg	gcc		1067	
Asp	Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala		
			295				300					305					
ctg	ctg	gcc	ggc	ctg	acc	atc	act	gtt	ttt	ggc	ttt	gcc	tat	tct	cag	1115	
Leu	Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln		
			310			315					320						
ctg	gct	ctg	gat	atc	tac	gga	ggg	acc	atg	ctt	agc	tca	gga	tcc	ggt	1163	
Leu	Ala	Leu	Asp	Ile	Tyr	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly		
325					330					335					340		
cct	gtt	ttg	ctg	cgt	tcc	tac	tgt	ctc	tat	gtt	ctc	ctg	ctt	gcc	atc	1211	
Pro	Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile		
				345					350					355			
aat	gga																

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gtt act gct gtt tcg gag gta ttc ctc tgc tgt gag cag ggc tgg cca 1547
Val Thr Ala Val Ser Glu Val Phe Leu Cys Cys Glu Gln Gly Trp Pro
      455      460      465
gcc aga ctg gca cac att gct gtg ggg gcc ttc tgt ctg gga gca act 1595
Ala Arg Leu Ala His Ile Ala Val Gly Ala Phe Cys Leu Gly Ala Thr
      470      475      480
ctc ggg aca gca ttc ctc aca gag acc aag ctg atc cat ttc ctc agg 1643
Leu Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg
485      490      495      500
act cag tta ggt gtg ccc aga cgc act gac aaa atg aca tgacttcagg 1692
Thr Gln Leu Gly Val Pro Arg Arg Thr Asp Lys Met Thr
      505      510
gaagcctgga caccgaggc acctggacca gctatgggta gttctgtggg tggaacacat 1752
tctgtgtaag agccccactg agggctctgc agcggagtga cagcaacccc agagatgagg 1812
caccagagag tgccactgca tgagacacct gtgaccattc gaagtctgaa atgcgggggg 1872
ggagtttcat ttttaagtga agaccaaag ccctttaaaa ataatagttt tttatcaaaa 1932
aaaaaaaaaa aaa 1945

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<210> 38
<211> 1330
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 198..998

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<220>
<221> sig_peptide
<222> 198..269
<223> Von Heijne matrix
      score 9.08017839002281
      seq LLLGPGLLATVRA/EC

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<400> 38
agaaatcagc cctttgcaga gggcgagag ggccctggaaa cctctgggac cttttcccag 60
gaactgttta tggtttcccc ctaggtctag gagacgtaga tgcataaggat gattggatac 120
atcgatggta gctataagag tcgtgtctga acccggcttt tccaattggc ctgctccatc 180
cgaacagcgt caactcc atg gcg cgg ttc ctg aca ctt tgc act tgg ctg 230
      Met Ala Arg Phe Leu Thr Leu Cys Thr Trp Leu
      -20      -15
ctg ttg ctc ggc ccc ggg ctc ctg gcg acc gtg cgg gcc gaa tgc agc 278
Leu Leu Leu Gly Pro Gly Leu Leu Ala Thr Val Arg Ala Glu Cys Ser
      -10      -5      1
cag gat tgc gcg acg tgc agc tac cgc cta gtg cgc ccg gcc gac atc 326
Gln Asp Cys Ala Thr Cys Ser Tyr Arg Leu Val Arg Pro Ala Asp Ile
      5      10      15
aac ttc ctg gct tgc gta atg gaa tgt gaa ggt aaa ctg cct tct ctg 374
Asn Phe Leu Ala Cys Val Met Glu Cys Glu Gly Lys Leu Pro Ser Leu
20      25      30      35
aaa att tgg gaa acc tgc aag gag ctc ctg cag ctg tcc aaa cca gat 422
Lys Ile Trp Glu Thr Cys Lys Glu Leu Leu Gln Leu Ser Lys Pro Asp
      40      45      50
ctt cct caa gat ggc acc agc acc ctc aga gaa aat agc aaa ccg gaa 470
Leu Pro Gln Asp Gly Thr Ser Thr Leu Arg Glu Asn Ser Lys Pro Glu
      55      60      65
gaa agc cat ttg cta gcc aaa agg tat ggg ggc ttc atg aaa agg tat 518
Glu Ser His Leu Leu Ala Lys Arg Tyr Gly Gly Phe Met Lys Arg Tyr

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      70      75      80
gga ggc ttc atg aag aaa atg gat gag ctt tat ccc atg gag cca gaa 566
Gly Gly Phe Met Lys Lys Met Asp Glu Leu Tyr Pro Met Glu Pro Glu
      85      90      95
gaa gag gcc aat gga agt gag atc ctc gcc aag cgg tat ggg ggc ttc 614
Glu Glu Ala Asn Gly Ser Glu Ile Leu Ala Lys Arg Tyr Gly Gly Phe
100      105      110      115
atg aag aag gat gca gag gag gac gac tcg ctg gcc aat tcc tca gac 662
Met Lys Lys Asp Ala Glu Glu Asp Asp Ser Leu Ala Asn Ser Ser Asp
      120      125      130
ctg cta aaa gag ctt ctg gaa aca ggg gac aac cga gag cgt agc cac 710
Leu Leu Lys Glu Leu Leu Glu Thr Gly Asp Asn Arg Glu Arg Ser His
      135      140      145
cac cag gat ggc agt gat aat gag gaa gaa gtg agc aag aga tat ggg 758
His Gln Asp Gly Ser Asp Asn Glu Glu Glu Val Ser Lys Arg Tyr Gly
      150      155      160
ggc ttc atg aga ggc tta aag aga agc ccc caa ctg gaa gat gaa gcc 806
Gly Phe Met Arg Gly Leu Lys Arg Ser Pro Gln Leu Glu Asp Glu Ala
      165      170      175
aaa gag ctg cag aag cga tat ggg ggc ttc atg aga aga gta ggt cgc 854
Lys Glu Leu Gln Lys Arg Tyr Gly Gly Phe Met Arg Arg Val Gly Arg
180      185      190      195
cca gag tgg tgg atg gac tac cag aaa cgg tat gga ggt ttc ctg aag 902
Pro Glu Trp Trp Met Asp Tyr Gln Lys Arg Tyr Gly Gly Phe Leu Lys
      200      205      210
cgc ttt gcc gag gct ctg ccc tcc gac gaa gaa ggc gaa agt tac tcc 950
Arg Phe Ala Glu Ala Leu Pro Ser Asp Glu Glu Gly Glu Ser Tyr Ser
      215      220      225
aaa gaa gtt cct gaa atg gaa aaa aga tac gga gga ttt atg aga ttt 998
Lys Glu Val Pro Glu Met Glu Lys Arg Tyr Gly Gly Phe Met Arg Phe
      230      235      240
taatattttt cccactagt gccccaggcc ccagcaagcc tccctccatc ctccagtggg 1058
aaactgttga tgggtgtttta ttgtcatgtg ttgcttgccct tgtatagttg acttcattgt 1118
ctggataact atacaacctg aaaactgtca ttccagggttc tgtgctcttt ttggagtctt 1178
taagctcagt attagtctat tgcagctatc tcgttttcat gctaaaatag tttttgttat 1238
cttgtctctt atttttgaca aacatcaata aatgcttact tgtatataga gataataaac 1298
ctattacccc aagtgcacaaa aaaaaaaaaa aa 1330

<210> 39
<211> 2124
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 505..1590

<220>
<221> sig_peptide
<222> 505..624
<223> Von Heijne matrix
      score 8.5056444915604
      seq VVMLMLLTLLVLG/MV

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cctggcataa ctgataggca tgtatgggag gaccacattc ctggggacag cctgggtatg 60
tgacatggca ggtgaccagg ttcccatgaa tgcccgaggc tgtgcccac ccatgagctg 120
gggcttccct ggaggtaaag agctaggggt ggggtggcagt gggtagaacc ccagctggac 180

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agtccttcc	ttagctctgt	gattgctaca	gctgggtctg	gaagccacag	gcgccctcag	240
gacaaatggg	gcttcttcag	cacagggtag	tgagtgtga	gctaagcaag	gacactgtcc	300
ccttctctgc	ccaggctcga	gctgtgcacc	tttaccctgg	caattgccct	gggtgctgtc	360
ctgctcctgc	ccttctccat	catcagcaat	gaggtgctgc	tctccctgcc	tcggaactac	420
tacatccagt	ggctcaacgg	ctccctcacc	catggcctct	ggaaccttgt	ttttctcttc	480
tccaacctgt	ccctcatctt	cctc	atg ccc ttt gca tat ttc ttc act gag			531
			Met Pro Phe Ala Tyr Phe Phe Thr Glu			
			-40		-35	
tct gag ggc ttt gct ggc tcc aga aag ggt gtc ctg ggc cgg gtc tat						579
Ser Glu Gly Phe Ala Gly Ser Arg Lys Gly Val Leu Gly Arg Val Tyr						
-30			-25		-20	
gag aca gtg gtg atg ttg atg ctc ctc act ctg ctg gtg cta ggt atg						627
Glu Thr Val Val Met Leu Met Leu Leu Thr Leu Leu Val Leu Gly Met						
-15			-10		-5	1
gtg tgg gtg gca tca gcc att gtg gac aag aac aag gcc aac aga gag						675
Val Trp Val Ala Ser Ala Ile Val Asp Lys Asn Lys Ala Asn Arg Glu						
5			10		15	
tca ctc tat gac ttt tgg gag tac tat ctc ccc tac ctc tac tca tgc						723
Ser Leu Tyr Asp Phe Trp Glu Tyr Tyr Leu Pro Tyr Leu Tyr Ser Cys						
20			25		30	
atc tcc ttc ctt ggg gtt ctg ctg ctc ctg gtg tgt act cca ctg ggt						771
Ile Ser Phe Leu Gly Val Leu Leu Leu Leu Val Cys Thr Pro Leu Gly						
35			40		45	
ctc gcc cgc atg ttc tcc gtc act ggg aag ctg cta gtc aag ccc cgg						819
Leu Ala Arg Met Phe Ser Val Thr Gly Lys Leu Leu Val Lys Pro Arg						
50			55		60	65
ctg ctg gaa gac ctg gag gag cag ctg tac tgc tca gcc ttt gag gag						867
Leu Leu Glu Asp Leu Glu Glu Gln Leu Tyr Cys Ser Ala Phe Glu Glu						
70			75		80	
gca gcc ctg acc cgc agg atc tgt aat cct act tcc tgc tgg ctg cct						915
Ala Ala Leu Thr Arg Arg Ile Cys Asn Pro Thr Ser Cys Trp Leu Pro						
85			90		95	
tta gac atg gag ctg cta cac aga cag gtc ctg gct ctg cag aca cag						963
Leu Asp Met Glu Leu Leu His Arg Gln Val Leu Ala Leu Gln Thr Gln						
100			105		110	
agg gtc ctg ctg gag aag agg cgg aag gct tca gcc tgg caa cgg aac						1011
Arg Val Leu Leu Glu Lys Arg Arg Lys Ala Ser Ala Trp Gln Arg Asn						
115			120		125	
ctg ggc tac ccc ctg gct atg ctg tgc ttg ctg gtg ctg acg ggc ctg						1059
Leu Gly Tyr Pro Leu Ala Met Leu Cys Leu Leu Val Leu Thr Gly Leu						
130			135		140	145
tct gtg ctc att gtg gcc atc cac atc ctg gag ctg ctc atc gat gag						1107
Ser Val Leu Ile Val Ala Ile His Ile Leu Glu Leu Leu Ile Asp Glu						
150			155		160	
gct gcc atg ccc cga ggc atg cag ggt acc tcc tta ggc cag gtc tcc						1155
Ala Ala Met Pro Arg Gly Met Gln Gly Thr Ser Leu Gly Gln Val Ser						
165			170		175	
ttc tcc aag ctg ggc tcc ttt ggt gcc gtc att cag gtt gta ctc atc						1203
Phe Ser Lys Leu Gly Ser Phe Gly Ala Val Ile Gln Val Val Leu Ile						
180			185		190	
ttt tac cta atg gtg tcc tca gtt gtg ggc ttc tat agc tct cca ctc						1251
Phe Tyr Leu Met Val Ser Ser Val Val Gly Phe Tyr Ser Ser Pro Leu						
195			200		205	
ttc cgg agc ctg cgg ccc aga tgg cac gac act gcc atg acg cag ata						1299
Phe Arg Ser Leu Arg Pro Arg Trp His Asp Thr Ala Met Thr Gln Ile						
210			215		220	225
att ggg aac tgt gtc tgt ctc ctg gtc cta agc tca gca ctt cct gtc						1347
Ile Gly Asn Cys Val Cys Leu Leu Val Leu Ser Ser Ala Leu Pro Val						

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                230                235                240
ttc tct cga acc ctg ggg ctc act cgc ttt gac ctg ctg ggt gac ttt    1395
Phe Ser Arg Thr Leu Gly Leu Thr Arg Phe Asp Leu Leu Gly Asp Phe
                245                250                255
gga cgc ttc aac tgg ctg ggc aat ttc tac att gtg ttc ctc tac aac    1443
Gly Arg Phe Asn Trp Leu Gly Asn Phe Tyr Ile Val Phe Leu Tyr Asn
                260                265                270
gca gcc ttt gca ggc ctc acc aca ctc tat ctg gtg aag acc ttc act    1491
Ala Ala Phe Ala Gly Leu Thr Thr Leu Tyr Leu Val Lys Thr Phe Thr
                275                280                285
gca gct gtg cgg gca gag ctg atc cgg gcc ttt ggg ctg gac aga ctg    1539
Ala Ala Val Arg Ala Glu Leu Ile Arg Ala Phe Gly Leu Asp Arg Leu
290                295                300                305
ccg ctg ccc gtc tcc ggt ttc ccc cag gca tct agg aag acc cag cac    1587
Pro Leu Pro Val Ser Gly Phe Pro Gln Ala Ser Arg Lys Thr Gln His
                310                315                320
cag tgacctccag ctgggggtgg gaagaaaaaa actggacact gccatctgct    1640
Gln
gcctaggcct ggaggggaagc ccaaggctac ttggacctca ggacctggaa tctgagaggg    1700
tgggtggcag aggggagcag agccatctgc actattgcat aatctgagcc agagtttggg    1760
accaggacct cctgcttttc cataacttaac tgtggcctca gcatggggta gggctgggtg    1820
actgggtcta gccctgatc ccaaactctgt ttacacatca atctgcctca ctgctgttct    1880
gggccatccc catagccatg tttacatgat ttgatgtgca atagggtggg gtaggggcag    1940
ggaaaggact gggccagggc aggctcggga gatagattgt ctcccttgcc tctggcccag    2000
cagagcctaa gcaactgtgct atcctggagg ggctttggac cacctgaaag accaagggga    2060
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aaaa    2124

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<210> 40
 <211> 1159
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 84..326

 <220>
 <221> sig_peptide
 <222> 84..146
 <223> Von Heijne matrix
 score 6.39000252120129
 seq LGLSVLLTAATVA/GV

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aggccgcggc cgccagcgtg ggg atg tct agg agc tcg aag gtg gtg ctg ggc    113
                Met Ser Arg Ser Ser Lys Val Val Leu Gly
                -20                -15
ctc tcg gtg ctg ctg acg gcg gcc aca gtg gcc ggc gta cat gtg aag    161
Leu Ser Val Leu Leu Thr Ala Ala Thr Val Ala Gly Val His Val Lys
                -10                -5                1                5
cag cag tgg gac cag cag agg ctt cgt gac gga gtt atc aga gac att    209
Gln Gln Trp Asp Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile
                10                15                20
gag agg caa att cgg aaa aaa gaa aac att cgt ctt ttg gga gaa cag    257
Glu Arg Gln Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln
                25                30                35

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att att ttg act gag caa ctt gaa gca aga gag aag atg tta ttg	305
Ile Ile Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu	
40 45 50	
gca aaa gga tct caa aaa tca tgacttgaat gtgaaatatc tgttggacag	356
Ala Lys Gly Ser Gln Lys Ser	
55 60	
acaacacgag tttgtgtgtg tgtgttgatg gagagtagct tagtagtatac ttcattctttt	416
tttttgggtca ctgtcctttt aaacttgatc aaataaagga cagtgggtca tataaggttac	476
tgctttcagg gtcccttata tctgaataaa ggagtggtggg cagacacttt ttggaagagt	536
ctgtctgggt gatcctggta gaagcccat tagggctact gtccagtgtc tagggttgtt	596
actgagaagc actgccgagc ttgtgagaag gaagggatgg atagtagcat ccacctgagt	656
agtctgatca gtccggcatga tgacgaagcc acgagaacat cgacctcaga aggactggag	716
gaaggtgaaa gtggagggag agacgctcct gatcgtcgaa tyccgaggat caggkcatca	776
gtggacttat cgcacgacca gagtggggat tccctcaaca gtgatgaagg agacgtgtct	836
tggtggagg agcagctgtc ctacttctgt gacaagtgcc aaaaatggat accagccagt	896
aaggagcttc tcaatttcct tgatttgtca attcctgtgt gaaggtttgt tttccaacc	956
tgtgaaagaa acgtgaatgt aaaagagacc taaataaaaag gataattata tttattctct	1016
agttgatcag ctataaattt atataaaaca taggcatgtt tgtactaatg aaacgtactg	1076
tcaacctcta tcacattgtt aaattaacac ttttggtggt aactcaataa aattgagaaa	1136
attgcacaaaa aaaaaaaaaaaa aaa	1159
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<211> 1953	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> 56..1678	
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<222> 56..139	
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score 3.75144398608723	
seq SGLLLQVLFRLIT/FV	
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	Met
ggc agc cag gag gtg ctg ggc cac gcg gcc cgg ctg gcc tcc tcc ggt	106
Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser Gly	
-25 -20 -15	
ctc ctc ctg cag gtg ttg ttt cgg ttg atc acc ttt gtc ttg aat gca	154
Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn Ala	
-10 -5 1 5	
ttt att ctt cgc ttc ctg tca aag gaa atc gtt ggc gta gta aat gta	202
Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn Val	
10 15 20	
aga cta acg ctg ctt tac tca acc acc ctc ttc ctg gcc aga gag gcc	250
Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu Ala	
25 30 35	
ttc cgc aga gca tgt ctc agt ggg ggc acc cag cga gac tgg agc cag	298
Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser Gln	
40 45 50	
acc ctc aac ctg ctg tgg cta aca gtc ccc ctg ggt gtg ttt tgg tcc	346
Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp Ser	
55 60 65	

tta	ttc	ctg	ggc	tgg	atc	tgg	tgt	cag	ctg	ctt	gaa	gtg	cct	gat	cct	394
Leu	Phe	Leu	Gly	Trp	Ile	Trp	Leu	Gln	Leu	Leu	Glu	Val	Pro	Asp	Pro	
70					75					80					85	
aat	gtt	gtc	cct	cac	tat	gca	act	gga	gtg	gtg	ctg	ttt	ggg	ctc	tcg	442
Asn	Val	Val	Pro	His	Tyr	Ala	Thr	Gly	Val	Val	Leu	Phe	Gly	Leu	Ser	
				90					95					100		
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Ala	Val	Val	Glu	Leu	Leu	Gly	Glu	Pro	Phe	Trp	Val	Leu	Ala	Gln	Ala	
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His	Met	Phe	Val	Lys	Leu	Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val	Ile	
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Leu	Lys	Ser	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His	Trp	
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Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val	Leu	
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Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu	Leu	
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Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala	Lys	
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Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe	Gly	
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Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe	Ala	
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Ala	Leu	Asp	Ile	Asn	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly	Pro	
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Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile	Asn	
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Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys	Phe	
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Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly	Leu	
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Arg	Leu	Ala	His	Ile	Ala	Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala	Thr	Leu	
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Gly	Thr	Ala	Phe	Leu	Thr	Glu	Thr	Lys	Leu	Ile	His	Phe	Leu	Arg	Thr	
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Gln	Leu	Gly	Val	Pro	Arg	Arg	Thr	Asp	Lys	Met	Thr					
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Lys	Gln	Val	Pro	Val	Leu	Asp	Asp	Gly	Ser	Leu	Glu	Asp	Phe	Thr	Asp	
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Lys	Val	Arg	Leu	Ser	Leu	Ala	Asn	Glu	Ala	Leu	Leu	Pro	Thr	Leu	Ile	
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Cys	Asp	Ile	Ala	Gly	Tyr	Tyr	Pro	Leu	Asp	Val	Val	Val	Thr	Trp	Thr	
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Thr His Ile Ser Leu Glu Gly Pro Leu Gly Ala Ser Thr Gln Val Val
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cca cca gag cgg aga aca gcc ttg gga gtc atc ttt gcc agc agt ctc 1366
Pro Pro Glu Arg Arg Thr Ala Leu Gly Val Ile Phe Ala Ser Ser Leu
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Thr Gly Leu Gly Leu Leu Gln Ala Glu Arg Trp Glu Thr Thr Ser Cys
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Ser Gln Pro Ser
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 seq TVFLLVTLQALDT/VE

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Lys Leu Leu Ala Ser Cys Leu Cys Val Thr Ala Thr Val Phe Leu Leu
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Trp	Pro	Leu	Ser	Asn	Thr	Arg	Ser	Ser	Glu	His	Ile	Lys	Glu	Val	Met	
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Gln	Gln	Leu	Lys	Asn	Pro	Ala	Ser	Met	Asp	Ala	Asp	Gly	Phe	Tyr	Arg	
	265				270					275					280	
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Ile	Ile	Ala	Gln	Tyr	Lys	Phe	Ile	Leu	Ala	Phe	Glu	Asn	Ala	Val	Cys	
			285					290						295		
gat	gac	tac	atc	act	gag	aag	ttc	tgg	agg	cca	ctg	aaa	ctg	ggg	gta	1362
Asp	Asp	Tyr	Ile	Thr	Glu	Lys	Phe	Trp	Arg	Pro	Leu	Lys	Leu	Gly	Val	

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gtc cct gta tat tac gga tcc ccc agc atc aca gac tgg ctt cca agt   1410
Val Pro Val Tyr Tyr Gly Ser Pro Ser Ile Thr Asp Trp Leu Pro Ser
          315          320          325
aac aaa agt gct att ctt gta tca gaa ttt tct cac ccc agg gaa ctg   1458
Asn Lys Ser Ala Ile Leu Val Ser Glu Phe Ser His Pro Arg Glu Leu
          330          335          340
gca agt tac atc aga cga ctg gat tct gat gac aga ttg tat gag gcc   1506
Ala Ser Tyr Ile Arg Arg Leu Asp Ser Asp Asp Arg Leu Tyr Glu Ala
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tat gta gaa tgg aag ctg aag ggt aga tct cta acc agc gac ttc   1551
Tyr Val Glu Trp Lys Leu Lys Gly Arg Ser Leu Thr Ser Asp Phe
          365          370          375
tgacagctct cagggaacgg aaatggggag tgcaagacgt caaccaggac aattacatcg   1611
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gcttaccacc caaaagatgg gaggcagaag ataccacct gagttgcca gagcccacag   1731
tgtttgcctt ctcaccactc cggactccac ctttgagctc tttgcgagag atgtggattt   1791
ccagctttga acaatccaag aaagaagccc aggcactaag gtggctggtt gataggaatc   1851
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 <213> Homo sapiens

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 seq GVGLVTLLGLAVG/SY

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          Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu
          -25          -20          -15
ggg gtg ggg ctg gtc act ctg ctc ggc ctg gct gtg ggc tcc tac ttg   158
Gly Val Gly Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu
          -10          -5          1
gtt cgg agg tcc cgc cgg cct cag gtc act ctc ctg gac ccc aat gaa   206
Val Arg Arg Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu
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aag tac ctg cta cga ctg cta gac aag acg act gtg agc cac aac acc   254
Lys Tyr Leu Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr
          20          25          30          35
aag agg ttc cgc ttt gcc ctg ccc acc gcc cac cac act ctg ggg ctg   302
Lys Arg Phe Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu
          40          45          50
cct gtg ggc aaa cat atc tac ctc tcc acc cga att gat ggc agc ctg   350
Pro Val Gly Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu
          55          60          65
gtc atc agg cca tac act cct gtc acc agt gat gag gat caa ggc tat   398

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Val	Ile	Arg	Pro	Tyr	Thr	Pro	Val	Thr	Ser	Asp	Glu	Asp	Gln	Gly	Tyr		
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Val	Asp	Leu	Val	Ile	Lys	Val	Tyr	Leu	Lys	Gly	Val	His	Pro	Lys	Phe		
	85					90					95						
cct	gag	gga	ggg	aag	atg	tct	cag	tac	ctg	gat	agc	ctg	aag	gtt	ggg		494
Pro	Glu	Gly	Gly	Lys	Met	Ser	Gln	Tyr	Leu	Asp	Ser	Leu	Lys	Val	Gly		
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gat	gtg	gtg	gag	ttt	cgg	ggg	cca	agc	ggg	ttg	ctc	act	tac	act	gga		542
Asp	Val	Val	Glu	Phe	Arg	Gly	Pro	Ser	Gly	Leu	Leu	Thr	Tyr	Thr	Gly		
				120					125					130			
aaa	ggg	cat	ttt	aac	att	cag	ccc	aac	aag	aaa	tct	cca	cca	gaa	ccc		590
Lys	Gly	His	Phe	Asn	Ile	Gln	Pro	Asn	Lys	Lys	Ser	Pro	Pro	Glu	Pro		
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Arg	Val	Ala	Lys	Lys	Leu	Gly	Met	Ile	Ala	Gly	Gly	Thr	Gly	Ile	Thr		
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cca	atg	cta	cag	ctg	atc	cgg	gcc	atc	ctg	aaa	gtc	cct	gaa	gat	cca		686
Pro	Met	Leu	Gln	Leu	Ile	Arg	Ala	Ile	Leu	Lys	Val	Pro	Glu	Asp	Pro		
	165				170					175							
acc	cag	tgc	ttt	ctg	ctt	ttt	gcc	aac	cag	aca	gaa	aag	gat	atc	atc		734
Thr	Gln	Cys	Phe	Leu	Phe	Ala	Asn	Gln	Thr	Glu	Lys	Asp	Ile	Ile			
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Leu	Arg	Glu	Asp	Leu	Glu	Glu	Leu	Gln	Ala	Arg	Tyr	Pro	Asn	Arg	Phe		
				200					205					210			
aag	ctc	tgg	ttc	act	ctg	gat	cat	ccc	cca	aaa	gat	tgg	gcc	tac	agc		830
Lys	Leu	Trp	Phe	Thr	Leu	Asp	His	Pro	Pro	Lys	Asp	Trp	Ala	Tyr	Ser		
			215				220						225				
aag	ggc	ttt	gtg	act	gcc	gac	atg	atc	cgg	gaa	cac	ctg	ccc	gct	cca		878
Lys	Gly	Phe	Val	Thr	Ala	Asp	Met	Ile	Arg	Glu	His	Leu	Pro	Ala	Pro		
		230			235						240						
ggg	gat	gat	gtg	ctg	gta	ctg	ctt	tgt	ggg	cca	ccc	cca	atg	gtg	cag		926
Gly	Asp	Asp	Val	Leu	Val	Leu	Leu	Cys	Gly	Pro	Pro	Pro	Met	Val	Gln		
	245				250				255								
ctg	gcc	tgc	cat	ccc	aac	ttg	gac	aaa	ctg	ggc	tac	tca	caa	aag	atg		974
Leu	Ala	Cys	His	Pro	Asn	Leu	Asp	Lys	Leu	Gly	Tyr	Ser	Gln	Lys	Met		
260				265					270					275			
cga	ttc	acc	tac	tgagcatcct	ccagcttccc	tggtgctggt	cgctgcagtt										1026
Arg	Phe	Thr	Tyr														
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gtctgtgatg	aaaggaacag	tctgtgcaat	gggttttact	taaaacttcac	tgttcaacct												1386
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atatctctgt	gtgtgtctct	ctcagccccct	gcccaggcta	gagggaaaca	gctactgata												1566
atcgaaaact	gctgtttgtg	gcaggaaccc	ctggctgtgc	aaataaatgg	ggctgaggcc												1626
cctgtgtgat	attaaaaaaaa	aaaaaaaaaaa	a														1657

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<211> 1733

<212> DNA

<213> Homo sapiens

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<221> CDS
<222> 157..1482

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seq LLLCLALSGAAET/KP

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ggcgtggggc aaggagggaa ctcgagagca gcctcc atg ggc aca cag gag ggc 174
Met Gly Thr Gln Glu Gly
-20
tgg tgc ctg ctg ctc tgc ctg gct cta tct gga gca gca gaa acc aag 222
Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser Gly Ala Ala Glu Thr Lys
-15 -10 -5 1
ccc cac cca gca gag ggg cag ttg cgg gca gtg gac gtg gtc cta gac 270
Pro His Pro Ala Glu Gly Gln Leu Arg Ala Val Asp Val Val Leu Asp
5 10 15
tgc ttc ctg gcg aag gac ggt gcg cac cgt gga gct ctc gcc agc agt 318
Cys Phe Leu Ala Lys Asp Gly Ala His Arg Gly Ala Leu Ala Ser Ser
20 25 30
gag gac agg gca agg gcc tcc ctt gtg ctg aag cag gtg cca gtg ctg 366
Glu Asp Arg Ala Arg Ala Ser Leu Val Leu Lys Gln Val Pro Val Leu
35 40 45
gac gat ggc tcc ctg gag gac ttc acc gat ttc caa ggg ggc aca ctg 414
Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp Phe Gln Gly Gly Thr Leu
50 55 60 65
gcc caa gat gac cca cct att atc ttt gag gcc tca gtg gac ctg gtc 462
Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu Ala Ser Val Asp Leu Val
70 75 80
cag att ccc cag gcc gag gcc ttg ctc cat gct gac tgc agt ggg aag 510
Gln Ile Pro Gln Ala Glu Ala Leu Leu His Ala Asp Cys Ser Gly Lys
85 90 95
gag gtg acc tgt gag atc tcc cgc tac ttt ctc cag atg aca gag acc 558
Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe Leu Gln Met Thr Glu Thr
100 105 110
act gtt aag aca gca gct tgg ttc atg gcc aac atg cag gtc tct gga 606
Thr Val Lys Thr Ala Ala Trp Phe Met Ala Asn Met Gln Val Ser Gly
115 120 125
ggg gga cst agc atc tcc ttg gtg atg aag act ccc agg gtc acc aag 654
Gly Gly Xaa Ser Ile Ser Leu Val Met Lys Thr Pro Arg Val Thr Lys
130 135 140 145
aat gag gcg ctc tgg cac ccg acg ctg aac ttg cca ctg agc ccc cag 702
Asn Glu Ala Leu Trp His Pro Thr Leu Asn Leu Pro Leu Ser Pro Gln
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ggg act gtg cga act gca gtg gag ttc cag gtg atg aca cag acc caa 750
Gly Thr Val Arg Thr Ala Val Glu Phe Gln Val Met Thr Gln Thr Gln
165 170 175
tcc ctg agc ttc ctg ctg ggg tcc tca gcc tcc ttg gac tgt ggc ttc 798
Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala Ser Leu Asp Cys Gly Phe
180 185 190
tcc atg gca ccg ggc ttg gac ctc atc agt gtg gag tgg cga ctg cag 846
Ser Met Ala Pro Gly Leu Asp Leu Ile Ser Val Glu Trp Arg Leu Gln
195 200 205

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His Lys Gly Arg Gly Gln Leu Val Tyr Ser Trp Thr Ala Gly Gln Gly
210                215                220                225
cag gct gtg cgg aag ggc gct acc ctg gag cct gca caa ctg ggc atg      942
Gln Ala Val Arg Lys Gly Ala Thr Leu Glu Pro Ala Gln Leu Gly Met
                230                235                240
gcc agg gat gcc tcc ctc acc ctg ccc ggc ctc act ata cag gac gag      990
Ala Arg Asp Ala Ser Leu Thr Leu Pro Gly Leu Thr Ile Gln Asp Glu
                245                250                255
ggg acc tac att tgc cag atc acc acc tct ctg tac cga gct cag cag      1038
Gly Thr Tyr Ile Cys Gln Ile Thr Thr Ser Leu Tyr Arg Ala Gln Gln
                260                265                270
atc atc cag ctc aac atc caa gct tcc cct aaa gta cga ctg agc ttg      1086
Ile Ile Gln Leu Asn Ile Gln Ala Ser Pro Lys Val Arg Leu Ser Leu
                275                280                285
gca aac gaa gct ctg ctg ccc acc ctc atc tgc gac att gct ggc tat      1134
Ala Asn Glu Ala Leu Leu Pro Thr Leu Ile Cys Asp Ile Ala Gly Tyr
290                295                300                305
tac cct ctg gat gtg gtg gtg acg tgg acc cga gag gag ctg ggt gga      1182
Tyr Pro Leu Asp Val Val Val Thr Trp Thr Arg Glu Glu Leu Gly Gly
                310                315                320
tcc cca gcc caa gtc tct ggt gcc tcc ttc tcc agc ctc agg caa agc      1230
Ser Pro Ala Gln Val Ser Gly Ala Ser Phe Ser Ser Leu Arg Gln Ser
                325                330                335
gtg gca ggc acc tac agc atc tcc tcc tct ctc acc gca gaa cct ggc      1278
Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser Leu Thr Ala Glu Pro Gly
                340                345                350
tct gca ggt gcc act tac acc tgc cag gtc aca cac atc tct ctg gag      1326
Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val Thr His Ile Ser Leu Glu
                355                360                365
gag ccc ctt ggg gcc agc acc cag gtt gtc cca cca gag cgg aga aca      1374
Glu Pro Leu Gly Ala Ser Thr Gln Val Val Pro Pro Glu Arg Arg Thr
370                375                380                385
gcc ttg gga gtc atc ttt gcc agc agt ctc ttc ctt ctt gca ctg atg      1422
Ala Leu Gly Val Ile Phe Ala Ser Ser Leu Phe Leu Leu Ala Leu Met
                390                395                400
ttc ctg ggg ctt cag aga cgg caa gca cct aca gga ctt ggg ctg ctt      1470
Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro Thr Gly Leu Gly Leu Leu
                405                410                415
cag gct gaa cgc taggagacca cttcctgtgc tgacacacag agctcccatc      1522
Gln Ala Glu Arg
420
tccatgaaga ccgcacagcg cgtgtaagcc agcccagctg acctaaagcg acatgagact      1582
actagaaaga aacgacaccc ttccccaagc ccccacagct actccaaccc aaacaacaac      1642
caagccagtt taatggtagg aatttgatt ttttgcttt gttcagaata catgacattg      1702
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1733

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 ttccttagac aagacacagt gtagggcccgg gcccggtgtg gcccaggac tcctttggaa 180
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 Val Ala Gly Phe Val Phe Tyr Leu Gly Val Phe Val Val Cys His Gln
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 Leu Ser Ser Ser Leu Asn Ala Thr Tyr Arg Ser Leu Val Ala Arg Glu
 1 5 10
 aag gtc ttc tgg gac ctg gcg gcc acg cgt gca gtc ttt ggt gtt cag 422
 Lys Val Phe Trp Asp Leu Ala Ala Thr Arg Ala Val Phe Gly Val Gln
 15 20 25
 agc aca gcc gca ggc ctg tgg gct ctg ctg ggg gac cct gtg ctg cat 470
 Ser Thr Ala Ala Gly Leu Trp Ala Leu Leu Gly Asp Pro Val Leu His
 30 35 40
 gcc gac aag gcg cgt ggc cag cag aac tgg tgc tgg ttt cac atc acg 518
 Ala Asp Lys Ala Arg Gly Gln Gln Asn Trp Cys Trp Phe His Ile Thr
 45 50 55 60
 aca gca acg gga ttc ttt tgc ttt gaa aat gtt gca gtc cac ctg tcc 566
 Thr Ala Thr Gly Phe Phe Cys Phe Glu Asn Val Ala Val His Leu Ser
 65 70 75
 aac ttg atc ttc cgg aca ttt gac ttg ttt ctg gtt atc cac cat ctc 614
 Asn Leu Ile Phe Arg Thr Phe Asp Leu Phe Leu Val Ile His His Leu
 80 85 90
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 Phe Ala Phe Leu Gly Phe Leu Gly Cys Leu Val Asn Leu Gln Ala Gly
 95 100 105
 cac tat cta gct atg acc acg ttg ctc ctg gag atg agc acg ccc ttt 710
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 110 115 120
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 Thr Cys Val Ser Trp Met Leu Leu Lys Ala Gly Trp Ser Glu Ser Leu
 125 130 135 140
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 Phe Trp Lys Leu Asn Gln Trp Leu Met Ile His Met Phe His Cys Arg
 145 150 155
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 Met Val Leu Thr Tyr His Met Trp Trp Val Cys Phe Trp His Trp Asp
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 Gly Leu Val Ser Ser Leu Tyr Leu Pro His Leu Thr Leu Phe Leu Val
 175 180 185
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 Gly Leu Ala Leu Leu Thr Leu Ile Ile Asn Pro Tyr Trp Thr His Lys
 190 195 200
 aag act cag cag ctt ctc aat ccg gtg gac tgg aac ttc gca cag cca 998

Lys Thr Gln Gln Leu Leu Asn Pro Val Asp Trp Asn Phe Ala Gln Pro
 205 210 215 220
 gaa gcc aag agc agg cca gaa ggc aac ggg cag ctg ctg cgg aag aag 1046
 Glu Ala Lys Ser Arg Pro Glu Gly Asn Gly Gln Leu Leu Arg Lys Lys
 225 230 235
 agg cca tagctgctcc agccgggggct ccgggggcggc agcagagctg gcacaccgat 1102
 Arg Pro
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 <213> Homo sapiens

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 ggctgaacc tggggccaga caccctctc ccggcc atg gtc aac gac cct cca 234
 Met Val Asn Asp Pro Pro
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 Val Pro Ala Leu Leu Trp Ala Gln Glu Val Gly Gln Val Leu Ala Gly
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 Arg Ala Arg Arg Leu Leu Leu Gln Phe Gly Val Leu Phe Cys Thr Ile
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 ctc ctt ttg ctc tgg gtg tct gtc ttc ctc tat ggc tcc ttc tac tat 378
 Leu Leu Leu Leu Trp Val Ser Val Phe Leu Tyr Gly Ser Phe Tyr Tyr
 20 25 30
 tcc tat atg ccg aca gtc agc cac ctc agc cct gtg cat ttc tac tac 426
 Ser Tyr Met Pro Thr Val Ser His Leu Ser Pro Val His Phe Tyr Tyr
 35 40 45
 agg acc gac tgt gat tcc tcc acc acc tca ctc tgc tcc ttc cct gtt 474
 Arg Thr Asp Cys Asp Ser Ser Thr Thr Ser Leu Cys Ser Phe Pro Val

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Gly Gln Pro Tyr Arg Val Thr Leu Glu Leu Pro Glu Ser Pro								
	85			90		95		
gtg aat caa gat ttg ggc atg ttc ttg gtc acc att tcc tgc tac acc								618
Val Asn Gln Asp Leu Gly Met Phe Leu Val Thr Ile Ser Cys Tyr Thr								
	100			105		110		
aga ggt ggc cga atc atc tcc act tct tcg cgt tcg gtg atg ctg cat								666
Arg Gly Gly Arg Ile Ile Ser Thr Ser Ser Arg Ser Val Met Leu His								
	115			120		125		
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Tyr Arg Ser Asp Leu Leu Gln Met Leu Asp Thr Leu Val Phe Ser Ser								
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ctc ctg cta ttt ggc ttt gca gag cag aag cag ctg ctg gag gtg gaa								762
Leu Leu Leu Phe Gly Phe Ala Glu Gln Lys Gln Leu Leu Glu Val Glu								
	150			155		160		
ctc tac gca gac tat aga gag aac tcg tac gtg ccg acc act gga gcg								810
Leu Tyr Ala Asp Tyr Arg Glu Asn Ser Tyr Val Pro Thr Thr Gly Ala								
	165			170		175		
atc att gag atc cac agc aag cgc atc cag ctg tat gga gcc tac ctc								858
Ile Ile Glu Ile His Ser Lys Arg Ile Gln Leu Tyr Gly Ala Tyr Leu								
	180			185		190		
cgc atc cac gcg cac ttc act ggg ctc aga tac ctg cta tac aac ttc								906
Arg Ile His Ala His Phe Thr Gly Leu Arg Tyr Leu Leu Tyr Asn Phe								
	195			200		205		
ccg atg acc tgc gcc ttc ata ggt gtt gcc agc aac ttc acc ttc ctc								954
Pro Met Thr Cys Ala Phe Ile Gly Val Ala Ser Asn Phe Thr Phe Leu								
	210			215		220		225
agc gtc atc gtg ctc ttc agc tac atg cag tgg gtg tgg ggg ggc atc								1002
Ser Val Ile Val Leu Phe Ser Tyr Met Gln Trp Val Trp Gly Gly Ile								
	230			235		240		
tgg ccc cga cac cgc ttc tct ttg cag gtt aac atc cga aaa aga gac								1050
Trp Pro Arg His Arg Phe Ser Leu Gln Val Asn Ile Arg Lys Arg Asp								
	245			250		255		
aat tcc cgg aag gaa gtc caa cga agg atc tct gct cat cag cca ggg								1098
Asn Ser Arg Lys Glu Val Gln Arg Arg Ile Ser Ala His Gln Pro Gly								
	260			265		270		
cct gaa ggc cag gag gag tca act ccg caa tca gat gtt aca gag gat								1146
Pro Glu Gly Gln Glu Glu Ser Thr Pro Gln Ser Asp Val Thr Glu Asp								
	275			280		285		
ggt gag agc cct gaa gat ccc tca ggg aca gag ggt cag ctg tcc gag								1194
Gly Glu Ser Pro Glu Asp Pro Ser Gly Thr Glu Gly Gln Leu Ser Glu								
	290			295		300		305
gag gag aaa cca gat cag cag ccc ctg agc gga gaa gag gag cta gag								1242
Glu Glu Lys Pro Asp Gln Gln Pro Leu Ser Gly Glu Glu Glu Leu Glu								
	310			315		320		
cct gag gcc agt gat ggt tca ggc tcc tgg gaa gat gca gct ttg ctg								1290
Pro Glu Ala Ser Asp Gly Ser Gly Ser Trp Glu Asp Ala Ala Leu Leu								
	325			330		335		
acg gag gcc aac ctg cct gct cct gct cct gct tct gct tct gcc cct								1338
Thr Glu Ala Asn Leu Pro Ala Pro Ala Pro Ala Ser Ala Ser Ala Pro								
	340			345		350		
gtc cta gag act ctg ggc agc tct gaa cct gct ggg ggt gct ctc cga								1386
Val Leu Glu Thr Leu Gly Ser Ser Glu Pro Ala Gly Gly Ala Leu Arg								
	355			360		365		

<210> 49
 <211> 831
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 234..491

<220>
 <221> sig_peptide
 <222> 234..293
 <223> Von Heijne matrix
 score 4.85037394589162
 seq AVAGLPALGFTGA/GI

<400> 49
 gtttactcgc tgctgtgccc atctatcagc aggetccggg ctgaagattg cttctcttct 60
 ctctccaag gtctagtac ggagcccgcg cgcggcgcca ccatgcggca gaaggcggta 120
 tcgttttct ctgctacctg ctgctcttca cttgcagtgg ggtggaggca ggtaagaaaa 180
 agtgcctgga gagctcggac agcggctccg ggttctggaa ggccctgacc ttc atg 236
 Met
 -20
 gcc gtc gga gga gga ctc gca gtc gcc ggg ctg ccc gcg ctg ggc ttc 284
 Ala Val Gly Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe
 -15 -10 -5
 acc ggc gcc ggc atc gcg gcc aac tcg gtg gct gcc tcg ctg atg agc 332
 Thr Gly Ala Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser
 1 5 10
 tgg tct gcg atc ctg aat ggg ggc ggc gtg ccc gcc ggg ggg cta gtg 380
 Trp Ser Ala Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu Val
 15 20 25
 gcc acg ctg cag agc ctc ggg gct ggt ggc agc agc gtc gtc ata ggt 428
 Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile Gly
 30 35 40 45
 aat att ggt gcc ctg atg ggc tac gcc acc cac aag tat ctc gat agt 476
 Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp Ser
 50 55 60
 gag gag gat gag gag tagccagcag ctcccagaac ctcttcttcc ttcttggcct 531
 Glu Glu Asp Glu Glu
 65
 aactcttcca gttaggatct agaactttgc cttttttttt tttttttttt tttttttgag 591
 atgggttctc actatattgt ccaggctaga gtgcagtggc tattcacaga tgcgaacata 651
 gtacactgca gcctccaact cctagcctca agtgatcctc ctgtctcaac ctcccaagta 711
 ggattacaag catgcgccga cgatgccag aatccagaac tttgtctatc actctcccca 771
 acaacctaga tgtgaaaaca gaataaactt caccagaaa gcaaaaaaaaa aaaaaaaaaa 831

<210> 50
 <211> 917
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 180..800

<220>
 <221> sig_peptide

<222> 180..248

<223> Von Heijne matrix

score 14.6828672385356

seq ILLLLWLIAPSRA/CT

<400> 50

acccttggct tctgcactga tgggtgggtgg atgagtaatg catccaggaa gcctggaggc	60
ctgtgggtttc cgcacccgct gccacccccg cccctagcgt ggacatttat cctctagcgc	120
tcaggccctg ccgccatcgc cgcagatcca gcgcccagag agacaccaga gaaccacc	179
atg gcc ccc ttt gag ccc ctg gct tct ggc atc ctg ttg ttg ctg tgg	227
Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp	
-20 -15 -10	
ctg ata gcc ccc agc agg gcc tgc acc tgt gtc cca ccc cac cca cag	275
Leu Ile Ala Pro Ser Arg Ala Cys Thr Cys Val Pro Pro His Pro Gln	
-5 1 5	
acg gcc ttc tgc aat tcc gac ctc gtc atc agg gcc aag ttc gtg ggg	323
Thr Ala Phe Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly	
10 15 20 25	
aca cca gaa gtc aac cag acc acc tta tac cag cgt tat gag atc aag	371
Thr Pro Glu Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys	
30 35 40	
atg acc aag atg tat aaa ggg ttc caa gcc tta ggg gat gcc gct gac	419
Met Thr Lys Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp	
45 50 55	
atc cgg ttc gtc tac acc ccc gcc atg gag agt gtc tgc gga tac ttc	467
Ile Arg Phe Val Tyr Thr Pro Ala Met Glu Ser Val Cys Gly Tyr Phe	
60 65 70	
cac agg tcc cac aac cgc agc gag gag ttt ctc att gct gga aaa ctg	515
His Arg Ser His Asn Arg Ser Glu Glu Phe Leu Ile Ala Gly Lys Leu	
75 80 85	
cag gat gga ctc ttg cac atc act acc tgc agt ttt gtg gct ccc tgg	563
Gln Asp Gly Leu Leu His Ile Thr Thr Cys Ser Phe Val Ala Pro Trp	
90 95 100 105	
aac agc ctg agc tta gct cag cgc cgg ggc ttc acc aag acc tac act	611
Asn Ser Leu Ser Leu Ala Gln Arg Arg Gly Phe Thr Lys Thr Tyr Thr	
110 115 120	
gtt ggc tgt gag gaa tgc aca gtg ttt ccc tgt tta tcc ttc ccc tgc	659
Val Gly Cys Glu Glu Cys Thr Val Phe Pro Cys Leu Ser Phe Pro Cys	
125 130 135	
aaa ctg cag agt ggc act cat tgc ttg tgg acg gac cag ctc ctc caa	707
Lys Leu Gln Ser Gly Thr His Cys Leu Trp Thr Asp Gln Leu Leu Gln	
140 145 150	
ggc tct gaa aag ggc ttc cag tcc cgt cac ctt gcc tgc ctg cct cgg	755
Gly Ser Glu Lys Gly Phe Gln Ser Arg His Leu Ala Cys Leu Pro Arg	
155 160 165	
gag cca ggg ctg tgc acc tgg cag tcc ctg cgg tcc cag ata gcc	800
Glu Pro Gly Leu Cys Thr Trp Gln Ser Leu Arg Ser Gln Ile Ala	
170 175 180	
tgaatcctgc ccggagtggg agctgaagcc tgcacagtgt ccaccctgtt cccactccca	860
tctttcttcc ggacaatgaa ataaagagtt accaccacgc aaaaaaaaaa aaaaaaa	917

<210> 51

<211> 621

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 140..472

<220>

<221> sig_peptide

<222> 140..211

<223> Von Heijne matrix

score 8.44884907465122

seq FVVFSFLICAMA/GD

<400> 51

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atatttttttt catatctgac atttctatgt cctatgacgg tttcacagct atcctacttt      60
ggagaagatg ctggaaattc agagtttccg ccagagaata tatgcctgaa ctaaaagagg      120
aagtgggtcta taggagaaa atg aaa tat gat tgt ccc ttc agt ggg aca tca      172
                               Met Lys Tyr Asp Cys Pro Phe Ser Gly Thr Ser
                               -20                               -15
ttt gtg gtc ttc tct ctc ttt ttg atc tgt gca atg gct gga gat gta      220
Phe Val Val Phe Ser Leu Phe Leu Ile Cys Ala Met Ala Gly Asp Val
                               -10                               -5                               1
gtc tac gct gac atc aaa act gtt cgg act tcc ccg tta gaa ctc gcg      268
Val Tyr Ala Asp Ile Lys Thr Val Arg Thr Ser Pro Leu Glu Leu Ala
                               5                               10                               15
ttt cca ctt cag aga tct gtt tct ttc aac ttt tct act gtc cat aaa      316
Phe Pro Leu Gln Arg Ser Val Ser Phe Asn Phe Ser Thr Val His Lys
20                               25                               30                               35
tca tgt cct gcc aaa gac tgg aag gtg cat aag gga aaa tgt tac tgg      364
Ser Cys Pro Ala Lys Asp Trp Lys Val His Lys Gly Lys Cys Tyr Trp
                               40                               45                               50
att gct gaa act aag aaa tct tgg aac aaa agt caa aat gac tgt gcc      412
Ile Ala Glu Thr Lys Lys Ser Trp Asn Lys Ser Gln Asn Asp Cys Ala
                               55                               60                               65
ata aac aat tca tat ctc atg gtg att caa gac att act gct atg gtg      460
Ile Asn Asn Ser Tyr Leu Met Val Ile Gln Asp Ile Thr Ala Met Val
70                               75                               80
aga ttt aac att tagaggtgac agcatccccc acactggcag ttaatttttt      512
Arg Phe Asn Ile
85
gtctacaaac ttggcaaaag tctgtgaaaa gaagtttcaa cttcatgtgt tattaactat      572
acaaatatta gttgaatgaa ttgttgaatt acaaaaaaaaa aaaaaaaaaa      621
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<210> 52

<211> 673

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 68..484

<220>

<221> sig_peptide

<222> 68..112

<223> Von Heijne matrix

score 4.93618539864455

seq AVVFVFSLLDCCA/LI

<400> 52

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ctatcagggg tgggtcgggg catccgagcg gggttgacgg aaggagcggc ggcgacggag      60
gaggagg atg gag gcg gtg gtg ttc gtc ttc tct ctc ctc gat tgt tgc      109
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      Met Glu Ala Val Val Phe Val Phe Ser Leu Leu Asp Cys Cys
      -15          -10          -5
gcg ctc atc ttc ctc tcg gtc tac ttc ata att aca ttg tct gat tta 157
Ala Leu Ile Phe Leu Ser Val Tyr Phe Ile Ile Thr Leu Ser Asp Leu
1          5          10          15
gaa tgt gat tac att aat gct aga tca tgt tgc tca aaa tta aac aag 205
Glu Cys Asp Tyr Ile Asn Ala Arg Ser Cys Cys Ser Lys Leu Asn Lys
          20          25          30
tgg gta att cca gaa ttg att ggc cat acc att gtc act gta tta ctg 253
Trp Val Ile Pro Glu Leu Ile Gly His Thr Ile Val Thr Val Leu Leu
          35          40          45
ctc atg tca ttg cac tgg ttc atc ttc ctt ctc aac tta cct gtt gcc 301
Leu Met Ser Leu His Trp Phe Ile Phe Leu Leu Asn Leu Pro Val Ala
          50          55          60
act tgg aat ata tat cga tac att atg gtg ccg agt ggt aac atg gga 349
Thr Trp Asn Ile Tyr Arg Tyr Ile Met Val Pro Ser Gly Asn Met Gly
          65          70          75
gtg ttt gat cca aca gaa ata cac aat cga ggg cag ctg aag lca cac 397
Val Phe Asp Pro Thr Glu Ile His Asn Arg Gly Gln Leu Lys Ser His
          80          85          90          95
atg aaa gaa gcc atg atc aag ctt ggt ttc cac ttg ctc tgc ttc ttc 445
Met Lys Glu Ala Met Ile Lys Leu Gly Phe His Leu Leu Cys Phe Phe
          100          105          110
atg tat ctt tat agt atg atc tta gct ttg ata aat gac tgaagctgga 494
Met Tyr Leu Tyr Ser Met Ile Leu Ala Leu Ile Asn Asp
          115          120
gaagccgtgg ttgaagtcag cctacactac agtgcacagt tgaggagcca gagacttctt 554
aaatcatcct tagaaccgtg accatagcag tatatatattt cctcttgga caaaaaacta 614
tttttgctgt atttttacca tataaagtat ttaaaaaaca cgaaaaaaaa aaaaaaaaaa 673

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<210> 53
 <211> 897
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..517

<220>
 <221> sig_peptide
 <222> 38..118
 <223> Von Heijne matrix
 score 7.20400999800742
 seq VLWLSGLSEPGAA/RQ

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<400> 53
agattgggac agtcgccagg gatggctgag cgtgaag atg cag cgg gtg tcc ggg 55
      Met Gln Arg Val Ser Gly
      -25
ctg ctc tcc tgg acg ctg agc aga gtc ctg tgg ctc tcc ggc ctc tct 103
Leu Leu Ser Trp Thr Leu Ser Arg Val Leu Trp Leu Ser Gly Leu Ser
      -20          -15          -10
gag ccg gga gct gcc cgg cag ccc cgg atc atg gaa gag aaa gcg cta 151
Glu Pro Gly Ala Ala Arg Gln Pro Arg Ile Met Glu Glu Lys Ala Leu
      -5          1          5          10
gag gtt tat gat ttg att aga act atc cgg gac cca gaa aag ccc aat 199
Glu Val Tyr Asp Leu Ile Arg Thr Ile Arg Asp Pro Glu Lys Pro Asn

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      15      20      25
act tta gaa gaa ctg gaa gtg gtc tcg gaa agt tgt gtg gaa gtt cag      247
Thr Leu Glu Glu Leu Glu Val Val Ser Glu Ser Cys Val Glu Val Gln
      30      35      40
gag ata aat gaa gaa gaa tat ctg gtt att atc agg ttc acg cca aca      295
Glu Ile Asn Glu Glu Glu Tyr Leu Val Ile Ile Arg Phe Thr Pro Thr
      45      50      55
gta cct cat tgc tct ttg gcg act ctt att ggg ctg tgc tta aga gta      343
Val Pro His Cys Ser Leu Ala Thr Leu Ile Gly Leu Cys Leu Arg Val
      60      65      70      75
aaa ctt cag cga tgt tta cca ttt aaa cat aag ttg gaa atc tac att      391
Lys Leu Gln Arg Cys Leu Pro Phe Lys His Lys Leu Glu Ile Tyr Ile
      80      85      90
tct gaa gga acc cac tca aca gaa gaa gac atc aat aag cag ata aat      439
Ser Glu Gly Thr His Ser Thr Glu Glu Asp Ile Asn Lys Gln Ile Asn
      95      100      105
gac aaa gag cga gtg gca gct gca atg gaa aac ccc aac tta cgg gaa      487
Asp Lys Glu Arg Val Ala Ala Ala Met Glu Asn Pro Asn Leu Arg Glu
      110      115      120
att gtg gaa cag tgt gtc ctt gaa cct gac tgatagctgt ttttaagagcc      537
Ile Val Glu Gln Cys Val Leu Glu Pro Asp
      125      130
actggcctgt aattgtttga tatatttgta actcttttgta taatgtcaga gactcatggt      597
taatacatag gtgatttgta cctcagagca ttttttaaag gattctttcc aagcgagatt      657
taattataag gtagtaccta atttgttcaa tgtataacat tctcaggatt tgtaacactt      717
aaatgatcag acagaataat attttctagt tattatgtgt aagatgagtt gctatttttc      777
tgatgctcat tctgatacaa ctatttttctg tgtcaaatat ctactgtgcc caaatgtact      837
caattttaat cattactctg taaaataaat aagcagatga ttcttataaa aaaaaaaaaa      897

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<210> 54
 <211> 1101
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 92..634

<220>
 <221> sig_peptide
 <222> 92..139
 <223> Von Heijne matrix
 score 7.36306712986597
 seq FLLLTCLFITGTS/VS

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<400> 54
cttaaaaaaa aaagtgcttg aaagagaagg ggacaaagga acaccagtat taagaggatt      60
ttccagtgtt tctggcagtt ggtccagaag g atg cct cca ttc ctg ctt ctc      112
                               Met Pro Pro Phe Leu Leu Leu
                               -15                               -10
acc tgc ctc ttc atc aca ggc acc tcc gtg tca ccc gtg gcc cta gat      160
Thr Cys Leu Phe Ile Thr Gly Thr Ser Val Ser Pro Val Ala Leu Asp
                               -5                               1                               5
cct tgt tct gct tac atc agc ctg aat gag ccc tgg agg aac act gac      208
Pro Cys Ser Ala Tyr Ile Ser Leu Asn Glu Pro Trp Arg Asn Thr Asp
                               10                               15                               20
cac cag ttg gat gag tct caa ggt cct cct cta tgt gac aac cat gtg      256
His Gln Leu Asp Glu Ser Gln Gly Pro Pro Leu Cys Asp Asn His Val

```

25	30	35	
aat ggg gag tgg tac cac ttc acg ggc atg gcg gga gat gcc atg cct			304
Asn Gly Glu Trp Tyr His Phe Thr Gly Met Ala Gly Asp Ala Met Pro			
40	45	50	55
acc ttc tgc ata cca gaa aac cac tgt gga acc cac gca cct gtc tgg			352
Thr Phe Cys Ile Pro Glu Asn His Cys Gly Thr His Ala Pro Val Trp			
	60	65	70
ctc aat ggc agc cac ccc cta gaa ggc gac ggc att gtg caa cgc cag			400
Leu Asn Gly Ser His Pro Leu Glu Gly Asp Gly Ile Val Gln Arg Gln			
	75	80	85
gct tgt gcc agc ttc aat ggg aac tgc tgt ctc tgg aac acc acg gtg			448
Ala Cys Ala Ser Phe Asn Gly Asn Cys Cys Leu Trp Asn Thr Thr Val			
	90	95	100
gaa gtc aag gct tgc cct gga ggc tac tat gtg tat cgt ctg acc aag			496
Glu Val Lys Ala Cys Pro Gly Gly Tyr Tyr Val Tyr Arg Leu Thr Lys			
	105	110	115
ccc agc gtc tgc ttc cac gtc tac tgt ggt cgt gag tac ctt ccc tgt			544
Pro Ser Val Cys Phe His Val Tyr Cys Gly Arg Glu Tyr Leu Pro Cys			
	120	125	130
gct ctt ttt ctc cac caa caa ggc cac agg tgg agt cca aaa gtg ccc			592
Ala Leu Phe Leu His Gln Gln Gly His Arg Trp Ser Pro Lys Val Pro			
	140	145	150
aat tat agg ata tgc agt tac agt ggc aac tat atc tca atc			634
Asn Tyr Arg Ile Cys Ser Tyr Ser Gly Asn Tyr Ile Ser Ile			
	155	160	165
tgaacaacat tgatgtgggg ctaaagatac tctgatttct gagatctctt cttagaactt			694
ctgaaaaatt cctgaagaaa tagaagggga aaggagctat gactttgatc agttcttttt			754
aattttgtct gaattccatt caaacaaaac attagaaaat gaaacattgg gccaggcgca			814
gtggctcatg cctgtaatcc cagcactttg ggaggctgag gcgggtggat cacaagatca			874
ggagttaaag accagcctgg ccaatatggt gaaaccctgt ctctactaga aatacaaaaa			934
ttagacaggc gtggtggcag gcaactgtaa ccccagctac ccgggaggct gaggcaggag			994
aattgcttga acccgggagg tggacgttgc ggtcaggcga aaatcgtgcc attgcactcc			1054
agcctgggtg acagagtgag actctgattc aaaaaaaaaa aaaaaaa			1101

<210> 55
 <211> 1047
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 27..767

<220>
 <221> sig_peptide
 <222> 27..80
 <223> Von Heijne matrix
 score 8.96664802487992
 seq LFCLAVLAASSFS/KA

<400> 55	
agcagaggcc ctacaccac cgaggc atg ggg ctc cct ggg ctg ttc tgc ttg	53
Met Gly Leu Pro Gly Leu Phe Cys Leu	
-15	-10
gcc gtg ctg gct gcc agc agc ttc tcc aag gca cgg gag gaa gaa att	101
Ala Val Leu Ala Ala Ser Ser Phe Ser Lys Ala Arg Glu Glu Glu Ile	
-5	1
acc cct gtg gtc tcc att gcc tac aaa gtc ctg gaa gtt ttc ccc aaa	149

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<220>
<221> CDS
<222> 4..399

<220>
<221> sig peptide
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<222> 4..126

<223> Von Heijne matrix

score 4.34454795165846

seq RVVSWLFSIVVFG/SI

<400> 56

acg atg gaa ggg ggt gcg tac gga gcg ggc aaa gcc ggg ggc gcc ttc	48
Met Glu Gly Gly Ala Tyr Gly Ala Gly Lys Ala Gly Gly Ala Phe	
-40 -35 -30	
gac ccc tac acc ctg gtc cgg cag ccg cac acc atc ctg cgc gtc gtg	96
Asp Pro Tyr Thr Leu Val Arg Gln Pro His Thr Ile Leu Arg Val Val	
-25 -20 -15	
tct tgg ctg ttc tcc ata gtg gtg ttc ggc tcc atc gtg aac gag ggc	144
Ser Trp Leu Phe Ser Ile Val Val Phe Gly Ser Ile Val Asn Glu Gly	
-10 -5 1 5	
tac ctc aac agc gcc tcc gag ggg gag cag ttc tgc atc tac aac cgc	192
Tyr Leu Asn Ser Ala Ser Glu Gly Glu Gln Phe Cys Ile Tyr Asn Arg	
10 15 20	
aac ccc aac gcc tgc agc tat ggc gtg gcc gtg ggc gtg ctc gcc ttc	240
Asn Pro Asn Ala Cys Ser Tyr Gly Val Ala Val Gly Val Leu Ala Phe	
25 30 35	
ctc acc tgc ctg ctg tac ctg gcc ctg gac gtg tac ttc ccg cag atc	288
Leu Thr Cys Leu Leu Tyr Leu Ala Leu Asp Val Tyr Phe Pro Gln Ile	
40 45 50	
agc agc gtc aag gac cgc aag aaa gcc gtc ctg tcc gac atc ggt gtc	336
Ser Ser Val Lys Asp Arg Lys Lys Ala Val Leu Ser Asp Ile Gly Val	
55 60 65 70	
tcg ggt gag ccc cac cca gca ggt acc ccc tgc aca gag tct aca gag	384
Ser Gly Glu Pro His Pro Ala Gly Thr Pro Cys Thr Glu Ser Thr Glu	
75 80 85	
ggc tgt ccc ggg cca taggaggcgg ctgccaccct tcttcccatg tttcagatga	439
Gly Cys Pro Gly Pro	
90	
gggaaatgag ccttctgggc tttcctctggt ttcgtgggat tctgctacct ggccaaccag	499
tggcaggtct ccaagcccaa ggacaaccca ctgaacgaag ggacggacgc agcccgggcc	559
gccatcgccct tctccttttt ctccatcttc acctggagcc tgaccgcagc cctggccgtg	619
cggagattca aggacctaag cttccaggag gagtacagca cactgttccc tgcttcggca	679
cagccgtagg cctccccggc ttgcagaggc cggcagccct gtatcaccac tggcagtgag	739
gtggcaggag cagcctagtg ccagaaatgt ccaagatgcc agggcatgca gggcagtgga	799
aggetggcct gaggaaccaa ttcaggttct ccactgactc attcattcct tcaccgcctc	859
cttcattgat tcttcatgcg ttcattcatt cagtaaacat ttattgagta aaaaaaaaaa	919
aaaaaa	925

<210> 57

<211> 1240

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 127..879

<220>

<221> sig_peptide

<222> 127..198

<223> Von Heijne matrix

score 5.38660866264012

seq ALCSVCSMSVLRA/YP

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<400> 57
agtctaggat cctcacacca gctacttgca agggagaagg aaaaggccag taaggcctgg      60
gccaggagag tcccgacagg agtgtcaggt ttcaatctca gcaccagcca ctcagagcag      120
ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc      168
      Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
      -20                               -15
agc gtc tgc agc atg agc gtc ctc aga gcc tat ccc aat gcc tcc cca      216
Ser Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
-10                               -5                               1                               5
ctg ctc ggc tcc agc tgg ggt ggc ctg atc cac ctg tac aca gcc aca      264
Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr
      10                               15                               20
gcc agg aac agc tac cac ctg cag atc cac aag aat ggc cat gtg gat      312
Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp
      25                               30                               35
ggc gca ccc cat cag acc atc tac agt gcc ctg atg atc aga tca gag      360
Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu
      40                               45                               50
gat gct ggc ttt gtg gtg att aca ggt gtg atg agc aga aga tac ctc      408
Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu
      55                               60                               65                               70
tgc atg gat ttc aga ggc aac att ttt gga tca cac tat ttc gac ccg      456
Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro
      75                               80                               85
gag aac tgc agg ttc caa cac cag acg ctg gaa aac ggg tac gac gtc      504
Glu Asn Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val
      90                               95                               100
tac cac tct cct cag tat cac ttc ctg gtc agt ctg ggc cgg gcg aag      552
Tyr His Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys
      105                               110                               115
aga gcc ttc ctg cca ggc atg aac cca ccc ccg tac tcc cag ttc ctg      600
Arg Ala Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu
      120                               125                               130
tcc cgg agg aac gag atc ccc cta att cac ttc aac acc ccc ata cca      648
Ser Arg Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro
      135                               140                               145                               150
cgg cgg cac acc cgg agc gcc gag gac gac tgc gag cgg gac ccc ctg      696
Arg Arg His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu
      155                               160                               165
aac gtg ctg aag ccc cgg gcc cgg atg acc ccg gcc ccg gcc tcc tgt      744
Asn Val Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys
      170                               175                               180
tca cag gag ctc ccg agc gcc gag gac aac agc ccg atg gcc agt gac      792
Ser Gln Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp
      185                               190                               195
cca tta ggg gtg gtc agg ggc ggt cga gtg aac acg cac gct ggg gga      840
Pro Leu Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly
      200                               205                               210
acg ggc ccg gaa ggc tgc cgc ccc ttc gcc aag ttc atc tagggctcgct      889
Thr Gly Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
      215                               220                               225
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ccttgacggt ccgaggatgg gaaagggtgac aggggcatgt atggaatttg ctgcttctct      1009
gggggtccctt ccacaggagg tctgtgaga accaaccttt gagggcccaag tcatgggggtt      1069
tcaccgcctt cctcactcca tatagaacac ctttcccaat aggaaacccc aacaggtaaa      1129
ctagaaattt ccccttcatt aaggtagaga gaaggggtct ctccaacat atttctcttc      1189
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> 156..566

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 <223> Von Heijne matrix
 score 5.67458379966095
 seq LVSMAGRVCLCQG/SA

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cctcactcct ggcgtctgag tctctggcgt agccc atg ctg agt ggg cgg ctg      173
                                Met Leu Ser Gly Arg Leu
                                -20
gtc ctg ggt ctg gtc tcc atg gct ggc cgc gtt tgt ttg tgc cag ggc      221
Val Leu Gly Leu Val Ser Met Ala Gly Arg Val Cys Leu Cys Gln Gly
-15 -10 -5
agc gcg gga tcc ggg gcc atc ggt ccg gtg gag gcc gcc att cgc acg      269
Ser Ala Gly Ser Gly Ala Ile Gly Pro Val Glu Ala Ala Ile Arg Thr
1 5 10 15
aag ttg gag gag gcc ctg agc ccc gag gtg cta gag ctt cgc aac gag      317
Lys Leu Glu Glu Ala Leu Ser Pro Glu Val Leu Glu Leu Arg Asn Glu
20 25 30
agc ggt ggc cac gcg gtc ccg cca ggc agt gag act cac ttc cgc gtg      365
Ser Gly Gly His Ala Val Pro Pro Gly Ser Glu Thr His Phe Arg Val
35 40 45
gct gtg gtg agc tct cgt ttc gag gga ctg agc ccc cta caa cga cac      413
Ala Val Val Ser Ser Arg Phe Glu Gly Leu Ser Pro Leu Gln Arg His
50 55 60
cgg ctg gtc cac gca gcg ctg gcc gag gag ctg gga ggt ccg gtc cat      461
Arg Leu Val His Ala Ala Leu Ala Glu Glu Leu Gly Gly Pro Val His
65 70 75 80
gcg ctg gcc atc cag gca cgg acc ccc gcc cag tgg aga gag aac tct      509
Ala Leu Ala Ile Gln Ala Arg Thr Pro Ala Gln Trp Arg Glu Asn Ser
85 90 95
cag ctg gac act agc ccc cca tgc ctg ggt ggg aac aag aaa act cta      557
Gln Leu Asp Thr Ser Pro Pro Cys Leu Gly Gly Asn Lys Lys Thr Leu
100 105 110
gga acc ccc tgaaccccaa gagagggagg accaggatcc gaatgggctg      606
Gly Thr Pro
115
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gacctctggg cccattctg ttgggggtcca tacatactct ccgaagatag caacttgctt      726
caggtcaaag tgaaccgag aaaagagaag aatcactcac tactgctctt gccctggact      786
attcaggaag ggcagcccg atgttccatg ttaaactctg acagaattgc accagacctg      846
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<212> DNA
<213> Homo sapiens

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<222> 35..1657

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seq SGLLLQVLFRLIT/FV

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-25
ggc cac gcg gcc cgg ctg gcc tcc tcc ggt ctc ctc ctg cag gtg ttg 103
Gly His Ala Ala Arg Leu Ala Ser Ser Gly Leu Leu Leu Gln Val Leu
-20 -15 -10
ttt cgg ttg atc acc ttt gtc ttg aat gca ttt att ctt cgc ttc ctg 151
Phe Arg Leu Ile Thr Phe Val Leu Asn Ala Phe Ile Leu Arg Phe Leu
-5 1 5 10
tca aag gaa atc gtt ggc gta gta aat gta aga cta acg ctg ctt tac 199
Ser Lys Glu Ile Val Gly Val Val Asn Val Arg Leu Thr Leu Leu Tyr
15 20 25
tca acc acc ctc ttc ctg gcc aga gag gcc ttc cgc aga gca tgt ctc 247
Ser Thr Thr Leu Phe Leu Ala Arg Glu Ala Phe Arg Arg Ala Cys Leu
30 35 40
agt ggg ggc acc cag cga gac tgg agc cag acc ctc aac ctg ctg tgg 295
Ser Gly Gly Thr Gln Arg Asp Trp Ser Gln Thr Leu Asn Leu Leu Trp
45 50 55
cta aca gtc ccc ctg ggt gtg ttt tgg tcc tta ttc ctg ggc tgg atc 343
Leu Thr Val Pro Leu Gly Val Phe Trp Ser Leu Phe Leu Gly Trp Ile
60 65 70 75
tgg ttg cag ctg ctt gaa gtg cct gat cct aat gtt gtc cct cac tat 391
Trp Leu Gln Leu Leu Glu Val Pro Asp Pro Asn Val Val Pro His Tyr
80 85 90
gca act gga gtg gtg ctg ttt ggt ctc tcg gca gtg gtg gag ctt cta 439
Ala Thr Gly Val Val Leu Phe Gly Leu Ser Ala Val Val Glu Leu Leu
95 100 105
gga gag ccc ttt tgg gtc ttg gca caa gca cat atg ttt gtg aag ctc 487
Gly Glu Pro Phe Trp Val Leu Ala Gln Ala His Met Phe Val Lys Leu
110 115 120
aag gtg att gca gag agc ctg tcg gta att ctt aag agc gtt ctg aca 535
Lys Val Ile Ala Glu Ser Leu Ser Val Ile Leu Lys Ser Val Leu Thr
125 130 135
gct ttt ctc gtg ctg tgg ttg cct cac tgg gga ttg tac att ttc tct 583
Ala Phe Leu Val Leu Trp Leu Pro His Trp Gly Leu Tyr Ile Phe Ser
140 145 150 155
ttg gcc cag ctt ttc tat acc aca gtt ctg gtg ctc tgc tat gtt att 631
Leu Ala Gln Leu Phe Tyr Thr Thr Val Leu Val Leu Cys Tyr Val Ile
160 165 170
tat ttc aca aag tta ctg ggt tcc cca gaa tca acc aag ctt caa act 679
Tyr Phe Thr Lys Leu Leu Gly Ser Pro Glu Ser Thr Lys Leu Gln Thr
175 180 185
ctt cct gtc tcc aga ata aca gat ctg tta ccc aat att aca aga aat 727

Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu	Leu	Pro	Asn	Ile	Thr	Arg	Asn	
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Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala	Lys	Leu	Thr	Trp	Ser	Phe	Phe	
		205					210				215					
aaa	cag	tct	ttc	ttg	aaa	cag	att	ttg	aca	gaa	ggc	gag	cga	tat	gtg	823
Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu	Thr	Glu	Gly	Glu	Arg	Tyr	Val	
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Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe	Gly	Asp	Gln	Gly	Val	Tyr	Asp	
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ata	gtg	aat	aat	ctt	ggc	tcc	ctt	gtg	gcc	aga	tta	att	ttc	cag	cca	919
Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val	Ala	Arg	Leu	Ile	Phe	Gln	Pro	
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Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe	Ala	Lys	Val	Leu	Glu	Arg	Gly	
		270					275					280				
aag	gat	gcc	aca	ctt	cag	aag	cag	gag	gac	ggt	gct	gtg	gct	gct	gca	1015
Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu	Asp	Val	Ala	Val	Ala	Ala	Ala	
		285				290					295					
gtc	ttg	gag	tcc	ctg	ctc	aag	ctg	gcc	ctg	ctg	gcc	ggc	ctg	acc	atc	1063
Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala	Leu	Leu	Ala	Gly	Leu	Thr	Ile	
300					305					310					315	
act	ggt	ttt	ggc	ttt	gcc	tat	tct	cag	ctg	gct	ctg	gat	atc	tac	gga	1111
Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln	Leu	Ala	Leu	Asp	Ile	Tyr	Gly	
				320				325						330		
ggg	acc	atg	ctt	agc	tca	gga	tcc	ggt	cct	ggt	ttg	ctg	cgt	tcc	tac	1159
Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly	Pro	Val	Leu	Leu	Arg	Ser	Tyr	
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tgt	ctc	tat	ggt	ctc	ctg	ctt	gcc	atc	aat	gga	gtg	aca	gag	tgt	tta	1207
Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile	Asn	Gly	Val	Thr	Glu	Cys	Leu	
		350					355					360				
aca	ttt	gct	gcc	atg	agc	aaa	gag	gag	gtc	gac	agg	tac	aat	ttt	gtg	1255
Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu	Val	Asp	Arg	Tyr	Asn	Phe	Val	
		365				370				375						
atg	ctg	gcc	ctg	tcc	tcc	tca	ttc	ctg	gtg	tta	tcc	tat	ctc	ttg	acc	1303
Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu	Val	Leu	Ser	Tyr	Leu	Leu	Thr	
380					385					390					395	
cgt	tgg	tgt	ggc	agc	gtg	ggc	ttc	atc	ttg	gcc	aac	tgc	ttt	aac	atg	1351
Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile	Leu	Ala	Asn	Cys	Phe	Asn	Met	
			400					405						410		
ggc	att	cgg	atc	acg	cag	agc	ctt	tgc	ttc	atc	cac	cgc	tac	tac	cga	1399
Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys	Phe	Ile	His	Arg	Tyr	Tyr	Arg	
			415				420					425				
agg	agc	ccc	cac	agg	ccc	ctg	gct	ggc	ctg	cac	cta	tcg	cca	gtc	ctg	1447
Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly	Leu	His	Leu	Ser	Pro	Val	Leu	
		430				435					440					
ctc	ggg	aca	ttt	gcc	ctc	agt	ggt	ggg	ggt	act	gct	ggt	tcg	gag	gta	1495
Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly	Val	Thr	Ala	Val	Ser	Glu	Val	
		445				450					455					
ttc	ctc	tgc	tgt	gat	cag	ggc	tgg	cca	gcc	aga	ctg	gca	cac	att	gct	1543
Phe	Leu	Cys	Cys	Asp	Gln	Gly	Trp	Pro	Ala	Arg	Leu	Ala	His	Ile	Ala	
460					465					470					475	
gtg	ggg	gcc	ttc	tgt	ctg	gga	gca	act	ctc	ggg	aca	gca	ttc	ctc	aca	1591
Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala	Thr	Leu	Gly	Thr	Ala	Phe	Leu	Thr	
				480				485						490		
gag	acc	aag	ctg	atc	cat	ttc	ctc	agg	act	cag	tta	ggt	gtg	ccc	aga	1639
Glu	Thr	Lys	Leu	Ile	His	Phe	Leu	Arg	Thr	Gln	Leu	Gly	Val	Pro	Arg	

495 500 505
 cgc act gac aaa atg aca tgacttcagg gaagcctgga cacccgaggc 1687
 Arg Thr Asp Lys Met Thr
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 acctggacca gctatgggta gttctgtggg tggaacacat tctgtgtaag agccccactg 1747
 agggctctgc agcggagtga cagcaacccc agagatgagg caccagagag tgccactgca 1807
 tgagacacct gtgaccattc gaagtctgaa atgcgggggg ggagtttcat ttttaagtga 1867
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 77..127
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 seq RIVSAALLAFVQT/HL

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 Met Glu Leu Glu Arg Ile Val Ser Ala Ala Leu Leu
 -15 -10
 gcc ttt gtc cag aca cac ctc ccg gag gcc gac ctc agt ggc ttg gat 160
 Ala Phe Val Gln Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp
 -5 1 5 10
 gag gtc atc ttc tcc tat gtg ctt ggg gtc ctg gag gac ctg ggc ccc 208
 Glu Val Ile Phe Ser Tyr Val Leu Gly Val Leu Glu Asp Leu Gly Pro
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 Ser Gly Pro Ser Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met
 30 35 40
 atg gag gcc tat gtg cct ggc ttc gcc cac atc ccc agg ggc aca ata 304
 Met Glu Ala Tyr Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile
 45 50 55
 ggg gac atg atg cag aag ctc tca ggg cag ctg agc gat gcc agg aac 352
 Gly Asp Met Met Gln Lys Leu Ser Gly Gln Leu Ser Asp Ala Arg Asn
 60 65 70 75
 aaa gag aac ctg caa ccg cag agc tct ggt gtc caa ggt cag gtg ccc 400
 Lys Glu Asn Leu Gln Pro Gln Ser Ser Gly Val Gln Gly Gln Val Pro
 80 85 90
 atc tcc cca gag ccc ctg cag cgg ccc gaa atg ctc aaa gaa gag act 448
 Ile Ser Pro Glu Pro Leu Gln Arg Pro Glu Met Leu Lys Glu Glu Thr
 95 100 105
 agg tct tcg gct gct gct gct gca gac acc caa gat gag gca act ggc 496
 Arg Ser Ser Ala Ala Ala Ala Ala Asp Thr Gln Asp Glu Ala Thr Gly
 110 115 120
 gct gag gag gag ctt ctg cca ggg gtg gat gta ctc ctg gag gtg ttc 544
 Ala Glu Glu Glu Leu Leu Pro Gly Val Asp Val Leu Leu Glu Val Phe
 125 130 135

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Pro Thr Cys Ser Val Glu Gln Ala Gln Trp Val Leu Ala Lys Ala Arg
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ggg gac ttg gaa gaa gct gtg cag atg ctg gta gag gga aag gaa gag      640
Gly Asp Leu Glu Glu Ala Val Gln Met Leu Val Glu Gly Lys Glu Glu
          160          165          170
ggg cct gca gcc tgg gag ggc ccc aac cag gac ctg ccc aga cgc ctc      688
Gly Pro Ala Ala Trp Glu Gly Pro Asn Gln Asp Leu Pro Arg Arg Leu
          175          180          185
aga ggc ccc caa aag gat gag ctg aag tcc ttc atc ctg cag aag tac      736
Arg Gly Pro Gln Lys Asp Glu Leu Lys Ser Phe Ile Leu Gln Lys Tyr
          190          195          200
atg atg gtg gat agc gca gag gat cag aag att cac cgg ccc atg gct      784
Met Met Val Asp Ser Ala Glu Asp Gln Lys Ile His Arg Pro Met Ala
          205          210          215
ccc aag gag gcc ccc aag aag ctg atc cga tac atc gac aac cag gta      832
Pro Lys Glu Ala Pro Lys Lys Leu Ile Arg Tyr Ile Asp Asn Gln Val
          220          225          230          235
gtg agc acc aaa ggg gag cga ttc aaa gat gtg cgg aac cct gag gcc      880
Val Ser Thr Lys Gly Glu Arg Phe Lys Asp Val Arg Asn Pro Glu Ala
          240          245          250
gag gag atg aag gcc aca tac atc aac ctc aag cca gcc aga aag tac      928
Glu Glu Met Lys Ala Thr Tyr Ile Asn Leu Lys Pro Ala Arg Lys Tyr
          255          260          265
cgc ttc cat tgaggcactc gccggactct gcccgagcct tctaggctca      977
Arg Phe His
          270
gatcccagag ggatgcagga gccctataacc cctacacagg ggccccctaa ctctgtccc      1037
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<213> Homo sapiens

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<222> 9..503

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<222> 9..113
<223> Von Heijne matrix
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Pro His Ala Leu Arg Pro Leu Leu Leu Leu Pro Leu Val Leu Leu Pro
      -20          -15          -10
ccc ctg gca gca gct gca gcg ggc cca aac cga tgt gac acc ata tac      146
Pro Leu Ala Ala Ala Ala Ala Gly Pro Asn Arg Cys Asp Thr Ile Tyr
      -5          1          5          10
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Gly Gly Glu Leu Glu Thr Ile Cys Arg Ser Trp Asn Tyr Phe His Ala	
30 35 40	
tgt gcc tct cag gtc ctg tca ggc tgt ccg gag gag gca gct gca gtg	290
Cys Ala Ser Gln Val Leu Ser Gly Cys Pro Glu Glu Ala Ala Ala Val	
45 50 55	
tgg gaa tca cta cag caa gaa gct cgc cag gcc ccc cgt ccg aat aac	338
Trp Glu Ser Leu Gln Gln Glu Ala Arg Gln Ala Pro Arg Pro Asn Asn	
60 65 70 75	
ttg cac act ctg tgc ggt gcc ccg gtg cat gtt cgg gag cgc ggc aca	386
Leu His Thr Leu Cys Gly Ala Pro Val His Val Arg Glu Arg Gly Thr	
80 85 90	
ggc tcc gaa acc aac cag gag acg ctg cgg gct aca gcg cct gca ctc	434
Gly Ser Glu Thr Asn Gln Glu Thr Leu Arg Ala Thr Ala Pro Ala Leu	
95 100 105	
ccc atg gcc cct gcg ccc cca ctg ctg gcg gct gct ctg gct ctg gcc	482
Pro Met Ala Pro Ala Pro Pro Leu Leu Ala Ala Ala Leu Ala Leu Ala	
110 115 120	
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Tyr Leu Leu Arg Pro Leu Ala	
125 130	
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Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala	
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Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly	
5 10 15	
gga aag tca tca ggc aga cgc caa ggc att aag aaa atg gaa ggt cac	197
Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His	
20 25 30	
tat gtt cat gct ggg aac atc att gca aca cag cgc cat ttc cgc tgg	245
Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp	
35 40 45 50	

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His Pro Gly Ala His Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala
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ctg gaa gag ggg ata gtc cgc tac act aag gag gtc tac gtg cct cat      341
Leu Glu Glu Gly Ile Val Arg Tyr Thr Lys Glu Val Tyr Val Pro His
                    70                                75                                80
ccc aga aac acg gag gct gtg gat ctg atc acc agg ctg ccc aag ggt      389
Pro Arg Asn Thr Glu Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly
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gct gtg ctc tac aag act ttt gtc cac gtg gtt cct gcc aag cct gag      437
Ala Val Leu Tyr Lys Thr Phe Val His Val Val Pro Ala Lys Pro Glu
                    100                               105                               110
ggc acc ttc aaa ctg gta gct atg ctt tgatgtcctg ttgaggccat      484
Gly Thr Phe Lys Leu Val Ala Met Leu
115                                120
cggacagaga ctggagccca ggtgacagga gatggtgata ccagaagtca aggggtgggg      544
tggcgacacg gcctcccag gaagaggtct gcttgatggt gactctgcag gagactctga      604
agtgactgct gggaaaccct ttgggaqacc tgacctgggg ccaaaaataa agtgagccag      664
cgatcatgaac gcatgctatt tagggacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      722

<210> 63
<211> 1442
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 178..1050

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<222> 178..279
<223> Von Heijne matrix
      score 10.0571391689271
      seq FLCLLSALLLTEG/KK

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agtgcattgc tggagcgagg agaagctcac gaatcagctg cagggtctctg ttttgaaaaa      60
gcagagatac agaggcagag gaaaagggca ctcctatgtg acctgttctt agagcaagac      120
aatcaccatc tgaattccag aagccctggt catggttggg gatattttct cgactgc      177
atg gaa tca gaa aga agc aaa agg atg gga aat gcc tgc att ccc ctg      225
Met Glu Ser Glu Arg Ser Lys Arg Met Gly Asn Ala Cys Ile Pro Leu
                    -30                                -25                                -20
aaa aga att gct tat ttc cta tgt ctc tta tct gcg ctt ttg ctg act      273
Lys Arg Ile Ala Tyr Phe Leu Cys Leu Leu Ser Ala Leu Leu Thr
                    -15                                -10                                -5
gag ggg aag aaa cca gcg aag cca aaa tgc cct gcc gtg tgt act tgt      321
Glu Gly Lys Lys Pro Ala Lys Pro Lys Cys Pro Ala Val Cys Thr Cys
                    1                                5                                10
acc aaa gat aat gct tta tgt gag aat gcc aga tcc att cca cgc acc      369
Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr
                    15                                20                                25                                30
gtt cct cct gat gtt atc tca tta tcc ttt gtg aga tct ggt ttt act      417
Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Gly Phe Thr
                    35                                40                                45
gaa atc tca gaa ggg agt ttt tta ttc acg cca tcg ctg cag ctc ttg      465
Glu Ile Ser Glu Gly Ser Phe Leu Phe Thr Pro Ser Leu Gln Leu Leu
                    50                                55                                60

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tta ttc aca tcg aac tcc ttt gat gtg atc agt gat gat gct ttt att	513
Leu Phe Thr Ser Asn Ser Phe Asp Val Ile Ser Asp Asp Ala Phe Ile	
65 70 75	
ggg ctt cca cat cta gag tat tta ttc ata gaa aac aac aac atc aag	561
Gly Leu Pro His Leu Glu Tyr Leu Phe Ile Glu Asn Asn Asn Ile Lys	
80 85 90	
tca att tca aga cat act ttc cgg gga cta aag tca tta att cac ttg	609
Ser Ile Ser Arg His Thr Phe Arg Gly Leu Lys Ser Leu Ile His Leu	
95 100 105 110	
agc ctt gca aac aac aat ctc cag aca ctc cca aaa gat att ttc aaa	657
Ser Leu Ala Asn Asn Asn Leu Gln Thr Leu Pro Lys Asp Ile Phe Lys	
115 120 125	
ggc ctg gat tct tta aca aat gtg gac ctg agg ggt aat tca ttt aat	705
Gly Leu Asp Ser Leu Thr Asn Val Asp Leu Arg Gly Asn Ser Phe Asn	
130 135 140	
tgt gac tgt aaa ctg aaa tgg cta gtg gaa tgg ctt ggc cac acc aat	753
Cys Asp Cys Lys Leu Lys Trp Leu Val Glu Trp Leu Gly His Thr Asn	
145 150 155	
gca act gtt gaa gac atc tac tgc gaa ggc ccc cca gaa tac aag aag	801
Ala Thr Val Glu Asp Ile Tyr Cys Glu Gly Pro Pro Glu Tyr Lys Lys	
160 165 170	
cgc aaa atc aat agt ctc tcc tcg aag gat ttc gat tgc atc att aca	849
Arg Lys Ile Asn Ser Leu Ser Ser Lys Asp Phe Asp Cys Ile Ile Thr	
175 180 185 190	
gaa ttt gca aag tct caa gac ctg cct tat caa tca ttg tcc ata gac	897
Glu Phe Ala Lys Ser Gln Asp Leu Pro Tyr Gln Ser Leu Ser Ile Asp	
195 200 205	
act ttt tct tat ttg aat gat gag tat gta gtc atc gct cag cct ttt	945
Thr Phe Ser Tyr Leu Asn Asp Glu Tyr Val Val Ile Ala Gln Pro Phe	
210 215 220	
act gga aaa tgc att ttc ctt gaa tgg gac cat gtg gaa aag acc ttc	993
Thr Gly Lys Cys Ile Phe Leu Glu Trp Asp His Val Glu Lys Thr Phe	
225 230 235	
cgg aat tat gac aac att aca gtt tta agg gaa ata cac aga ttt aca	1041
Arg Asn Tyr Asp Asn Ile Thr Val Leu Arg Glu Ile His Arg Phe Thr	
240 245 250	
aac atg tca tagttgactt aagcgcata gacaccaa tctgtggctg	1090
Asn Met Ser	
255	
ccatcagaaa ttttctacag tacatgaccc ggatgaactc aatgcatgat gactcttctt	1150
atcacacttg caaatgaatg cctttcaaac attgagactg ctagaaccaa gcactaccag	1210
tatctccatc cttaactgtc cagtccagtg atgtgggaag ttacctttta taagacaaaa	1270
tttaattgtg taactgttct ttgcagtga gatgtgtaaa taagcgttta atggatatctg	1330
ttactccaaa aagaaatatt aatatgtact ttccattta ttattcatg tgtacagaaa	1390
caactgccaa ataaaatggt tacattttct ttcagaaaaa aaaaaaaaaa aa	1442

<210> 64

<211> 795

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 32..274

<220>

<221> sig_peptide

<222> 32..178

<223> Von Heijne matrix
 score 4.30837886795471
 seq LMVELLKVFFVEA/AV

<400> 64

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gttccggttg gcgcgcgttg aggctgcggt c atg gag gga gca gga gct gga      52
                               Met Glu Gly Ala Gly Ala Gly
                               -45
tcc ggc ttc cgg aag gag ctg gtg agc agg ctg ctg cac ctg cac ttc      100
Ser Gly Phe Arg Lys Glu Leu Val Ser Arg Leu Leu His Leu His Phe
-40                               -35                               -30
aag gat gac aag acc aaa gtg agc ggg gac gcg ctg cag ctc atg gtg      148
Lys Asp Asp Lys Thr Lys Val Ser Gly Asp Ala Leu Gln Leu Met Val
-25                               -20                               -15
gag ttg ctg aag gtc ttc gtt gtg gaa gca gca gtc cgc ggc gtg cgg      196
Glu Leu Leu Lys Val Phe Val Val Glu Ala Ala Val Arg Gly Val Arg
-10                               -5                               1                               5
cag gcc cag gca gaa gac gcg ctc cgt gtg gac gtg gac cag ctg gag      244
Gln Ala Gln Ala Glu Asp Ala Leu Arg Val Asp Val Asp Gln Leu Glu
10                               15                               20
aag gtg ctt ccg cag ctg ctc ctg gac ttc tagggatctc agccgtggct      294
Lys Val Leu Pro Gln Leu Leu Leu Asp Phe
25                               30
gaggccaccc ccagaggagc ccctggtcca cagaagcagg ccttggtgtt ccagcggcct      354
ctgataagag gcaggaagg acctgaagga tttggagttg attcaaaca gatctctggg      414
agtctccagc ctgtgcagaa ggggcaggac tgcagtgcac tgcgggcctt ggagtgtcca      474
gtggggacac tgggtgtgga aggggcagca cctggggagt cctgcctct cctccctggg      534
acaatagtgt gcatgccacc cggggtccta caggcagggt ctgggaaagg cctggccagc      594
aggtagcctg tgtgtttgac aaacagcagc tggcagcgct gcctcctgcc cacattcctg      654
ccacccgaca tcaaagctgg cgtgtgacct ttccagccat gcgatattcc ccttgggaaga      714
tgcttcccca ggctataaat ttgttctcac aaagcaacat caataaatca aaactgtctc      774
tctcaaaaaa aaaaaaaaaa a                                         795

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<210> 65
 <211> 1236
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 222..920

<220>
 <221> sig_peptide
 <222> 222..311
 <223> Von Heijne matrix
 score 4.35083245061594
 seq VAHALSLPAESYG/ND

<400> 65

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accgaaaatt actgacgagt caatcacctc agatctctca agcagtcag cctacgcaac      60
agtactccac ctctgcgcct gtgcggggag ggtaaggcgg ggccagcaac ttcctcagct      120
ggagggagag cgcacgggtg agccgccagt tgagaaggac tctgatccgg ctacgcttcc      180
caatcagctg cggaaggagc cacgctttcg ggggttgcaa g atg gcg gcc acc agt      236
                               Met Ala Ala Thr Ser
                               -30
gga act gat gag ccg gtt tcc ggg gag ttg gtg tct gtg gca cat gcg      284
Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val Ser Val Ala His Ala

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<220>
 <221> sig_peptide
 <222> 101..160
 <223> Von Heijne matrix
 score 9.32665652007071
 seq LFLCYLLLFTCSG/VE

<400> 66
 ttactcgctg ctgtgcccac ctatcagcag gctccgggct gaagattgct tctcttctct 60
 cctccaaggt ctagtgacgg agcccgcgcg cggcgccacc atg cgg cag aag gcg 115
 Met Arg Gln Lys Ala
 -20
 gta tcg ctt ttc ttg tgc tac ctg ctg ctc ttc act tgc agt ggg gtg 163
 Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe Thr Cys Ser Gly Val
 -15 -10 -5 1
 gag gca ggt aag aaa aag tgc tcg gag agc tcg gac agc ggc tcc ggg 211
 Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser Gly
 5 10 15
 ttc tgg aag gcc ctg acc ttc atg gcc gtc gga gga gga ctc gca gtc 259
 Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly Gly Gly Leu Ala Val
 20 25 30
 gcc ggg ctg ccc gcg ctg ggc ttc acc ggc gcc ggc atc gcg gcc aac 307
 Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala Asn
 35 40 45
 tcg gtg gct gcc tcg ctg atg agc tgg tct gcg atc ctg aat ggg ggc 355
 Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly Gly
 50 55 60 65
 tagtggccac gctgcagagc ctccggggctg gtggcagcag cgtcgtcata ggtaatatg 415
 gtgccttgat gggctacgcc acccacaagt atctcgatag tgaggaggat gaggagtagc 475
 cagcagctcc cagaacctct tcttccttct tggcctaact ctccagtta ggatctagaa 535
 ctttgccctt tttttttttt tttttttttt ttgagatggg ttctcactat attgtccagg 595
 ctagagtgcg gkggctattc acagatgcga acatagtaca ctgcagcctc caactcctag 655
 cctcaagtga tcctcctgtc tcaacctccc aagtaggatt acaagcatgc gccgacgatg 715
 cccaraatcc araactttgt ctatcactct ccccaacaac ctagatgtga aaacagaata 775
 aacttcaccc agaaaaaaaa aaammacaar aaaaaaaaaa aaaaaaaaaa aaaaaaaaaam 835
 aaaaaaaaaa rrraaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 881

<210> 67
 <211> 524
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 173..487
 <220>
 <221> sig_peptide
 <222> 173..301
 <223> Von Heijne matrix
 score 4.27484469223909
 seq AGSLVATLQSVGA/AG

<400> 67
 agggcagagt aggcgcgtcc ctactggatg gagggggaag taacacccca agaacgctgt 60
 catttcctgg gccaaagtgg gaccgggacg gcctcaccat gatgaaacgg gcagctgctg 120
 ctgcagtggg aggagccctg gcagtggggg ctgtgccgtg gtgctcagtg cc atg ggc 178
 Met Gly


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ttc act ggg gca gga atc gcc gcg tcc tcc ata gca gcc aag atg atg      226
Phe Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met
   -40                -35                -30
tcc gca gca gcc att gcc aac ggg ggt ggt gtt tct gcg ggg agc ctg      274
Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu
  -25                -20                -15                -10
gtg gct act ctg cag tcc gtg ggg gca gct gga ctc tcc aca tca tcc      322
Val Ala Thr Leu Gln Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser
           -5                1                5
aac atc ctc ctg gcc tct gtt ggg tca gtg ttg ggg gcc tgc ttg ggg      370
Asn Ile Leu Leu Ala Ser Val Gly Ser Val Leu Gly Ala Cys Leu Gly
           10                15                20
aat tca cct tct tct tct ctc cca gct gaa ccc gag gct aaa gaa gat      418
Asn Ser Pro Ser Ser Ser Leu Pro Ala Glu Pro Glu Ala Lys Glu Asp
           25                30                35
gag gca aga gaa aat gta ccc caa ggt gaa cct cca aaa ccc cca ctc      466
Glu Ala Arg Glu Asn Val Pro Gln Gly Glu Pro Pro Lys Pro Pro Leu
  40                45                50                55
aag tca gag aaa cat gag gaa taaaggtcac atgcagatgc aaaaaaaaaa      517
Lys Ser Glu Lys His Glu Glu
           60
aaaaaaa      524

<210> 68
<211> 1472
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 210..1082

<220>
<221> sig_peptide
<222> 210..311
<223> Von Heijne matrix
      score 10.0571391689271
      seq FLCLLSALLLTEG/KK

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gaatcagctg caggtctctg ttttgaaaaa gcagagatac agaggcagag gaaaaggggtg      120
gactcctatg tgacctgttc ttagagcaag acaatcacca tctgaattcc agaagccctg      180
ttcatgggtg gggatatttt ctcgactgc atg gaa tca gaa aga agc aaa agg      233
                                Met Glu Ser Glu Arg Ser Lys Arg
                                -30
atg gga aat gcc tgc att ccc ctg aaa aga att gct tat ttc cta tgt      281
Met Gly Asn Ala Cys Ile Pro Leu Lys Arg Ile Ala Tyr Phe Leu Cys
  -25                -20                -15
ctc tta tct gcg ctt ttg ctg act gag ggg aag aaa cca gcg aag cca      329
Leu Leu Ser Ala Leu Leu Leu Thr Glu Gly Lys Lys Pro Ala Lys Pro
  -10                -5                1                5
aaa tgc cct gcc gtg tgt act tgt acc aaa gat aat gct tta tgt gag      377
Lys Cys Pro Ala Val Cys Thr Cys Thr Lys Asp Asn Ala Leu Cys Glu
           10                15                20
aat gcc aga tcc att cca cgc acc gtt cct cct gat gtt atc tca tta      425
Asn Ala Arg Ser Ile Pro Arg Thr Val Pro Pro Asp Val Ile Ser Leu
           25                30                35

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tcc ttt gtg aga tct gtt ttt act gaa atc tca gaa ggg agt ttt tta      473
Ser Phe Val Arg Ser Val Phe Thr Glu Ile Ser Glu Gly Ser Phe Leu
40 45 50
ttc acg cca tcg ctg cag ctc ttg tta ttc aca tcg aac tcc ttt gat      521
Phe Thr Pro Ser Leu Gln Leu Leu Leu Phe Thr Ser Asn Ser Phe Asp
55 60 65 70
gtg atc agt gat gat gct ttt att ggt ctt cca cat cta gag tat tta      569
Val Ile Ser Asp Asp Ala Phe Ile Gly Leu Pro His Leu Glu Tyr Leu
75 80 85
ttc ata gaa aac aac aac atc aag tca att tca aga cat act ttc cgg      617
Phe Ile Glu Asn Asn Asn Ile Lys Ser Ile Ser Arg His Thr Phe Arg
90 95 100
gga cta aag tca tta att cac ttg agc ctt gca aac aac aat ctc cag      665
Gly Leu Lys Ser Leu Ile His Leu Ser Leu Ala Asn Asn Asn Leu Gln
105 110 115
aca ctc cca aaa gat att ttc aaa ggc ctg gat tct tta aca aat gtg      713
Thr Leu Pro Lys Asp Ile Phe Lys Gly Leu Asp Ser Leu Thr Asn Val
120 125 130
gac ctg agg ggt aat tca ttt aat tgt gac tgt aaa ctg aaa tgg cta      761
Asp Leu Arg Gly Asn Ser Phe Asn Cys Asp Cys Lys Leu Lys Trp Leu
135 140 145 150
gtg gaa tgg ctt ggc cac acc aat gca act gtt gaa gac atc tac tgc      809
Val Glu Trp Leu Gly His Thr Asn Ala Thr Val Glu Asp Ile Tyr Cys
155 160 165
gaa ggc ccc cca gaa tac aag aag cgc aaa atc aat agt ctc tcc tcg      857
Glu Gly Pro Pro Glu Tyr Lys Lys Arg Lys Ile Asn Ser Leu Ser Ser
170 175 180
aag gat ttc gat tgc atc att aca gaa ttt gca aag tct caa gac ctg      905
Lys Asp Phe Asp Cys Ile Ile Thr Glu Phe Ala Lys Ser Gln Asp Leu
185 190 195
cct tat caa tca ttg tcc ata gac act ttt tct tat ttg aat gat gag      953
Pro Tyr Gln Ser Leu Ser Ile Asp Thr Phe Ser Tyr Leu Asn Asp Glu
200 205 210
tat gta gtc atc gct cag cct ttt act gga aaa tgc att ttc ctt gaa      1001
Tyr Val Val Ile Ala Gln Pro Phe Thr Gly Lys Cys Ile Phe Leu Glu
215 220 225 230
tgg gac cat gtg gaa aag acc ttc cgg aat tat gac aac att aca gtt      1049
Trp Asp His Val Glu Lys Thr Phe Arg Asn Tyr Asp Asn Ile Thr Val
235 240 245
tta agg gaa ata cac aga ttt aca aac atg tca tagttgactt aagcgcatga      1102
Leu Arg Glu Ile His Arg Phe Thr Asn Met Ser
250 255
gacaccaaatt tctgtggctg ccacacagaaa ttttctacag tacatgaccc ggatgaactc      1162
aatgcatgat gactcttctt atcacacttg caaatgaatg cctttcaaac attgagactg      1222
ctagaaccaa gcactaccag tatctccatc cttaactgtc cagtccagtg atgtgggaag      1282
ttacctttta taagacaaaa tttaattgtg taactgttct ttgcagtga gatgtgtaaa      1342
taagcgttta atggtatctg ttactccaaa aagaaatatt aatatgtact tttccattta      1402
tttattcatg tgtacagaaa caactgccaa ataaaatgtt tacattttct tacaaaaaaa      1462
aaaaaaaaa      1472

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<210> 69

<211> 1737

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 172..1449

<220>
 <221> sig_peptide
 <222> 172..255
 <223> Von Heijne matrix
 score 5.94825670923113
 seq XVLLEPFVHQVGG/HS

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 caagccaagg agccaagacg agagggacac acggacaaac aacagacaga agacgtactg 120
 gccgctggac tccgctgcct ccccatctc cccgccatct gcgcccggag g atg agc 177
 Met Ser
 cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc gtc ctt 225
 Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu
 -25 -20 -15
 ctg gag ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc 273
 Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg
 -10 -5 1 5
 ttc aat gag aca acc ctg tgc aag ccc ctg gtc cca agg gaa cat cag 321
 Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln
 10 15 20
 ttc tac gag acc ctc cct gct gag atg cgc aaa ttc act ccc cag tac 369
 Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro Gln Tyr
 25 30 35
 aaa ggt gtg gta tct gtg cgc ttt gaa gaa gat gaa gac agg aac ttg 417
 Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg Asn Leu
 40 45 50
 tgt cta ata gca tat cca ttg aaa ggg gac cat gga att gtg gac att 465
 Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val Asp Ile
 55 60 65 70
 gta gat aat tca gac tgt gaa cca aaa agt aag ctc cta agg tgg aca 513
 Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg Trp Thr
 75 80 85
 aca aac aaa aaa cat cat gtc tta gaa aca gaa aag acc cct aag gac 561
 Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro Lys Asp
 90 95 100
 tgg gtg cgt cag cac cgt aaa gag gag aaa atg aag agc cat aag tta 609
 Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His Lys Leu
 105 110 115
 gaa gaa gaa ttt gag tgg cta aag aaa tct gaa gtc ttg tac tac act 657
 Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr Tyr Thr
 120 125 130
 gta gag aag aag ggg aat ata agt tcc cag ctt aaa cac tat aac cct 705
 Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr Asn Pro
 135 140 145 150
 tgg agc atg aaa tgt cac cag caa cag tta cag aga atg aag gag aat 753
 Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys Glu Asn
 155 160 165
 gca aag cat cgg aac cag tac aaa ttt atc tta ctg gaa aac ctg act 801
 Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn Leu Thr
 170 175 180
 tcc cgc tat gag gtg cct tgt gtc ctt gac ctc aag atg ggc aca cga 849
 Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly Thr Arg
 185 190 195
 caa cat ggt gat gat gct tca gag gag aag gca gcc aac cag atc cga 897
 Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala Ala Asn Gln Ile Arg
 200 205 210

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aaa tgt cag cag agc aca tct gca gtc att ggt gtg cgt gtg tgt ggc      945
Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly Val Arg Val Cys Gly
215                220                225                230
atg cag gtg tac caa gca ggc agt ggg cag ctc atg ttc atg aac aag      993
Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu Met Phe Met Asn Lys
                235                240                245
tac cat gga cgg aag cta tct atg cag ggc ttc aag gag gca ctt ttc      1041
Tyr His Gly Arg Lys Leu Ser Met Gln Gly Phe Lys Glu Ala Leu Phe
                250                255                260
cag ttc ttc cac aat ggg cgg tac ctg cgc cgt gaa ctc ctg ggc cct      1089
Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg Glu Leu Leu Gly Pro
                265                270                275
gtg ctc aag aag ctg act gag ctc aag gca gtg ttg gag cga cag gag      1137
Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val Leu Glu Arg Gln Glu
                280                285                290
tcc tac cgc ttc tac tca agc tcc ctg ctg gtc att tat gat ggc aag      1185
Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val Ile Tyr Asp Gly Lys
295                300                305                310
gag cgg ccc gaa gtg gtc ctg gac tca gat gct gag gat ttg gag gac      1233
Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala Glu Asp Leu Glu Asp
                315                320                325
ctg tca gag gaa tca gct gat gag tct gct ggt gcc tat gcc tac aaa      1281
Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly Ala Tyr Ala Tyr Lys
                330                335                340
ccc atc ggc gcc agc tct gta gat gtg cgc atg atc gac ttt gca cac      1329
Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met Ile Asp Phe Ala His
                345                350                355
acc acc tgc agg ctg tat ggc gag gac acc gtg gtg cat gag ggc cag      1377
Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val Val His Glu Gly Gln
                360                365                370
gat gct ggc tat atc ttc ggg ctc cag agc ctg ata gac att gtc aca      1425
Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu Ile Asp Ile Val Thr
375                380                385                390
gag ata agt gag gag agt ggg gag tgagcttgct agctgctcca gtacttgaga      1479
Glu Ile Ser Glu Glu Ser Gly Glu
                395
gcgactctgt gtcccaggca cagctgtgct gcgctcaggga ggaagccagt atggccaggt      1539
ggtggctcct gcagcctgga gctgatgtgc agtggcctct gtgagcccca gcctgagcca      1599
gtcccagctg tgcttgaggt ctttatttat tttaactatt tcttcaacat tccacatttg      1659
atgatgatac ctctttcttc cctgagtgtg tatgtttctaa tacaaatctt tttgtttatt      1719
gaaaaaaaaa aaaaaaaaaa      1737

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<210> 70

<211> 1637

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 30..1427

<220>

<221> sig_peptide

<222> 30..77

<223> Von Heijne matrix

score 3.71064775937629

seq YAAAAGVLAGVES/RQ

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 His Glu Val His Tyr Ile Leu Leu Asp Pro Ser Cys Ser Gly Ser Gly
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 atg ccg agc aga cag ctg gag gag ccc ggg gca ggc aca cct agc ccg 1013
 Met Pro Ser Arg Gln Leu Glu Glu Pro Gly Ala Gly Thr Pro Ser Pro
 300 305 310
 gtg cgt ctg cat gcc ctg gca ggc ttc cag cag cga gcc ctg tgc cac 1061
 Val Arg Leu His Ala Leu Ala Gly Phe Gln Gln Arg Ala Leu Cys His
 315 320 325
 gcg ctc act ttc cct tcc ctg cag cgg ctc gtc tac tcc acg tgc tcc 1109
 Ala Leu Thr Phe Pro Ser Leu Gln Arg Leu Val Tyr Ser Thr Cys Ser
 330 335 340
 ctc tgc cag gag gag aat gaa gac gtg gtg cga gat gcg ctg cag cag 1157
 Leu Cys Gln Glu Glu Asn Glu Asp Val Val Arg Asp Ala Leu Gln Gln
 345 350 355 360
 aac ccg ggc gcc ttc agg cta gct ccc gcc ctg cct gcc tgg ccc cac 1205
 Asn Pro Gly Ala Phe Arg Leu Ala Pro Ala Leu Pro Ala Trp Pro His
 365 370 375
 cga ggc ctg agc acg ttc ccg ggt gcc gag cac tgc ctc cgg gcc tcc 1253
 Arg Gly Leu Ser Thr Phe Pro Gly Ala Glu His Cys Leu Arg Ala Ser
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 cct gag acc aca ctc agc agt ggc ttc ttc gtt gct gta att gaa cgg 1301
 Pro Glu Thr Thr Leu Ser Ser Gly Phe Phe Val Ala Val Ile Glu Arg
 395 400 405
 gtc gag gtg cca agc tca gcc tca cag gcc aaa gca tca gca cca gaa 1349
 Val Glu Val Pro Ser Ser Ala Ser Gln Ala Lys Ala Ser Ala Pro Glu
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 cgc aca ccc agc cca gcc cca aag aga aag aag aga cag caa aga gcc 1397
 Arg Thr Pro Ser Pro Ala Pro Lys Arg Lys Lys Arg Gln Gln Arg Ala
 425 430 435 440
 gca gcc ggt gct tgc aca ccg cct tgc aca tagcagaggc tccgggctga 1447
 Ala Ala Gly Ala Cys Thr Pro Pro Cys Thr
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 <223> Von Heijne matrix
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 seq YAAAAGVLAGVES/RQ

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Val Arg Leu His Ala Leu Ala Ala Ser Ser Ser Glu Pro Cys Ala Thr
      315      320      325
cgc tca ctt tcc ctt ccc tgc agc ggc tcg tct act cca cgt gct ccc      1109
Arg Ser Leu Ser Leu Pro Cys Ser Gly Ser Ser Thr Pro Arg Ala Pro
      330      335      340
tct gcc agg agg aga atg aag acg tgg tgc gag atg cgc tgc agc aga      1157
Ser Ala Arg Arg Arg Met Lys Thr Trp Cys Glu Met Arg Cys Ser Arg
345      350      355      360
acc cgg gcg cct tca ggc tagctcccg cctgcctgcc tggccccacc      1205
Thr Arg Ala Pro Ser Gly
      365
gaggcctgag cacgttcccg ggtgccgagc actgcctccg ggcttcccct gagaccacac      1265
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aggccaaagc atcagcacca gaacgcacac ccagcccagc cccaaagaga aagaagagac      1385
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tcgcc atg gag gag ctc cag gag cct ctg aga gga gag ctc cgg ctc tgc      110
      Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Glu Leu Arg Leu Cys
      -35      -30      -25
ttc acg caa gct gcc cgg act agc ctc tta ctg ctc agg ctc aac gac      158
Phe Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp
      -20      -15      -10
gct gcc ctg cgg gcg ctg caa gag tgt cag cgg caa cag gta cgg ccg      206
Ala Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro
      -5      1      5      10
gtg att gct ttc caa ggc cac cga ggg tat ctg aga ctc cca ggc cct      254
Val Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro
      15      20      25
ggg tgg tcc tgc ctc ttc tcc ttc ata gtg tcc cag tgt tgt cag gag      302
Gly Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu
      30      35      40
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Gly Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser

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Gly Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile			
60	65	70	75
att tgg gca gcc atg gat tct atc cca gcc cca tca tca gtt cag gga			446
Ile Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly			
80	85	90	
cac aac ctg act gaa gat gcc aga cat cct gag agt tgg cag aac aca			494
His Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr			
95	100	105	
gga ggc tat tct gaa gga gat gca gta tca cag cca cag atg gca cta			542
Gly Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu			
110	115	120	
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Glu Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser			
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ctc cca gga tcc tca agg gag cac atg gca cag tgg gaa gtg aga agc			638
Leu Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser			
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cag acc cat gtt cca aac aga gaa cct gtt cag gca ctg cct tcc tct			686
Gln Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser			
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gcc agc cgg aaa cgt ctg gac aag aaa cgt tca gtg cct gta gcc act			734
Ala Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr			
175	180	185	
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Val Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Pro			
190	195	200	
cct aca agg cct gac caa tca gga ttt aca aga ggg aga aga ttg gga			830
Pro Thr Arg Pro Asp Gln Ser Gly Phe Thr Arg Gly Arg Arg Leu Gly			
205	210	215	
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Ala Arg Arg			
220			
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gaataaccgca tcctgcatgc ccgtgttgagg actgcaagcc aaagggttcat agagctggga			1059
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atttttagcct ggtagcctct ctaaggaaac agtaataata acttctgata agagttaaaa			1659
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 seq LLLLPFLPLLLA/AP

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 -15 -10 -5
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 Leu Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val
 1 5 10
 gtg cat ggg ctc ttc gac agc tcg tac agc ttc cgc cac ctg ctg gaa 252
 Val His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu
 15 20 25 30
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 Tyr Ile Asn Glu Thr His Pro Gly Thr Val Val Thr Val Leu Asp Leu
 35 40 45
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 Phe Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly
 50 55 60
 ttc cga gag gct gtg gtc ccc atc atg gca aag gcc cct caa ggg gtg 396
 Phe Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val
 65 70 75
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 His Leu Ile Cys Tyr Ser Gln Gly Gly Leu Val Cys Arg Ala Leu Leu
 80 85 90
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 Ser Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser
 95 100 105 110
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 Pro Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe
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 Pro Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro Leu
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 Ile Asn Gly Glu Arg Asp His Pro Asn Ala Thr Val Trp Arg Lys Asn
 145 150 155
 ttt ctg cgt gtg ggc cac ctg gtg ctg att ggg ggc cct gat gat ggt 684
 Phe Leu Arg Val Gly His Leu Val Leu Ile Gly Gly Pro Asp Asp Gly
 160 165 170
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 Val Ile Thr Pro Trp Gln Ser Ser Phe Phe Phe Tyr Asp Ala Asn
 175 180 185 190
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 Glu Thr Val Leu Glu Met Glu Glu Gln Leu Val Tyr Leu Arg Asp Ser
 195 200 205
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 Phe Gly Leu Lys Thr Leu Leu Ala Arg Gly Ala Ile Val Arg Cys Pro
 210 215 220

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Met Ala Gly Ile Ser His Thr Ala Trp His Ser Asn Arg Thr Leu Tyr	
225 230 235	
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Glu Thr Cys Ile Glu Pro Trp Leu Ser	
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Pro Ala Ala Trp Val Leu Leu Leu Leu Pro Phe Leu Pro Leu Leu Leu	
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Leu Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val	
1 5 10	
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Val His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu	
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35 40 45	
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Phe Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly	
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Phe Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val	

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Pro	Gln	Met	Gly	Gln	Tyr	Gly	Asp	Thr	Asp	Tyr	Leu	Lys	Trp	Leu	Phe	
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			-15														

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Phe Cys Tyr Met Leu Ser Leu Val Leu Cys Ala Ala Leu Ile Phe Phe	

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agc ccc ata gac cag tgc aat cct gtt cat gcg agg gaa cgg ttg agg      438
Ser Pro Ile Asp Gln Cys Asn Pro Val His Ala Arg Glu Arg Leu Arg
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aac atc gag cgc atc tgc ttc ctt ctg cga aag ctg gtg ctg cca gaa      486
Asn Ile Glu Arg Ile Cys Phe Leu Leu Arg Lys Leu Val Leu Pro Glu
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Tyr Ser Ile His Ser Leu Phe Cys Ile Met Phe Leu Cys Ala Gln Glu
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Pro Val Val Met Asn Pro Asp Thr Leu Ser Tyr Cys Gln Lys Glu Ala
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Trp Cys Lys Leu Ala Phe Tyr Leu Leu Ser Phe Phe Tyr Tyr Leu Tyr
          120          125          130
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Cys Met Ile Tyr Thr Leu Val Ser Ser
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 Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ser Glu Met Arg Lys
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 Phe Thr Pro Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp
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 Glu Asp Arg Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His
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 Gly Ile Val Asp Ile Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys
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 Leu Leu Arg Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu
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 Lys Thr Pro Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met
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 Lys Ser His Lys Leu Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu
 115 120 125
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 130 135 140 145
 aaa cac tat aac cct tgg agc atg aaa tgt cac cag caa cag tta cag 757
 Lys His Tyr Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln
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gaa ctc ctg ggc cct gtg ctc aag aag ctg act gag ctc aag gca gtg      1141
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Ala Tyr Ala Tyr Lys Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met
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Ile Asp Phe Ala His Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val
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Val His Glu Gly Gln Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu
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Ala Gly Arg Asp Leu Glu Lys Pro Pro Arg Leu His Cys Ser Gly Arg	
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	Met	Asp	Tyr	Ser	Arg	Val	Phe	Gln	Gly	Val	Phe	Phe	Thr	Phe			
					-35					-30							
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Lys	His	Ala	Phe	Ala	Asp	Gly	Ala	Trp	Asp	Leu	Ser	Phe	Leu	Cys	Ala		
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Leu	Cys	Ser	Phe	Cys	Pro	Ile	Ser	Ala	Ala	Ser	Gly	Arg	Pro	Tyr	Arg		
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Phe Asp Ile Glu Arg Lys Gly Lys Ser Ser Val Cys Pro Phe Cys Tyr
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Tyr Ala Phe His Phe Pro His Leu Leu Ser Pro Gln Ile Gln Arg Ser
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gcc cac agg gct ctg tac cga cga cac gtc ctg ggc atc gtc ctc caa 483
Ala His Arg Ala Leu Tyr Arg Arg His Val Leu Gly Ile Val Leu Gln
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Gly Pro Ala Leu Cys Phe Ala Ala Ile Phe Ser Leu Phe Phe Val
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Pro Leu Ser Tyr Leu Leu Met Val Thr Val Ile Leu Leu Pro Tyr Val
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Leu Thr Phe Gln Arg Arg Phe

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                                     Met Ser Ser Pro
                                     -35
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Gln Leu Pro Ala Phe Leu Trp Asp Lys Gly Thr Leu Thr Thr Ala Ile
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Met Thr Leu Val Thr Leu Leu Ile Leu Val Trp Lys Val Thr Lys Asp
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Lys Ser Asn Lys Asn Arg Glu Thr His Pro Arg Lys Glu Ala Thr Trp
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Leu Pro
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 gagccatgtc gcttgcccct tacgttctgt tacccttttt cttttttgtc atctctcgtg 540
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 ttcttttctc ttctttcctt gttttcattc cagacttcag cactgggctg ggaaactttc 720
 tggcttccat ctcgcttact catgtagcct tcgctttgca aggtggag atg agg ggt 777
 Met Arg Gly

-25
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 Pro Thr Ala Gly Pro Ser Val Leu Ser Ala Ala His Leu Leu Val Val
 -20 -15 -10
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 Ile Leu Pro Ala Asn Ala Ala Leu Lys Leu Leu Ser Trp Glu Arg Leu
 -5 1 5 10
 gcg gcc ccc gcc atc gag gtg gaa gta cct tcc aag gag gtg ctt gca 921
 Ala Ala Pro Ala Ile Glu Val Glu Val Pro Ser Lys Glu Val Leu Ala
 15 20 25
 gca ccc acc aag gcc aag cta ata ccc tct gag gat atg ttg gca gca 969
 Ala Pro Thr Lys Ala Lys Leu Ile Pro Ser Glu Asp Met Leu Ala Ala
 30 35 40
 cct gcc atg gac ttg ctg gat tca ttt tct cct gga ttt ttg ata gct 1017
 Pro Ala Met Asp Leu Leu Asp Ser Phe Ser Pro Gly Phe Leu Ile Ala
 45 50 55
 gct ccc gcc agc gct gtg atc act tgg cct ggg cct gca gat ttg gtt 1065
 Ala Pro Ala Ser Ala Val Ile Thr Trp Pro Gly Pro Ala Asp Leu Val
 60 65 70
 gtt gct atg ctc ata gca cct gtt gca gga ctc att gct gcc cct gct 1113
 Val Ala Met Leu Ile Ala Pro Val Ala Gly Leu Ile Ala Ala Pro Ala
 75 80 85 90
 att gcc aca tct gtt cta ggt cct gtt gct gtt cct gcc act gcc atg 1161

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Ile Ala Thr Ser Val Leu Gly Pro Val Ala Val Pro Ala Thr Ala Met
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cca cct gct gtc ctt gct gct cct cct tca gca gcc cct gga gtg ctc      1209
Pro Pro Ala Val Leu Ala Ala Pro Pro Ser Ala Ala Pro Gly Val Leu
          110                      115                      120
gtg gat gga gaa gcc gca cta gcc gtt ccg tgg gag gca tgt tgg att      1257
Val Asp Gly Glu Ala Ala Leu Ala Val Pro Trp Glu Ala Cys Trp Ile
          125                      130                      135
ccc tct ccc cca gca taagcagaag aggtggctgc agatacatca caaggcttgt      1312
Pro Ser Pro Pro Ala
          140
agagcccagt ctactctga tcccccttctc tgtggagctc tgcagcctat accaagggga      1372
agagaaacag atgagattga gatgactgaa agggagatca gaactttcta ctctctctt      1432
atcctggagt taattcaagg gcttataatt agaagaacct gggtcgggtg tggaggctca      1492
cgctgtaat cccaacactt tgggaggcca aggagggcag atcgcttgag gccaggagtt      1552
caagaccagc cttgccaaca tagcaaaacc ccgactctac taaaaatata aaaaattagc      1612
tggacaggat ggcgcatgcc tgtaatccca gctactcagt aggctgaggt aggagtatcg      1672
cttgaactcg gatggcggag gctgcagtga gccaaagactg cgccactcca ctgcactcca      1732
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                               Met Leu Pro Leu Leu Ile Ile Cys
                               -15                      -10
ctc ctg cct gcc att gaa ggg aag aac tgc ctc cgc tgc tgg cca gaa      101
Leu Leu Pro Ala Ile Glu Gly Lys Asn Cys Leu Arg Cys Trp Pro Glu
          -5                      1                      5
ctg tct gcc ttg ata gac tat gac ctg cag atc ctc tgg gtg acc cca      149
Leu Ser Ala Leu Ile Asp Tyr Asp Leu Gln Ile Leu Trp Val Thr Pro
          10                      15                      20                      25
ggg cca ccc aca gaa ctt tct caa aat cgt gac cat ttg gaa gaa gaa      197
Gly Pro Pro Thr Glu Leu Ser Gln Asn Arg Asp His Leu Glu Glu Glu
          30                      35                      40
aca gcc aaa ttc ttc act caa gta cac caa gcc att aaa acg tta cga      245
Thr Ala Lys Phe Phe Thr Gln Val His Gln Ala Ile Lys Thr Leu Arg
          45                      50                      55
gat gat aaa aca gta ctt ctg gaa gag atc tac acg cac aag aat ctc      293
Asp Asp Lys Thr Val Leu Leu Glu Glu Ile Tyr Thr His Lys Asn Leu
          60                      65                      70
ttt act gag agg ctg aat aag ata tct gat ggg ctg aag gag aag gac      341
Phe Thr Glu Arg Leu Asn Lys Ile Ser Asp Gly Leu Lys Glu Lys Asp
          75                      80                      85

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ata cag tcc aca ctg aag gtc acc agc tgt gct gac tgc agg act cac 389
 Ile Gln Ser Thr Leu Lys Val Thr Ser Cys Ala Asp Cys Arg Thr His
 90 95 100 105
 ttc ctc tcc tgc aat gac ccc act ttc tgc cca gcc agg aac cgg cgg 437
 Phe Leu Ser Cys Asn Asp Pro Thr Phe Cys Pro Ala Arg Asn Arg Arg
 110 115 120
 acc tcc ctg tgg gct gtg agt ctc agc agt gct cta ctc ctg gcc ata 485
 Thr Ser Leu Trp Ala Val Ser Leu Ser Ser Ala Leu Leu Leu Ala Ile
 125 130 135
 gct gga gat gtt tct ttt act ggc aaa gga aga agg agg cag 527
 Ala Gly Asp Val Ser Phe Thr Gly Lys Gly Arg Arg Arg Gln
 140 145 150
 taaagcagga acagggcagc ccgcatgtct tccagaagtg aacagaggcc gcagctacca 587
 ccgtcacaaa gttcactcat ctctgggtcc cgggtgacccc atccccccat accctccatc 647
 ctgggtcctg gggcccaaaa gctctgaggg ctaggagact gcgctgtctc gtggtttgcc 707
 tactcctaca cctttgtaaa gagtctcttc attaaaaccc ctcttcataa aaaaaaaaaa 767
 aaaaaaaaaa aaaaaaaaaa aataaaaaaaaa aaaaaaaaaa 805

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 <213> Homo sapiens

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 <222> 39..506

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 <221> sig_peptide
 <222> 39..83
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 seq ILMLTFIICGLLT/RV

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 Met Asn Ile Leu Met Leu
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 acc ttc att atc tgt ggg ttg cta act cgg gtg acc aaa ggt agc ttt 104
 Thr Phe Ile Ile Cys Gly Leu Leu Thr Arg Val Thr Lys Gly Ser Phe
 -5 1 5
 gaa ccc caa aaa tgt tgg aag aat aat gta gga cat tgc aga aga cga 152
 Glu Pro Gln Lys Cys Trp Lys Asn Asn Val Gly His Cys Arg Arg Arg
 10 15 20
 tgt tta gat act gaa agg tac ata ctt ctt tgt agg aac aag cta tca 200
 Cys Leu Asp Thr Glu Arg Tyr Ile Leu Leu Cys Arg Asn Lys Leu Ser
 25 30 35
 tgc tgc att tct ata ata tca cat gaa tat act cga cga cca gca ttt 248
 Cys Cys Ile Ser Ile Ile Ser His Glu Tyr Thr Arg Arg Pro Ala Phe
 40 45 50 55
 cct gtg att cac cta gag gat ata aca ttg gat tat agt gat gtg gac 296
 Pro Val Ile His Leu Glu Asp Ile Thr Leu Asp Tyr Ser Asp Val Asp
 60 65 70
 tct ttt act ggt tcc cca gta tct atg ttg aat gat ctg ata aca ttt 344
 Ser Phe Thr Gly Ser Pro Val Ser Met Leu Asn Asp Leu Ile Thr Phe
 75 80 85
 gac aca act aaa ttt gga gaa acc atg aca cct gag acc aat act cct 392
 Asp Thr Thr Lys Phe Gly Glu Thr Met Thr Pro Glu Thr Asn Thr Pro

ttacatacta ttatataatg tacagtgtta ttttctgtac ttctgaataa atgtgcaata 579
 ttgcaaaaaa aaaaaaaaaa 598

<210> 87
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 <213> Homo sapiens

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 <222> 332..574

<220>
 <221> sig_peptide
 <222> 332..412
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 seq ILGLFCCLPLAIP/AV

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 gcagaaagga gagtctcgct ctgtcaccca ggctggagtg cagtggcagg atcttggctc 180
 acttcaacct ccacctcccg agttctgcct cagcctcca agtagctggg attacaggtc 240
 cagtcactcc acgcttgag agtccaatta acaagagcaa gttctggtag aaagaagggtg 300
 actttattcc agagctcagg tgtttgaact g atg tct gat gag gat gaa tcc 352
 Met Ser Asp Glu Asp Glu Ser
 -25
 agc gac tac ctc tgc ctg tcc atc ctg ggc ctc ttc tgt tgc ctt ccc 400
 Ser Asp Tyr Leu Cys Leu Ser Ile Leu Gly Leu Phe Cys Cys Leu Pro
 -20 -15 -10 -5
 cta gcc atc cca gcc gtg atc ttt tct tgc ctg aca aag aac tac aat 448
 Leu Ala Ile Pro Ala Val Ile Phe Ser Cys Leu Thr Lys Asn Tyr Asn
 1 5 10
 aaa tcc agt gac tat gag ctg gca gcc aag acc tcc aaa caa gcc tac 496
 Lys Ser Ser Asp Tyr Glu Leu Ala Ala Lys Thr Ser Lys Gln Ala Tyr
 15 20 25
 tac tgg gcc atc gcg agc atc act gtg gga atc tta ggt acc atc ttg 544
 Tyr Trp Ala Ile Ala Ser Ile Thr Val Gly Ile Leu Gly Thr Ile Leu
 30 35 40
 tac acc tac ctg ata tac tta ctt aga ttg taaactgctt cccagctctt 594
 Tyr Thr Tyr Leu Ile Tyr Leu Leu Arg Leu
 45 50
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gaaaaaaaaa aaaaaa 699

<210> 88
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 <212> DNA
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 <222> 133..417

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 <222> 133..213

<223> Von Heijne matrix
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 seq LTSLILVTLISA/FV

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 gccagtttcc tcccagggcc attgttacca cctgatcatt tgagtttttag tttctctagc 120
 agatgctgac ta atg act gac cag gat cga atc atc aat tta gtt gtt ggc 171
 Met Thr Asp Gln Asp Arg Ile Ile Asn Leu Val Val Gly
 -25 -20 -15
 agc tta aca tcc tta ttg att cta gta acg ctg ata agt gct ttt gtt 219
 Ser Leu Thr Ser Leu Leu Ile Leu Val Thr Leu Ile Ser Ala Phe Val
 -10 -5 1
 ttc cct caa cta cct cca aaa ccg ttg aat ata ttc ttt gct gtc tgc 267
 Phe Pro Gln Leu Pro Pro Lys Pro Leu Asn Ile Phe Phe Ala Val Cys
 5 10 15
 atc tct ttg agt agt att act gcc tgc ata atc tac tgg tat cga caa 315
 Ile Ser Leu Ser Ser Ile Thr Ala Cys Ile Ile Tyr Trp Tyr Arg Gln
 20 25 30
 gga gac tta gaa ccg aaa ttt aga aag cta att tac tat atc ata ttt 363
 Gly Asp Leu Glu Pro Lys Phe Arg Lys Leu Ile Tyr Tyr Ile Ile Phe
 35 40 45 50
 tct atc atc atg ttg tgt ata tgt gca aac ctg tac ttc cat gat gtg 411
 Ser Ile Ile Met Leu Cys Ile Cys Ala Asn Leu Tyr Phe His Asp Val
 55 60 65
 gga agg tgaggctgcc aaggagaagt acttaccagg actcttcaaa atgatacatt 467
 Gly Arg
 aggacagtga gtaatttttg gataaggat gctgaagaat ctctgcaga agtctgatac 527
 atgattttca tgtaattgt aaatgttaat tccctcttgc aaggagagaca tatcctagat 587
 cactttgctt tttctttaag gagctgatgt tgcacctaaa cattccaacc cttaaagcta 647
 aaacagcaca aaaaaatttc acttttgaaa tgaaattttt ataattgtat ggcaaaaggc 707
 tatgtaaaaa caaatcttgc atcttaagac aaatattctt ttatttctgt taaactgaat 767
 atacaattgt tccctaggca accaactttt gcttataact acaatttaat ttcacgttga 827
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<210> 89
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 113..364

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 <222> 113..172
 <223> Von Heijne matrix
 score 4.37180298395146
 seq SLLLSLPPHQGLT/FS

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 tcgctggacc ctagaaaagc caccacgacc tgtgggccat gatgctaccc ca atg gct 118
 Met Ala
 -20
 gct gct gct gtt cct tct ctt ctt ctt tct ctt cct cct cac cag ggg 166

Ala Ala Ala Val Pro Ser Leu Leu Leu Ser Leu Pro Pro His Gln Gly
-15 -10 -5
ctc act ttc tcc aac aaa ata caa cct ttt gga gct caa gga gtc ttg 214
Leu Thr Phe Ser Asn Lys Ile Gln Pro Phe Gly Ala Gln Gly Val Leu
1 5 10
cat ccg gaa cca gga ctg cga gac tgg ctg ctg cca acg tgc tcc aga 262
His Pro Glu Pro Gly Leu Arg Asp Trp Leu Leu Pro Thr Cys Ser Arg
15 20 25 30
caa ttg cga gtc gca ctg ccg gag aag ggg tcc gag ggc agt ctg tgt 310
Gln Leu Arg Val Ala Leu Pro Glu Lys Gly Ser Glu Gly Ser Leu Cys
35 40 45
caa acg cag ctg cca gct act cca tgc ttc ctg cct tgc aat acg gtg 358
Gln Thr Gln Leu Pro Ala Thr Pro Cys Phe Leu Pro Ser Asn Thr Val
50 55 60
aga acg tgaagtcag agctgctgct aaggcatgtg gcaaccttga agagaaggtc 414
Arg Thr
aagagctacc agccaccaaaa agaagtcag cacttcctgt gtctttgctt tggattcatg 474
agaaatatac gttcctattt gcttcaaaaa aaaaaaaaaa 514

<210> 90
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<212> DNA
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<222> 9..380

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<223> Von Heijne matrix
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Met Val Val Val Glu Pro Gly Ala Ser Leu Phe Pro Asn Gly
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gtt cct tgg ctg tat gct gtg ttt gct gtg ctt ttt gta ttt ttt ctt 98
Val Pro Trp Leu Tyr Ala Val Phe Ala Val Leu Phe Val Phe Phe Leu
-15 -10 -5
ttt gcc atg tta tct ccc ttt tta ctt gag ata gac cag cac ata aag 146
Phe Ala Met Leu Ser Pro Phe Leu Leu Glu Ile Asp Gln His Ile Lys
1 5 10
aaa ttc ttg atc aga tgc agg tat tct ctg cat aac act gtg cat aag 194
Lys Phe Leu Ile Arg Cys Arg Tyr Ser Leu His Asn Thr Val His Lys
15 20 25 30
gac aaa aaa aac agt gag ata aag atg gac cat cta gaa agg cca ggc 242
Asp Lys Lys Asn Ser Glu Ile Lys Met Asp His Leu Glu Arg Pro Gly
35 40 45
tgt cca ctg gag tca cca agg aga gga gtt ctg gga ggg aag aaa aat 290
Cys Pro Leu Glu Ser Pro Arg Arg Gly Val Leu Gly Gly Lys Lys Asn
50 55 60
ggg atg gga aac gac cca tta cta ttt gtg aaa gtg aca aaa gaa ccc 338
Gly Met Gly Asn Asp Pro Leu Leu Phe Val Lys Val Thr Lys Glu Pro
65 70 75
agg gat tct gag gct gaa atc tat acc cct ggg cct tca gtt 380

Arg Asp Ser Glu Ala Glu Ile Tyr Thr Pro Gly Pro Ser Val
80 85 90
tgagagtcatt ttagcctata tggattacc tgtgacatta cattccagag agatgagaaa 440
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ccccaaaaaa aaaaaaaa 518

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<212> DNA
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<222> 155..340

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<222> 155..292
<223> Von Heijne matrix
score 8.64329745298384
seq AVLLLLILFAIVFG/LL

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cttcagctca gccctccaca aagtgtgagc ctgaaggacc accctgaatt gccctttag 120
gaccagaac agctaccagc agaatcagat tctc atg gac caa ctg gta ttc aaa 175
Met Asp Gln Leu Val Phe Lys
-45 -40
gag aca atc tgg aat gat gcg ttc tgg cag aac ccc tgg gac cag ggg 223
Glu Thr Ile Trp Asn Asp Ala Phe Trp Gln Asn Pro Trp Asp Gln Gly
-35 -30 -25
ggc ctg gca gtg att atc tta ttc atc acc gct gtc ctg ctt ctc atc 271
Gly Leu Ala Val Ile Ile Leu Phe Ile Thr Ala Val Leu Leu Leu Ile
-20 -15 -10
tta ttt gcc atc gtg ttt ggt tta ctc act tcc aca gaa aac act cag 319
Leu Phe Ala Ile Val Phe Gly Leu Leu Thr Ser Thr Glu Asn Thr Gln
-5 1 5
tgt gaa gcg ggt gaa gag gag tgacctgact tgctggggac tgagatggca 370
Cys Glu Ala Gly Glu Glu
10 15
gcaggggagg cgagctgacc tgccccatt ccagtggtgg gccccttcgc gggtccctct 430
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<210> 92
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<212> DNA
<213> Homo sapiens

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<222> 185..634

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 <221> sig_peptide
 <222> 185..253
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 seq SLLFICFFGESFC/IC

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 agctaattta gctattttta aatagctaaa ttttagctac ttttttttca attgacaaag 180
 aagg atg tct aat caa aga cta ccg ctg att ttt tct ctg ttg ttt atc 229
 Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile
 -20 -15 -10
 tgc ttc ttc ggg gag agt ttc tgc att tgt gat gga act gtc tgg aca 277
 Cys Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr
 -5 1 5
 aag gtt gga tgg gag att ctt cca gaa gaa gta cat tat tgg aaa ggt 325
 Lys Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Gly
 10 15 20
 tgt tta tat ctc att tat aat tta tta caa gct gtc ttc ttc gtc tta 373
 Cys Leu Tyr Leu Ile Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu
 25 30 35 40
 ttt gtt ttg tct gtg cat tac ctg tgg aag aaa tgg aag aaa cac caa 421
 Phe Val Leu Ser Val His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln
 45 50 55
 aaa aag ctg aaa aag caa gcc tcc tta gaa aaa cct ggt aat gat cta 469
 Lys Lys Leu Lys Lys Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu
 60 65 70
 gaa agc cca ttg atc aac aac att gac caa aca ctc cac aga gtg gca 517
 Glu Ser Pro Leu Ile Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala
 75 80 85
 acc aca gca tca gtg ata tac aag atc tgg gag cac agg tct cac cat 565
 Thr Thr Ala Ser Val Ile Tyr Lys Ile Trp Glu His Arg Ser His His
 90 95 100
 cct tcc tct aag aaa att aag cac tgc aaa tta aag aag aag agt aaa 613
 Pro Ser Ser Lys Lys Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys
 105 110 115 120
 gaa gaa gga gcc aga tac taaataaatg catatgcaaa tgtagcttag 664
 Glu Glu Gly Ala Arg Arg Tyr
 125
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 aaaaaaaaaaaa aaa 737

<210> 93
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 <213> Homo sapiens

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 <222> 53..646

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 score 4.95353272042967

seq MLLGRLTSQLLRA/VP

<400> 93

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ctg ggg cgc ctg act tcc cag ctg ttg agg gcc gtt cct tgg gca ggc      106
Leu Gly Arg Leu Thr Ser Gln Leu Leu Arg Ala Val Pro Trp Ala Gly
   -10                               -5                               1           5
ggc cgc ccg cct tgg ccc gtc tct gga gtg ctg ggc agc cgg gtc tgc      154
Gly Arg Pro Pro Trp Pro Val Ser Gly Val Leu Gly Ser Arg Val Cys
                               10                               15           20
ggg ccc ctt tac agc aca tcg ccg gcc ggc cca ggt agg gcg gcc tct      202
Gly Pro Leu Tyr Ser Thr Ser Pro Ala Gly Pro Gly Arg Ala Ala Ser
                               25                               30           35
ctc cct cgc aag ggg gcc cag ctg gag ctg gag gag atg gtc ccc agg      250
Leu Pro Arg Lys Gly Ala Gln Leu Glu Leu Glu Glu Met Val Pro Arg
                               40                               45           50
aag atg tcc gtc agc ccc ctg gag agc tgg ctc acg gcc cgc lgc ttc      298
Lys Met Ser Val Ser Pro Leu Glu Ser Trp Leu Thr Ala Arg Cys Phe
                               55                               60           65
ctg ccc aga ctg gat acc ggg acc gca ggg act gtg gct cca ccg caa      346
Leu Pro Arg Leu Asp Thr Gly Thr Ala Gly Thr Val Ala Pro Pro Gln
   70                               75                               80           85
tcc tac cag tgt ccg ccc agc cag ata ggg gaa ggg gcc gag cag ggg      394
Ser Tyr Gln Cys Pro Pro Ser Gln Ile Gly Glu Gly Ala Glu Gln Gly
                               90                               95           100
gat gaa ggc gtc gcg gat gcg cct caa att cag tgc aaa aac gtg ctg      442
Asp Glu Gly Val Ala Asp Ala Pro Gln Ile Gln Cys Lys Asn Val Leu
                               105                              110           115
aag atc cgc cgg cgg aag atg aac cac cac aag tac cgg aag ctg gtg      490
Lys Ile Arg Arg Arg Lys Met Asn His His Lys Tyr Arg Lys Leu Val
                               120                              125           130
aag aag acg cgg ttc ctg cgg agg aag gtc cag gag gga cgc ctg aga      538
Lys Lys Thr Arg Phe Leu Arg Arg Lys Val Gln Glu Gly Arg Leu Arg
                               135                              140           145
cgc aag cag atc aag ttc gag aaa gac ctg agg cgc atc tgg ctg aag      586
Arg Lys Gln Ile Lys Phe Glu Lys Asp Leu Arg Arg Ile Trp Leu Lys
   150                              155                              160           165
gcg ggg cta aag gaa gcc ccc gaa ggc tgg cag acc ccc aag atc tac      634
Ala Gly Leu Lys Glu Ala Pro Glu Gly Trp Gln Thr Pro Lys Ile Tyr
                               170                              175           180
ctg cgg ggc aaa tgagtctggc gccgcccttc ccgcccgttg ctgctgtgat      686
Leu Arg Gly Lys
                               185
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<211> 582

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 247..510

<220>

<221> sig_peptide

<222> 247..318

<223> Von Heijne matrix
 score 5.20026065148038
 seq FCALEVVLPS CDC/RS

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 gggaacattc tttaagcggg tcgtcttggc acgagacata aggcagttca acatcaagcc 120
 cttgccctga acagttccaa atgccaagaa ctggcgaatt actactttgg tttcaatggg 180
 tgttccaaaa ggatcatcaa gcttcaggag ctttctgacc ttgaagaaag ggaaaatgaa 240
 gatagc atg gtg cca ctt ccg aag caa agc ctg aag ttc ttc tgt gct 288
 Met Val Pro Leu Pro Lys Gln Ser Leu Lys Phe Phe Cys Ala
 -20 -15
 tta gaa gtg gtg ttg cca tcc tgt gat tgc agg agt cct ggc att ggc 336
 Leu Glu Val Val Leu Pro Ser Cys Asp Cys Arg Ser Pro Gly Ile Gly
 -10 -5 1 5
 ttg gtg gag gag cct atg gat aag gtg gag gaa gga cca tta tca ttc 384
 Leu Val Glu Glu Pro Met Asp Lys Val Glu Glu Gly Pro Leu Ser Phe
 10 15 20
 ctt atg aaa agg aag aca gcc cag aag ctt gct att cag aag gct ttg 432
 Leu Met Lys Arg Lys Thr Ala Gln Lys Leu Ala Ile Gln Lys Ala Leu
 25 30 35
 tca gat gca ttc cag aaa ctg ttg att gtt gtt cta ggt aag act gtc 480
 Ser Asp Ala Phe Gln Lys Leu Leu Ile Val Val Leu Gly Lys Thr Val
 40 45 50
 ttg atc atc ctt gaa gta ctt cag ttt cag taagcaaata aactcatttt 530
 Leu Ile Ile Leu Glu Val Leu Gln Phe Gln
 55 60
 gaaaagttaa ttgaataaaa atattgatat ctaaagcaaa aaaaaaaaaa aa 582

<210> 95
 <211> 1913
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 143..592

<220>
 <221> sig_peptide
 <222> 143..277
 <223> Von Heijne matrix
 score 5.94057630118762
 seq VLVDLAILGQAYA/FA

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 ggacatgagg ccagaccttg tgaccttggt ggcagtgggc agtggttga tgtgaggtcc 120
 cagagacggc aggttcatca ag atg gtg ctc atg tgg acc agt ggt gac gcc 172
 Met Val Leu Met Trp Thr Ser Gly Asp Ala
 -45 -40
 ttc aag acg gcc tac ttc ctg ctg aag ggt gcc cct ctg cag ttc tcc 220
 Phe Lys Thr Ala Tyr Phe Leu Leu Lys Gly Ala Pro Leu Gln Phe Ser
 -35 -30 -25 -20
 gtg tgc ggc ctg ctg cag gtg ctg gtg gac ctg gcc atc ctg ggg cag 268
 Val Cys Gly Leu Leu Gln Val Leu Val Asp Leu Ala Ile Leu Gly Gln
 -15 -10 -5
 gcc tac gcc ttc gcc cca ccc cca gaa gcc ggc gcc cca cgc cgt gca 316

Ala	Tyr	Ala	Phe	Ala	Pro	Pro	Pro	Glu	Ala	Gly	Ala	Pro	Arg	Arg	Ala		
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ccc	cac	tgg	cac	caa	ggc	cct	ctg	aca	gtg	ggg	agg	acg	agg	atg	tgg		364
Pro	His	Trp	His	Gln	Gly	Pro	Leu	Thr	Val	Gly	Arg	Thr	Arg	Met	Trp		
	15					20					25						
gac	cgc	cag	ccg	cgg	gca	ctg	gtg	ggc	cct	gac	ctc	ccc	gcg	ggg	agg		412
Asp	Arg	Gln	Pro	Arg	Ala	Leu	Val	Gly	Pro	Asp	Leu	Pro	Ala	Gly	Arg		
	30				35				40					45			
gtg	ggt	gcc	gtg	gcc	cct	gca	ggg	gtg	gca	gag	atg	ggg	cac	ggg	cat		460
Val	Gly	Ala	Val	Ala	Pro	Ala	Gly	Val	Ala	Glu	Met	Gly	His	Gly	His		
			50					55					60				
tgg	ggt	ctc	cat	cag	cct	ctg	tgg	ggg	gtc	tca	ggg	tgg	gca	gtg	ggg		508
Trp	Gly	Leu	His	Gln	Pro	Leu	Trp	Gly	Val	Ser	Gly	Trp	Ala	Val	Gly		
	65					70				75							
gtg	ggg	ctg	gga	cgc	tgt	ttg	tgc	tca	gcg	ggg	aca	gcc	agg	gtt	gat		556
Val	Gly	Leu	Gly	Arg	Cys	Leu	Cys	Ser	Ala	Gly	Thr	Ala	Arg	Val	Asp		
	80					85				90							
ctg	gcc	ccg	agg	gtt	ttg	gat	gtt	ttt	agg	atg	aca	taaaaagcaa					602
Leu	Ala	Pro	Arg	Val	Leu	Asp	Val	Phe	Arg	Met	Thr						
	95				100					105							
gtgttttccc	catttccctct	tatgaaacac	cgtctgagcc	caaggtacac	attgggcggc												662
ctgcaggaac	ctgctccagg	tggacacacg	ggccagcagc	cgcgaacctt	gaagctgggg												722
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cagacaccct	gcttggactg	gggtggcctc	tgctaccag	gggtctggca	cgggggaggg												842
ctggggcctt	ctctgcctgg	tacacacgga	aaggcggctg	tgccggacgca	gggtcaccgt												902
gctccggggt	ttctgacagt	cgggtgtttcc	tgggcctttg	gagtggctgc	gaggcctgaa												962
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cgccagtctg	acccttgtca	ccgcacgctc	tgccccacc	ccgttgcaag	aggtcacacc												1502
atgtcagcag	ccttgcaactg	accgcagccg	gccccaggc	ctcagagttc	tggatgcttc												1562
cgtgcggctc	caacaggcat	cgtcttccct	tccgcagggtg	gaggggcccgc	ttcccgcagg												1622
catctgagct	ctgtgccggg	gccgtggcca	tggaagatg	ttccacgctg	cctcctcctc												1682
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ttgctcaca	ttaaactgtc	gccgactgca	ggcgcagtga	ctgctgaatg	taccctgtgt												1862
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<210> 96

<211> 670

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 33..458

<220>

<221> sig_peptide

<222> 33..89

<223> Von Heijne matrix

score 6.45239823575329

seq SVFLLMVNGQVES/AQ

[illegible]

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<221> CDS
<222> 1..336

<400> 97
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Thr Ser Glu Glu Arg Thr Ala Met Lys Arg Glu Gly Gly Ala Ala His
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ctc tgc tcc gac agc ctc ccg gag tcc cag cag caa gac ggc aac cac 96

Leu	Cys	Ser	Asp	Ser	Leu	Pro	Glu	Ser	Gln	Gln	Gln	Asp	Gly	Asn	His	
-10						-5					1				5	
gca	ccc	aac	ttc	tcc	agc	cac	ggc	tca	tgc	cgc	cgt	cgc	cag	cgg	scc	144
Ala	Pro	Asn	Phe	Ser	Ser	His	Gly	Ser	Cys	Arg	Arg	Arg	Gln	Arg	Xaa	
			10					15					20			
gac	atg	aca	agg	cgc	tgc	atg	ccc	gct	agg	cca	ggg	ttc	ccc	tca	tcc	192
Asp	Met	Thr	Arg	Arg	Cys	Met	Pro	Ala	Arg	Pro	Gly	Phe	Pro	Ser	Ser	
			25				30					35				
cca	gcc	ccg	ggg	tcg	tcg	ccc	ccg	cgc	tgc	cat	ctg	aga	ccc	ggg	agt	240
Pro	Ala	Pro	Gly	Ser	Ser	Pro	Pro	Arg	Cys	His	Leu	Arg	Pro	Gly	Ser	
			40				45					50				
acc	gcc	cat	gct	gca	gcg	gga	aag	aga	aca	gag	agt	cct	ggg	gac	agg	288
Thr	Ala	His	Ala	Ala	Ala	Gly	Lys	Arg	Thr	Glu	Ser	Pro	Gly	Asp	Arg	
			55			60					65					
tac	cgt	gca	gag	ggc	ttg	aga	agg	ggc	cgg	gtc	gcg	ggg	gca	agg	gta	336
Tyr	Arg	Ala	Glu	Gly	Leu	Arg	Arg	Gly	Arg	Val	Ala	Gly	Ala	Arg	Val	
70					75					80					85	
tgaggggagg	gctgcagacc	gcogetcttcc	cagttcccgcc	catcctccgc	gagctcaggc											396
ggtggcattt	cggggcctgg	caaateccccg	ccccgcctcc	gcgcaggggc	tactgggagt											456
tggagtttgc	ttctctgtag	ttgggcagct	gctcttggtc	tagtgaccac	cagcctggac											516
agctacggag	aaccgcctt	aggtagaaag	aaagtgattt	tttcccttg	caagagtttg											576
acccgggacc	ctaactgctt	aatgcatatt	tagatcggtt	tctgtacgtt	gtcagttcta											636
ctgatacctag	tggttttagta	atataaacct	tttctatggt	gtgggtgaaa	ttatgtaacc											696
tgtgatgagg	gaatcccttc	cacgaattac	ttttagtcc	agcgtgcacg	ctagttcata											756
cttaaaagaa	cttgcagatt	tggaaatgtga	cgtgttttct	ctttcagtaa	cttcacgcct											816
ctccaagagg	ctaatttttt	tgtaaagatt	ttgtgggagc	tatgtaatga	gatggggagt											876
ttcatcta	gacatcctct	gacaataaaa	aatgttttaa	ttccccaaaa	aaaaaaaaaa											936
aaa																939

<210> 98
 <211> 661
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 174..443

<220>
 <221> sig_peptide
 <222> 174..269
 <223> Von Heijne matrix
 score 4.13107367257584
 seq SSLAFCQVGFLTA/QP

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ctagatgacc	gactttaccc	acttcaaagt	ctaccttgac	cctagcactc	tctccaccct											120
gcatactcac	ctcagaccat	cagttgggta	ggccaacagc	tcaccatcaa	ttc atg											176
					Met											
ccc tgc cta	gac caa	cag ctc	act gtt	cat gcc	cta ccc	tgc cct	gcc									224
Pro Cys Leu	Asp Gln	Gln Leu	Thr Val	His Ala	Leu Pro	Cys Pro	Ala									
-30			-25				-20									
cag ccc tcc	tct ctg	gcc ttc	tgc caa	gtg ggg	ttc tta	aca gca	cag									272
Gln Pro Ser	Ser Leu	Ala Phe	Cys Gln	Val Gly	Phe Leu	Thr Ala	Gln									
-15			-10				-5					1				
cct tca cct	ccg aga	agg cgc	aat ggg	aaa gac	aga tac	acg ttg	gtt									320
Pro Ser Pro	Pro Arg	Arg Arg	Asn Gly	Lys Asp	Arg Tyr	Thr Leu	Val									

	5		10		15											
ctg	caa	cac	cag	gaa	tgc	cag	gat	gat	tta	gcc	acc	tcc	tca	ctt	gtc	368
Leu	Gln	His	Gln	Glu	Cys	Gln	Asp	Asp	Leu	Ala	Thr	Ser	Ser	Leu	Val	
	20		25		30											
tac	ctt	tcc	ctc	ccc	tgc	ttc	aaa	gac	ttg	ggt	cga	tcg	aag	cac	caa	416
Tyr	Leu	Ser	Leu	Pro	Cys	Phe	Lys	Asp	Leu	Gly	Arg	Ser	Lys	His	Gln	
	35		40		45											
agc	atc	act	gtt	gct	gac	act	aac	aag	tagtgccaag	ggattgcctt						463
Ser	Ile	Thr	Val	Ala	Asp	Thr	Asn	Lys								
50			55													
taaggaagat	caggagcggg	acatctggtg	gcaaagaaaa	tcttttcta	at	agccccattc										523
tagtgaccac	cttcaacctc	ctcatagcag	gagagtttgg	gagtagggga	cttaggatgt											583
tttgttcttt	taatcaattc	agaaaatatg	tatgtttgaa	ataaaaataa	aaatacttga											643
gccaaaaaaa	aaaaaaaa															661

<210> 99
 <211> 647
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 282..521

<220>
 <221> sig_peptide
 <222> 282..386
 <223> Von Heijne matrix
 score 3.64439944832387
 seq LEPGLSSSAACNG/KE

<400> 99																
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tgtgaaagaa	tctcctgatg	tcataatttc	cgggtgtcac	cggaacattt	gatcatcatt											180
cctttggcaa	ttccagcctt	ctgtggaaag	gccagtagaa	agcattgatt	tattcacctc											240
tacaggaatc	agactcagcc	tcttttggtt	ttcagtgaa	t atg cct ttt caa ttt												296
				Met Pro Phe Gln Phe												
				-35												
gga acc cag cca agg agg ttt cca gtg gaa gga gga gat tct tca att																344
Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly Gly Asp Ser Ser Ile																
-30		-25		-20		-15										
gag ctg gaa cct ggg ctg agc tcc agt gct gcc tgt aat ggg aag gag																392
Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala Cys Asn Gly Lys Glu																
-10		-5		1												
atg tca cca acc agg caa ctc cgg agg tgc cct gga agt cat tgc ctg																440
Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro Gly Ser His Cys Leu																
5		10		15												
aca ata act gat gtt ccc gtc act gtt tat gca aca acg aga aag cca																488
Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala Thr Thr Arg Lys Pro																
20		25		30												
cct gca caa agc agc aag gaa atg cat cct aaa tagcaccatt aagtcttttg																541
Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys																
35		40		45												
tcaaggtctg actaggtcaa gggtaatgga ccagtatcat ctggtgatct ggtaaacaaa																601
taaaagtggg ggcaccttta gatgatgaca aaaaaaaaaa aaaaaa																647

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<211> 1006
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 251..643

<220>
 <221> sig_peptide
 <222> 251..295
 <223> Von Heijne matrix
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 seq LLMFTQLLLCGFL/YV

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 ttcttgactt taattagtat ctaggaaagt ctaaactttg gacctacctc tttttttgat 180
 actcattttt gtacttttgc tctctgggat tggttttctta aagaatctgg atccttttta 240
 atatgtcaaaa atg agt ctg ctg atg ttt aca caa cta ctg ctc tgt gga 289
 Met Ser Leu Leu Met Phe Thr Gln Leu Leu Cys Gly
 -15 -10 -5
 ttt tta tat gtt cgg gtt gat gga tcg cgt ctt cgc cag gag gac ttt 337
 Phe Leu Tyr Val Arg Val Asp Gly Ser Arg Leu Arg Gln Glu Asp Phe
 1 5 10
 ccc ccg cgg att gtg gag cat cct tcc gat gtc atc gtc tct aag ggc 385
 Pro Pro Arg Ile Val Glu His Pro Ser Asp Val Ile Val Ser Lys Gly
 15 20 25 30
 gag ccc acg act ctg aac tgc aag gcg gag ggc cgg cca acg ccc acc 433
 Glu Pro Thr Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr Pro Thr
 35 40 45
 att gag tgg tac aaa gat ggg gag cga gtg gag act gac aag gac gat 481
 Ile Glu Trp Tyr Lys Asp Gly Glu Arg Val Glu Thr Asp Lys Asp Asp
 50 55 60
 ccc cgg tcc cac agg atg ctt ctg ccc agc gga tcc tta ttc ttc ttg 529
 Pro Arg Ser His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe Phe Leu
 65 70 75
 cgc atc gtg cac ggg cgc agg agt aaa cct gat gaa gga agc tac gtt 577
 Arg Ile Val His Gly Arg Arg Ser Lys Pro Asp Glu Gly Ser Tyr Val
 80 85 90
 tgt gtt gcg agg aac tat ctt ggt gaa gca gtg agt cga aat gcg tct 625
 Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser Arg Asn Ala Ser
 95 100 105 110
 ctg gaa gtg gca tgt aag tgaacataat gaacctcatg tgcacattta 673
 Leu Glu Val Ala Cys Lys
 115
 cttttattta tttcaagtaa gttttgatgt gttcccatag acgctgaaac ctaaagaatc 733
 aatcaacaca ctgcataatt ttacttggtc ttcttcagag aagtctggtc aagatagtat 793
 caagccaggg tgtttagta agtttgttta tatgaaatca agatgaccaa tatgttatta 853
 taagaaagca ggccgggcgc ggtgggtcac gcctgtaatc ccagcacttt gggaggcgga 913
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 tctctacaaa aaatacaaaa aaaaaaaaaa aaa 1006

<210> 101
 <211> 1059
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 179..475

<220>
 <221> sig_peptide
 <222> 179..295
 <223> Von Heijne matrix
 score 4.14109371250204
 seq PSLIAGLFVGCILA/GY

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 gacttctgtc ttttcagctg cagtgaaggc tcggggctgc agaattgcaa ccttgcca 178
 atg gac ctg atc ggt ttt ggt tat gca gcc ctc gtg aca ttt gga agc 226
 Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser
 -35 -30 -25
 att ttt gga tat aag cgg aga ggt ggt gtt ccg tct ttg att gct ggt 274
 Ile Phe Gly Tyr Lys Arg Arg Gly Gly Val Pro Ser Leu Ile Ala Gly
 -20 -15 -10
 ctt ttt gtt gga tgt ttg gcc ggc tat gga gct tac cgt gtc tcc aat 322
 Leu Phe Val Gly Cys Leu Ala Gly Tyr Gly Ala Tyr Arg Val Ser Asn
 -5 1 5
 gac aaa cga gat gta aaa gtg tca ctg ttt aca gct ttc ttc ctg gct 370
 Asp Lys Arg Asp Val Lys Val Ser Leu Phe Thr Ala Phe Phe Leu Ala
 10 15 20 25
 acc ata atg ggt gtg aga ttt aag agg tcc aag aaa ata atg cct gct 418
 Thr Ile Met Gly Val Arg Phe Lys Arg Ser Lys Lys Ile Met Pro Ala
 30 35 40
 ggt ttg gtt gca ggt tta agc ctc atg atg atc ctg aga ctt gtc ttg 466
 Gly Leu Val Ala Gly Leu Ser Leu Met Met Ile Leu Arg Leu Val Leu
 45 50 55
 ttg ctg ctc tgagcatctg gaggaacaga aaactaagtt catgtcatcc 515
 Leu Leu Leu
 60
 tgctgtaatg ggcagagcat attttttttg tattttaaag ataaacttca atatggaatg 575
 ctagaaacac aaatagcact gtcacctcta atatgaacat tagtttgagg tagttttttt 635
 ctaaagcaaa aattttaact gtttttcta tgtcaagcac tattttcatt aaaagtgtct 695
 aatgaatcat gatatactct tccatttggt gtgtctatatt tttatatatt tggatatttt 755
 tgaaaattcc aaatactcat gtctcaagta agcttaaaact acaacttgtc acataaagga 815
 agtcttaagt ggagttcaca gaatgataat gtatctatatt gtcatttggt ttatatattga 875
 aattattaga aattatgctt tttccatttt aattgtattg ctgccagtgc tatttttttc 935
 tttaaaaaat tttattctta gcacactggt atgtcctaac tgaatgtatt cagtattcaa 995
 ataaaagaca ttttgggtcca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1055
 aaaa 1059

<210> 102
 <211> 514
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 34..327

<220>

<221> sig_peptide
 <222> 34..162
 <223> Von Heijne matrix
 score 5.69273078757386
 seq LGDALLFLRPAGS/CA

<400> 102
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 Met Cys Glu Thr Leu Leu Thr
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 agt aaa tgg gct tca gta tcc ccc atc cct gca ctc ctg cag gaa ggt 102
 Ser Lys Trp Ala Ser Val Ser Pro Ile Pro Ala Leu Leu Gln Glu Gly
 -35 -30 -25
 gag aat cgg gac agt cgc agg ctg gga gac gct ctg ctt ttc ctg cgt 150
 Glu Asn Arg Asp Ser Arg Arg Leu Gly Asp Ala Leu Leu Phe Leu Arg
 -20 -15 -10 -5
 cct gct ggg agc tgc gcg ctc cag gta tcc tgg cct gcc gcc cta gcc 198
 Pro Ala Gly Ser Cys Ala Leu Gln Val Ser Trp Pro Ala Ala Leu Ala
 1 5 10
 ggc cca agg agc cac aca gga cag ttg acc caa cac ttc tgc cac ctg 246
 Gly Pro Arg Ser His Thr Gly Gln Leu Thr Gln His Phe Cys His Leu
 15 20 25
 aag aac gac acc tgc att cct cca tct ctg gga cca cca agg aac tca 294
 Lys Asn Asp Thr Cys Ile Pro Pro Ser Leu Gly Pro Pro Arg Asn Ser
 30 35 40
 ggg agc ttg gaa tct ctc aga tca aaa aga tac tgactcatcg gatagccatg 347
 Gly Ser Leu Glu Ser Leu Arg Ser Lys Arg Tyr
 45 50 55
 gcatcctgaa aacggccttc cttgtgtgta cattatttgc aacaagcaac aagtttataa 407
 gcaatttggg aaaattgcat gtgagggtta aaatattaaa gtcagtgcgt caacttgaaa 467
 taaatgatga gttattgatt actgctaaag aaaaaaaaaa aaaaaaa 514

<210> 103
 <211> 1158
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 303..953

<220>
 <221> sig_peptide
 <222> 303..359
 <223> Von Heijne matrix
 score 5.47911600153114
 seq LCCSGCVPSLCCS/SY

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 atcaggtttt taacttaagt cgtgaggat acaacgggtga acacaagatt cattttatatt 180
 tcatcaccat gggacgtatc ctgttggtga gttctctggg tcagacctct gaagacttct 240
 cagatggatc ctagtctctg ggcttgccct gaaattactc gctgctcagg gagagagttg 300
 aa atg gtt ggc atc ctc cca ctc tgt tgc tcc ggc tgt gtc ccc tcg 347
 Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser
 -15 -10 -5
 ctc tgt tgt tcc agc tat gtc ccc tct gtt gct cca act gca gct cat 395

Leu	Cys	Cys	Ser	Ser	Tyr	Val	Pro	Ser	Val	Ala	Pro	Thr	Ala	Ala	His	
				1				5					10			
tct	ggt	aga	ggt	cct	cat	tca	gct	ggg	cac	tgt	ggc	cag	agg	gtg	ttg	443
Ser	Val	Arg	Val	Pro	His	Ser	Ala	Gly	His	Cys	Gly	Gln	Arg	Val	Leu	
		15					20					25				
gcc	tgc	tcc	ctt	cct	caa	gta	ttc	tta	aag	cca	tgg	att	ttt	gtg	gag	491
Ala	Cys	Ser	Leu	Pro	Gln	Val	Phe	Leu	Lys	Pro	Trp	Ile	Phe	Val	Glu	
	30					35				40						
cat	ttt	tct	tcc	tgg	ctc	tcc	ctt	gag	tta	ttt	tcc	ttt	ctt	cgc	tat	539
His	Phe	Ser	Ser	Trp	Leu	Ser	Leu	Glu	Leu	Phe	Ser	Phe	Leu	Arg	Tyr	
45					50					55					60	
ctt	ggg	act	ctt	ctt	tgt	gct	tgc	gga	cat	cgg	ttg	aga	gaa	gga	cga	587
Leu	Gly	Thr	Leu	Leu	Cys	Ala	Cys	Gly	His	Arg	Leu	Arg	Glu	Gly	Arg	
				65					70					75		
ctt	ctt	cct	tgt	ctc	ctt	ggg	ggt	ggc	tgc	tgg	ttg	ctc	ttc	aac	aac	635
Leu	Leu	Pro	Cys	Leu	Leu	Gly	Val	Gly	Ser	Trp	Leu	Leu	Phe	Asn	Asn	
		80						85					90			
tgg	act	gga	ggc	tct	tgg	ttt	tct	ctt	cat	ctt	caa	caa	gtc	agt	ctc	683
Trp	Thr	Gly	Gly	Ser	Trp	Phe	Ser	Leu	His	Leu	Gln	Gln	Val	Ser	Leu	
	95					100					105					
tct	caa	ggg	tct	cac	ggt	gca	gca	ttc	tta	cca	gag	gcc	att	ggg	cct	731
Ser	Gln	Gly	Ser	His	Val	Ala	Ala	Phe	Leu	Pro	Glu	Ala	Ile	Gly	Pro	
	110					115					120					
gga	ggt	cca	ggt	cca	gtg	tct	gga	gag	tcc	acc	tca	gct	cag	caa	tct	779
Gly	Val	Pro	Val	Pro	Val	Ser	Gly	Glu	Ser	Thr	Ser	Ala	Gln	Gln	Ser	
125					130					135					140	
cat	gcc	ggg	tgg	caa	ttg	tca	gca	gaa	gcc	gat	gcc	tgc	cca	tca	ggt	827
His	Ala	Gly	Trp	Gln	Leu	Ser	Ala	Glu	Ala	Asp	Ala	Cys	Pro	Ser	Val	
				145					150					155		
ctt	tac	tct	gag	gtg	tta	gag	tgg	aat	aaa	aat	ata	aat	act	tat	act	875
Leu	Tyr	Ser	Glu	Val	Leu	Glu	Trp	Asn	Lys	Asn	Ile	Asn	Thr	Tyr	Thr	
		160						165					170			
agt	ttt	cat	gac	ttc	tgc	tta	ata	ttg	ggg	att	ttt	ktt	ggt	ttg	ttt	923
Ser	Phe	His	Asp	Phe	Cys	Leu	Ile	Leu	Gly	Ile	Phe	Xaa	Val	Leu	Phe	
	175					180					185					
tgt	ttt	ggc	ggg	gat	agg	ctt	acc	tta	cat	taaaccaggc	cttagccttt					973
Cys	Phe	Gly	Gly	Asp	Arg	Leu	Thr	Leu	His							
	190					195										
ctgtggccttt	ggttatggcaa	agcctcatat	tactctctag	tctggttcag	caggacagtc											1033
aggtccacac	ctggggctgt	ttgttttcta	cgtttacctc	aacataaggt	accttatcat											1093
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 <213> Homo sapiens

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 <222> 97..645

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 seq AVVGCLLVPPAEA/NK

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 <222> 972
 <223> n=a, g, c or t

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gtgtccggct ttgctggccc agcaagcctg ataagc atg aag ctc tta tct ttg      114
                                     Met Lys Leu Leu Ser Leu
                                     -20                               -15

gtg gct gtg gtc ggg tgt ttg ctg gtg ccc cca gct gaa gcc aac aag      162
Val Ala Val Val Gly Cys Leu Leu Val Pro Pro Ala Glu Ala Asn Lys
                                     -10                               -5                               1

agt tct gaa gat atc cgg tgc aaa tgc atc tgt cca cct tat aga aac      210
Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile Cys Pro Pro Tyr Arg Asn
                                     5                               10                               15

atc agt ggg cac att tac aac cag aat gta tcc cag aag gac tgc aac      258
Ile Ser Gly His Ile Tyr Asn Gln Asn Val Ser Gln Lys Asp Cys Asn
                                     20                               25                               30

tgc ctg cac gtg gtg gag ccc atg cca gtg cct ggc cat gac gtg gag      306
Cys Leu His Val Val Glu Pro Met Pro Val Pro Gly His Asp Val Glu
35                               40                               45                               50

gcc tac tgc ctg ctg tgc gag tgc agg tac gag gag cgc agc acc acc      354
Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr
                                     55                               60                               65

acc atc aag gtc atc att gtc atc tac ctg tcc gtg gtg ggt gcc ctg      402
Thr Ile Lys Val Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu
                                     70                               75                               80

ttg ctc tac atg gcc ttc ctg atg ctg gtg gac cct ctg atc cga aag      450
Leu Leu Tyr Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys
85                               90                               95

ccg gat gca tac act gag caa ctg cac aat gag gag gag aat gag gat      498
Pro Asp Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp
100                               105                               110

gct cgc tct atg gca gca gct gct gca tcc ctc ggg gga ccc cga gca      546
Ala Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
115                               120                               125                               130

aac aca gtc ctg gag cgt gtg gaa ggt gcc cag cag cgg tgg aag ctg      594
Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys Leu
135                               140                               145

cag gtg cag gag cag cgg aag aca gtc ttc gat cgg cac aag atg ctc      642
Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys Met Leu
150                               155                               160

agc tagatgggct ggtgtggttg ggtcaaggcc ccaacacccat ggctgccagc      695
Ser

ttccaggctg gacaaagcag ggggctactt ctcccttccc tcggttccag tcttcccttt      755
aaaagcctgt ggcatttttc ctcccttctcc ctaacttttag aaatgttgta cttggctatt      815
ttgattaggg aagaggggatg tgggtctctga tctctgttgt cttcttgggg ctttggggtt      875
gaagggaggg ggaaggcagg cccasaaggg aatggagaca ttcgaggcgg cctcaggagt      935
ggatgcgac ttgtctctcc tkggcctccc actcttngcc gccttccagc tctgagtctt      995
gggaatgttg ttacccttgg aagataaagy ctgggtcttc aggaactcag tgtctgggag      1055
gaaagcatgg ccagcattc agcatgtgtt cctttctgca gtggttctta tcaccacctc      1115
cctcccagcc ccagcgcctc agccccagcc ccagctccag ccctgaggac agctctgatg      1175
ggagagctgg gccccctgag cccactgggt cttcagggtg cactggaagc tgggtgttcgc      1235
tgtccctgt gcacttctcg cactggggca tggagtgcc atgcatactc tgctgccggg      1295
cccctcacct gcacttgagg ggtctgggca gtccctctc tccccagtgt ccacagtcac      1355
tgagccagac ggtcgggttg aacatgagac tcgaggctga gcgtggatct gaacaccaca      1415

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gccctgtac ttgggttgcc tcttgtccct gaacttcgtt gtaccagtgc atggagagaa 1475
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tatttctctc taaaaaaaaa aaaaaaaaaa 1563

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<222> 80..118
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tcagcgccga agccgcgcc atg ctc gtc ctc aga agc gcc ctg act cgg gcg 112
               Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala
               -10                               -5
ctg gcc tca cgg acg ctg gcg cct cag atg tgc tca tct ttt gct acg 160
Leu Ala Ser Arg Thr Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr
               1           5           10
gga ccc aga caa tac gat gga ata ttc tat gaa ttt cgt tct tat tac 208
Gly Pro Arg Gln Tyr Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr
15           20           25           30
ctt aag ccc tca aag atg aat gag ttc ctg gaa aat ttt gag aaa aac 256
Leu Lys Pro Ser Lys Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn
               35           40           45
gct cat ctt cgg aca gct cac tct gaa ttg gtt gga tac tgg agt gta 304
Ala His Leu Arg Thr Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val
               50           55           60
gaa ttt gga ggc aga atg aat aca gtg ttt cat att tgg aag tat gat 352
Glu Phe Gly Gly Arg Met Asn Thr Val Phe His Ile Trp Lys Tyr Asp
65           70           75
aat ttt gct cat cga act gaa gtt cag aaa gcc ttg gcc aaa gat aag 400
Asn Phe Ala His Arg Thr Glu Val Gln Lys Ala Leu Ala Lys Asp Lys
80           85           90
gaa tgg caa gaa caa ttc ctc att cca aat ttg gct ctc att gat aaa 448
Glu Trp Gln Glu Gln Phe Leu Ile Pro Asn Leu Ala Leu Ile Asp Lys
95           100           105           110
caa gag agt gag att act tat ctg gta cca tgg tgc aaa tta gaa aaa 496
Gln Glu Ser Glu Ile Thr Tyr Leu Val Pro Trp Cys Lys Leu Glu Lys
115           120           125
cct cca aaa gaa gga gtc tat gaa ctg gcc act ttt cag atg aaa cct 544
Pro Pro Lys Glu Gly Val Tyr Glu Leu Ala Thr Phe Gln Met Lys Pro
130           135           140
ggg ggg cca gct ctg tgg ggt gat gca ttt aaa agg gca gtt cat gct 592
Gly Gly Pro Ala Leu Trp Gly Asp Ala Phe Lys Arg Ala Val His Ala
145           150           155
cat gtc aat cta ggc tac aca aaa cta gtt gga gtg ttc cac aca gag 640
His Val Asn Leu Gly Tyr Thr Lys Leu Val Gly Val Phe His Thr Glu
160           165           170

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tac gga gca ctc aac aga gtt cat gtt ctt tgg tgg aat gag agt gca      688
Tyr Gly Ala Leu Asn Arg Val His Val Leu Trp Trp Asn Glu Ser Ala
175                      180                      185                      190
gat agt cgt gca gct ggg aga cat aag tcc cat gag gat ccc aga gtt      736
Asp Ser Arg Ala Ala Gly Arg His Lys Ser His Glu Asp Pro Arg Val
                      195                      200                      205
gtg gca gct gtt cgg gaa agt gtc aac tac cta gta tct cag cag aat      784
Val Ala Ala Val Arg Glu Ser Val Asn Tyr Leu Val Ser Gln Gln Asn
                      210                      215                      220
atg ctt ctg att cct aca tcg ttt tca cca ctg aaa tagtttttcta      830
Met Leu Leu Ile Pro Thr Ser Phe Ser Pro Leu Lys
                      225                      230
ctgaaataca aaacatttca ttaactgcta taggatctct ctgctaattgg tgcttaaatt      890
ctcccaagag gttctcactt ttatttgaag gaggtggtaa gttaatttgc tatgtttctt      950
gcattatgaa ggctacatct gtgctttgta agtaccactt caaaaaatag ttctgtttac    1010
tttctgcatg gtatttcagt gtctgtcata cattaaaaat acttgtcact gttttaagat    1070
cttgactctt catttgtttc agaatagctc ttctactgta ttctgacaac tctttgcttt    1130
atagcattttt gttgtattca aatgataatg gtagcatttc catgcttgtg acagcattttl    1190
taagttatta atatatttta tcaacctttc catcatgtct gttttcctgg ttttttttgg    1250
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tttcacatta gttatttgtc acttacttgg aaaatgatgc tgtttaggtcc tggattataa    1430
aatctagaaa agacttgttg gtttatgtgc tgaaatgtct ttatttataa ttaatttttaa    1490
ctactattta ctttatttcg gatcctgttt aacaaagata cttgagacat ccatttgttt    1550
taatgaaatc tgtatggata tggaaatgct tgcctaata aaagcctaca tatacaaaaa    1610
aaaaaaaaaa a                                     1621

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<211> 557
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<213> Homo sapiens

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<222> 77..388

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<222> 77..217
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      seq FLYLTLNQSCIFA/NY

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cctcccaaac caaaag atg ttc tct ccg cgc caa gct ttg acg ccc gac ccc      112
      Met Phe Ser Pro Arg Gln Ala Leu Thr Pro Asp Pro
                      -45                      -40
ctg cac tct ccc gcc tac tca ccg gtc cta ggg ggt tgg tcc cgc ttt      160
Leu His Ser Pro Ala Tyr Ser Pro Val Leu Gly Gly Trp Ser Arg Phe
-35                      -30                      -25                      -20
cgt agt gtg gat ttt cgt ttc ctc tac ttg act cta aat caa tcc tgt      208
Arg Ser Val Asp Phe Arg Phe Leu Tyr Leu Thr Leu Asn Gln Ser Cys
                      -15                      -10                      -5
ata ttc gca aac tac aaa gag gcg cat gca aat aga tac tgt act gag      256
Ile Phe Ala Asn Tyr Lys Glu Ala His Ala Asn Arg Tyr Cys Thr Glu
      1                      5                      10
ggc aga tac acg cgc gag atc cag agg ctt aca tcc cca gcc gct tgg      304

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Gly Arg Tyr Thr Arg Glu Ile Gln Arg Leu Thr Ser Pro Ala Ala Trp
15 20 25
ccc acc aga gac aag aac agg atg ata agc aat gga atg gca ttg aac 352
Pro Thr Arg Asp Lys Asn Arg Met Ile Ser Asn Gly Met Ala Leu Asn
30 35 40 45
tct cct gct gaa gga ctt gca ttt caa tgt aga ttc tgaggctggg 398
Ser Pro Ala Glu Gly Leu Ala Phe Gln Cys Arg Phe
50 55
tgaaaacttc tctgtcacct ttactacagc attctcacc atttatattt ctttcccctt 458
ctacatctct attactgttg cactatgtta tgcattacac catggcaaaa ttaatcaatt 518
aatacaataa aagcttaatt ttaaaaaaaaa aaaaaaaaaa 557

<210> 107
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<213> Homo sapiens

<220>
<221> CDS
<222> 139..513

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<221> sig_peptide
<222> 139..201
<223> Von Heijne matrix
score 5.86857787719223
seq IVMGVQVVGRAFA/RA

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tgacccgccg accacgcttg atccccggcc gcggggccag gaagtcggag tttgagcccc 120
ggaggcagag cggctgcc atg gcc aag tac ctg gcc cag atc att gtg atg 171
Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met
-20 -15
ggc gtg cag gtg gtg ggc agg gcc ttt gca cgg gcc ttg cgg cag gag 219
Gly Val Gln Val Val Gly Arg Ala Phe Ala Arg Ala Leu Arg Gln Glu
-10 -5 1 5
ttt gca gcc agc cgg gcc gca gct gat gcc cga gga cgc gct gga cac 267
Phe Ala Ala Ser Arg Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His
10 15 20
cgg tct gca gcc gct tcc aac ctc tcc ggc ctc agc ctc cag gag gca 315
Arg Ser Ala Ala Ala Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala
25 30 35
cag cag att ctc aac gtg tcc aag ctg agc cct gag gag gtc cag aag 363
Gln Gln Ile Leu Asn Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys
40 45 50
aac tat gaa cac tta ttt aag gtg aat gat aaa tcc gtg ggt ggc tcc 411
Asn Tyr Glu His Leu Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser
55 60 65 70
ttc tac ctg cag tca aag gtg gtc cgc gca aag gag cgc ctg gat gag 459
Phe Tyr Leu Gln Ser Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu
75 80 85
gaa ctc aaa atc cag gcc cag gag gac aga gaa aaa ggg cag atg ccc 507
Glu Leu Lys Ile Gln Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro
90 95 100
cat acg tgactgctcg gctccccccg cccaccccg cgcctctaatt ttatagcttg 563
His Thr
gtaataaatt tcttttctac aaaaaaaaaa aaaaaaa 600

<210> 108
 <211> 1129
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> 81..986

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 <221> sig_peptide
 <222> 81..134
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 score 5.03543461931947
 seq ITLLGLAVNVVTT/LV

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 Met Ala Pro Asn Ser Ile Thr Leu Leu Gly Leu
 -15 -10
 gcc gtc aac gtg gtc acc acg ctc gtg ctc atc tcc tac tgt ccc acg 161
 Ala Val Asn Val Val Thr Thr Leu Val Leu Ile Ser Tyr Cys Pro Thr
 -5 1 5
 gcc acc gaa gag gca cca tac tgg aca tac ctt tta tgt gca ctg gga 209
 Ala Thr Glu Glu Ala Pro Tyr Trp Thr Tyr Leu Leu Cys Ala Leu Gly
 10 15 20 25
 ctt ttt att tac cag tca ctg gat gct att gat ggg aaa caa gcc aga 257
 Leu Phe Ile Tyr Gln Ser Leu Asp Ala Ile Asp Gly Lys Gln Ala Arg
 30 35 40
 aga aca aac tct tgt tcc cct tta ggg gag ctc ttt gac cat ggc tgt 305
 Arg Thr Asn Ser Cys Ser Pro Leu Gly Glu Leu Phe Asp His Gly Cys
 45 50 55
 gac tct ctt tcc aca gta ttt atg gca gtg gga gct tca att gcc gct 353
 Asp Ser Leu Ser Thr Val Phe Met Ala Val Gly Ala Ser Ile Ala Ala
 60 65 70
 cgc tta gga act tat cct gac tgg ttt ttt ttc tgc tct ttt att ggg 401
 Arg Leu Gly Thr Tyr Pro Asp Trp Phe Phe Phe Cys Ser Phe Ile Gly
 75 80 85
 atg ttt gtg ttt tat tgc gct cat tgg cag act tat gtt tca ggc atg 449
 Met Phe Val Phe Tyr Cys Ala His Trp Gln Thr Tyr Val Ser Gly Met
 90 95 100 105
 ttg aga ttt gga aaa gtg gat gta act gaa att cag ata gct tta gtg 497
 Leu Arg Phe Gly Lys Val Asp Val Thr Glu Ile Gln Ile Ala Leu Val
 110 115 120
 att gtc ttt gtg ttg tct gca ttt gga gga gca aca atg tgg gac tat 545
 Ile Val Phe Val Leu Ser Ala Phe Gly Gly Ala Thr Met Trp Asp Tyr
 125 130 135
 acg ggc acc agt gtc ttg tca cct gga ctc cac ata gga cta att att 593
 Thr Gly Thr Ser Val Leu Ser Pro Gly Leu His Ile Gly Leu Ile Ile
 140 145 150
 ata ctg gca ata atg atc tat aaa aag tca gca act gat gtg ttt gaa 641
 Ile Leu Ala Ile Met Ile Tyr Lys Lys Ser Ala Thr Asp Val Phe Glu
 155 160 165
 aag cat cct tgt ctt tat atc cta atg ttt gga tgt gtc ttt gct aaa 689
 Lys His Pro Cys Leu Tyr Ile Leu Met Phe Gly Cys Val Phe Ala Lys
 170 175 180 185

gtc tca caa aaa tta gtg gta gct cac atg acc aaa agt gaa cta tat	737
Val Ser Gln Lys Leu Val Val Ala His Met Thr Lys Ser Glu Leu Tyr	
190 195 200	
ctt caa gac act gtc ttt ttg ggg cca ggt ctt ttg ttt tta gac cag	785
Leu Gln Asp Thr Val Phe Leu Gly Pro Gly Leu Leu Phe Leu Asp Gln	
205 210 215	
tac ttt aat aac ttt ata gac gaa tat gtt gtt cta tgg atg gca atg	833
Tyr Phe Asn Asn Phe Ile Asp Glu Tyr Val Val Leu Trp Met Ala Met	
220 225 230	
gtg att tct tca ttt gat atg gtg ata tac ttt agt gct ttg tgc ctg	881
Val Ile Ser Ser Phe Asp Met Val Ile Tyr Phe Ser Ala Leu Cys Leu	
235 240 245	
caa att tca aga cac ctt cat cta aat ata ttc aag act gca tgt cat	929
Gln Ile Ser Arg His Leu His Leu Asn Ile Phe Lys Thr Ala Cys His	
250 255 260 265	
caa gca cct gaa cag gtt caa gtt ctt tct tca aag agt cat cag aat	977
Gln Ala Pro Glu Gln Val Gln Val Leu Ser Ser Lys Ser His Gln Asn	
270 275 280	
aac atg gat tgaagagact tccgaacact tgctatctct tgctgctgct	1026
Asn Met Asp	
gtttcatgga aggagatatt aaacatttgt ttaattttta ttttaagtgtt atacctattt	1086
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 <213> Homo sapiens

<220>
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 <222> 266..586

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 <222> 266..307
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taaattaatg cctcttttta aataactaact tgtactactt ttgtggctgt gaatggtatc	180
ttttattgaa ctgaggcagc ttttaaaaga cttgcctgat catttagagc actccattg	240
aggttaaatt agacttgaat ctgta atg att ctc gta act gtt cct ggt gtg	292
Met Ile Leu Val Thr Val Pro Gly Val	
-10	
tgt cca gca caa tgt tgc tgg gca gag cag agg ggc aga ggc tca ggt	340
Cys Pro Ala Gln Cys Cys Trp Ala Glu Gln Arg Gly Arg Gly Ser Gly	
-5 1 5 10	
atg tac ttc att gac aag tgg gca agg cca tcc tgg gta cca cat tgg	388
Met Tyr Phe Ile Asp Lys Trp Ala Arg Pro Ser Trp Val Pro His Trp	
15 20 25	
ctt aat gat ctc ttc att gtg aag tcc ggc tac ctc gtt tgc ata aga	436
Leu Asn Asp Leu Phe Ile Val Lys Ser Gly Tyr Leu Val Cys Ile Arg	
30 35 40	
act aca gta atc agg caa ggc att gtc aga att ggg agg aat aaa atc	484
Thr Thr Val Ile Arg Gln Gly Ile Val Arg Ile Gly Arg Asn Lys Ile	

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agt gag tct gga agg agt gct ctg tat aca att gca aag aac aaa atg      532
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gtc atc ttt aag gta cct gat tgc atg cac tta aat gca gat tat ttt      580
Val Ile Phe Lys Val Pro Asp Cys Met His Leu Asn Ala Asp Tyr Phe
      80              85              90
gga gtt tgaaaaggga ctattaatga aatctttctt ttcctcctt tctctttttc      636
Gly Val
ccttccccgc cactgattca gtgagctgga gattggatca cagccgaagg agtaaagggtg      696
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Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
      -30              -25              -20
att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc      154
Ile Gly Ala Gly Ala Leu Gly Ala Ala Leu Ala Leu Leu Ala
      -15              -10              -5
aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac      202
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
      1              5              10
ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc      250
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
      15              20              25              30
aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg      298
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
      35              40              45
cgg agg cca ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc      346
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
      50              55              60
tcc ctg aaa agc atg ttg gac cag ctg ggc gtc ccc ctc tat gca gtg      394
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
      65              70              75
gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct tat ttc      442
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
      80              85              90
aaa gga gaa atc ttc ctg gat gaa aag aaa aag ttc tat ggt cca caa      490
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
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agg cgg aag atg atg ttt atg gga ttt atc cgt ctg gga gtg tgg tac      538
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
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aac ttc ttc cga gcc tgg aac gga ggc ttc tct gga aac ctg gaa gga      586
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
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gaa ggc ttc atc ctt ggg gga gtt ttc gtg gtg gga tca gga aag cag      634
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln
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ggc att ctt ctt gag cac cga gaa aaa gaa ttt gga gac aaa gta aac      682
Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn
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Ala Ser Glu Lys Lys
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<223> Von Heijne matrix
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      seq LGAAALALLLANT/DV

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Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
                               -30                               -25                               -20
att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc      154
Ile Gly Ala Gly Ala Leu Gly Ala Ala Leu Ala Leu Leu Ala
                               -15                               -10                               -5
aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac      202
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
                               1                               5                               10
ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc      250
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
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aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg      298
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
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cgg agg cca ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc      346
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
                               50                               55                               60
tcc ctg aaa agc atg ttg gac cag ctg ggc gtc ccc ctc tat gca gtg      394
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
                               65                               70                               75
gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct tat ttc      442
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
                               80                               85                               90
aaa gga gaa atc ttc ctg gat gaa aag aaa aag ttc tat ggt cca caa      490
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
                               95                               100                               105                               110
agg cgg aag atg atg ttt atg gga ttt atc cgt ctg gga gtg tgg tac      538
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
                               115                               120                               125
aac ttc ttc cga gcc tgg aac gga ggc ttc tct gga aac ctg gaa gga      586
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
                               130                               135                               140
gaa ggc ttc atc ctt ggg gga gtt ttc gtg gtg gga tca gga agc agg      634
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Ser Arg
                               145                               150                               155
gca ttc ttc ttg agc acc gag aaa aag aat ttg gag aca aag      676
Ala Phe Phe Leu Ser Thr Glu Lys Lys Asn Leu Glu Thr Lys
                               160                               165                               170
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<222> 15..278

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<223> Von Heijne matrix

score 12.2610572403264

seq PLFLLLLLGSVTA/DI

<400> 112

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Pro	Thr	Thr	Pro	Leu	Phe	Leu	Leu	Leu	Leu	Gly	Ser	Val	Thr	Ala													
			-15				-10				-5																
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cctggggaat agtctggccc gctccttgga accacactca gactca atg gac tct 175
Met Asp Ser
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gcc tca aat ccc acc aac ctt gtc agc acc tcc caa agg cac cgg ccc 223
Ala Ser Asn Pro Thr Asn Leu Val Ser Thr Ser Gln Arg His Arg Pro
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Leu Leu Ser Ser Cys Gly Leu Pro Pro Ser Thr Ala Ser Ala Val Arg
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Arg Leu Cys Ser Arg Gly Val Leu Lys Gly Ser Asn Glu Arg Arg Asp
5 10 15
atg gaa tca ttt tgg aaa cta aat cgt tcc cca ggg tcg gac cga tac 367
Met Glu Ser Phe Trp Lys Leu Asn Arg Ser Pro Gly Ser Asp Arg Tyr
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tgg aca gtc gag gat gtg atg cag ttt gtc cgg gaa gct gat cct cag 463
Trp Thr Val Glu Asp Val Met Gln Phe Val Arg Glu Ala Asp Pro Gln
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ctt gga ccc cac gct gac ctg ttt cgc aaa cac gag atc gat ggc aag 511
Leu Gly Pro His Ala Asp Leu Phe Arg Lys His Glu Ile Asp Gly Lys
70 75 80
gcc ctg ctg ctg ctg cgc agt gac atg atg atg aag tac atg ggc ctg 559
Ala Leu Leu Leu Leu Arg Ser Asp Met Met Met Lys Tyr Met Gly Leu
85 90 95
aag ctg ggg cct gca ctc aag ctc tcc tac cac att gac cgg ctg aag 607
Lys Leu Gly Pro Ala Leu Lys Leu Ser Tyr His Ile Asp Arg Leu Lys
100 105 110 115
cag ggc aag ttc tgaaccagga gaggcagcct agacaaccaa gtggcagcag 659
Gln Gly Lys Phe
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<221> sig_peptide

<222> 223..270

<223> Von Heijne matrix

score 4.19788230215007

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cctatccccg gccccgctcg ggcctttccc cttgcgcctt ggctcggctg gctcgacgag    180
cagtaagttc gtagccgccc tccgaagccg ggcgtgcatg gg atg gca gag ttg    234
                                     Met Ala Glu Leu
                                     -15
gcg tgc gtg cgt gag tcc acc agt gtg gca tgg gca tgt aag gtg cgc    282
Ala Cys Val Arg Glu Ser Thr Ser Val Ala Trp Ala Cys Lys Val Arg
      -10                -5                1
gga ggg act gca cct tct cca tca ggt gca gaa ggc cac gtc atg ctg    330
Gly Gly Thr Ala Pro Ser Pro Ser Gly Ala Glu Gly His Val Met Leu
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aac aag agc cga gaa gta gaa tcg cca gtg tca agc cgt cca cgt tgt    378
Asn Lys Ser Arg Glu Val Glu Ser Pro Val Ser Ser Arg Pro Arg Cys
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Gly Met Pro Thr Val Pro Pro Gly Ser Leu Lys Thr Leu
      40          45
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tccacatgca aatccatcca gaggcaggaa ctgggaatag gcttgagggt ggccaggaca    547
gcaagtgggc tgtctgtata aacctcccct ccacttgga aggaaaatca cccccaagt    607
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<221> sig_peptide

<222> 166..237

<223> Von Heijne matrix

score 6.60662787180923

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tccgggtgct gcggattgag gtcccggttc ctaacggact gcaag atg gag gaa ggc    177
                                     Met Glu Glu Gly
ggg aac cta gga ggc ctg att aag atg gtc cat cta ctg gtc ttg tca    225
Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu Leu Val Leu Ser
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Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys
      15      20      25
ctc ttc ccc ttc tac ttc cac atc tcc atg ggc tgt gsc ttc atc aac      369
Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys Xaa Phe Ile Asn
      30      35      40
ctc tgc atc ttg gct tca cag cat gct tgg gct cag ctc aca ttc tgg      417
Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp
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gag gcc agc cag ctt tac ctg ctg ttc ctg agc ctt acg ctg gcc act      465
Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr
      65      70      75
gtc aac gcc cgc tgg ctg gaa ccc cgc acc aca gct gcc atg tgg gcc      513
Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala
      80      85      90
ctg caa acc gtg gag aag gag cga ggc ctg ggt ggg gag gta cca ggc      561
Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly
      95      100      105
agc cac cag ggt ccc gat ccc tac cgc cag ctg cga gag aag gac ccc      609
Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro
      110      115      120
aag tac agt gct ctc cgc cag aat ttc ttc cgc tac cat ggg ctg tcc      657
Lys Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser
      125      130      135      140
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Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala
      145      150      155
ggc ctt gcc ctg gaa ata agg agc ctc tagcatgggc cctgcatgct      752
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<211> 804

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 75..623

<220>

<221> sig_peptide

<222> 75..215

<223> Von Heijne matrix

score 8.34104221735598

seq RLLLPCLVRMALC/AP

<400> 116

agtacggtgg ccgacgggag tcagacgctg gggatgaatg aaggtgctgg gtgcaggatc 60

aacaaacagt aata atg act gaa tgt aca agt ctt cag ttt gtc agc cct 110

Met Thr Glu Cys Thr Ser Leu Gln Phe Val Ser Pro

-45 -40

ttt gct ttt gag gca atg cag aag gtg gat gtt gtt tgc ctg gca tct 158

Phe Ala Phe Glu Ala Met Gln Lys Val Asp Val Val Cys Leu Ala Ser

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-35          -30          -25          -20
tta agt gat cca gaa tta aga ctt ctt ctg ccc tgt ttg gta cgg atg      206
Leu Ser Asp Pro Glu Leu Arg Leu Leu Leu Pro Cys Leu Val Arg Met

          -15          -10          -5
gca ctt tgt gca cct gct gac cag agc caa agc tgg gct cag gat aag      254
Ala Leu Cys Ala Pro Ala Asp Gln Ser Gln Ser Trp Ala Gln Asp Lys

          1          5          10
aaa ctc atc ctt cgc ctt ctt tct gga gtg gaa gct gtc aac tcc att      302
Lys Leu Ile Leu Arg Leu Leu Ser Gly Val Glu Ala Val Asn Ser Ile

          15          20          25
gtt gca ttg ttg tcc gtg gac ttt cat gct tta gaa caa gat gcc agc      350
Val Ala Leu Leu Ser Val Asp Phe His Ala Leu Glu Gln Asp Ala Ser

          30          35          40          45
aaa gaa cag cag ctt aga ccg agt ctt gcc ctg ttg ccc agg ctg gag      398
Lys Glu Gln Gln Leu Arg Pro Ser Leu Ala Leu Leu Pro Arg Leu Glu

          50          55          60
tgc ggt ggc gtg atc tcg gct cac tgc aac ctc cac ctc ctg ggt tca      446
Cys Gly Gly Val Ile Ser Ala His Cys Asn Leu His Leu Leu Gly Ser

          65          70          75
agt gat tct tct gcc tca gtc tcc cga gta gat ggg act aca ggc acg      494
Ser Asp Ser Ser Ala Ser Val Ser Arg Val Asp Gly Thr Thr Gly Thr

          80          85          90
cgc cac cat gcc cgg ctt ttt tgt att att agt aga gac gag gtt tca      542
Arg His His Ala Arg Leu Phe Cys Ile Ile Ser Arg Asp Glu Val Ser

          95          100          105
cca tat tgg cca ggc tgg tct cga act ccc aac ctt gtg atc cac ctg      590
Pro Tyr Trp Pro Gly Trp Ser Arg Thr Pro Asn Leu Val Ile His Leu

          110          115          120          125
cct cag cct ccc aaa gta ctg gga tta ccg gcg tgagccactg tgcctggcct      643
Pro Gln Pro Pro Lys Val Leu Gly Leu Pro Ala

          130          135
atgtggtgga gtatttatta tacgtaggat gtgaatccct gaaatacaca ggcaaactaa      703
atagcatttc agaagtaaca gaacatttta gaacacttta tacatccttt tatagcttat      763
ttcaataaaaa gataattttt atacaaaaaa aaaaaaaaaa a      804

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<210> 117
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 <213> Homo sapiens

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 <222> 30..335

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 <223> Von Heijne matrix
 score 4.49063834776683
 seq FLTALLWRGRIPG/RQ

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gcagagtctt gagcagcgcg gcaggcacc atg ttc ctg act gcg ctc ctc tgg      53
Met Phe Leu Thr Ala Leu Leu Trp

          -10
cgc ggc cgc att ccc ggc cgt cag tgg atc ggg aag cac cgg cgg ccg      101
Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg Arg Pro

          -5          1          5          10

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cgg ttc gtg tcg ttg cgc gcc aag cag aac atg atc cgc cgc ctg gag	149
Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg Leu Glu	
15 20 25	
atc gag gcg gag aac cat tac tgg ctg agc atg ccc tac atg acc cgg	197
Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met Thr Arg	
30 35 40	
gag cag gag cgc ggc cac gcc gcg gtg cgc agg agg gag gcc ttc gag	245
Glu Gln Glu Arg Gly His Ala Ala Val Arg Arg Arg Glu Ala Phe Glu	
45 50 55	
gcc ata aag gcg gcc gcc act tcc aag ttc ccc ccg cat aga ttc att	293
Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro Pro His Arg Phe Ile	
60 65 70	
gcg gac cag ctc gac cat ctc aat gtc acc aag aaa tgg tcc	335
Ala Asp Gln Leu Asp His Leu Asn Val Thr Lys Lys Trp Ser	
75 80 85	
taatcctgag tcgtcaccct tggattttat ggatcacgga gctgaccatc tttacctggt	395
cctggaactg aaaaactgta gcttgtgtga aaatgagcct ttggaccagt ctttattaaa	455
acaaacaaac acaaaaaaaaaa aaaaaaaaaa	484

<210> 118
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 21..752

<220>
 <221> sig_peptide
 <222> 21..107
 <223> Von Heijne matrix
 score 3.61056351168286
 seq FPLYLLNFLGLWS/WI

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gttttttttcc cttctgagca atg gag ctt acc atc ttt atc ctg aga ctg gcc	53
Met Glu Leu Thr Ile Phe Ile Leu Arg Leu Ala	
-25 -20	
att tac atc ctg aca ttt ccc ttg tac ctg ctg aac ttt ctg ggc ttg	101
Ile Tyr Ile Leu Thr Phe Pro Leu Tyr Leu Leu Asn Phe Leu Gly Leu	
-15 -10 -5	
tgg agc tgg ata tgc aaa aaa tgg ttc ccc tac ttc ttg gtg agg ttc	149
Trp Ser Trp Ile Cys Lys Lys Trp Phe Pro Tyr Phe Leu Val Arg Phe	
1 5 10	
act gtg ata tac aac gaa cag atg gca agc aag aag cgg gag ctc ttc	197
Thr Val Ile Tyr Asn Glu Gln Met Ala Ser Lys Lys Arg Glu Leu Phe	
15 20 25 30	
agt aac ctg cag gag ttt gcg ggc ccc tcc ggg aaa ctc tcc ctg ctg	245
Ser Asn Leu Gln Glu Phe Ala Gly Pro Ser Gly Lys Leu Ser Leu Leu	
35 40 45	
gaa gtg ggc tgt ggc acg ggg gcc aac ttc aag ttc tac cca cct ggg	293
Glu Val Gly Cys Gly Thr Gly Ala Asn Phe Lys Phe Tyr Pro Pro Gly	
50 55 60	
tgc agg gtg acc tgt att gac ccc aac ccc aac ttt gag aag ttt ttg	341
Cys Arg Val Thr Cys Ile Asp Pro Asn Pro Asn Phe Glu Lys Phe Leu	
65 70 75	
atc aag agc att gca gag aac cga cac ctg cag ttt gag cgc ttt gtg	389

Ile	Lys	Ser	Ile	Ala	Glu	Asn	Arg	His	Leu	Gln	Phe	Glu	Arg	Phe	Val		
80						85					90						
gta	gct	gcc	ggg	gag	aac	atg	cac	cag	gtg	gct	gat	ggc	tct	gtg	gat	437	
Val	Ala	Ala	Gly	Glu	Asn	Met	His	Gln	Val	Ala	Asp	Gly	Ser	Val	Asp		
95					100					105				110			
gtg	gtg	gtc	tgc	acc	ctg	gtg	ctg	tgc	tct	gtg	aag	aac	cag	gag	cgg	485	
Val	Val	Val	Cys	Thr	Leu	Val	Leu	Cys	Ser	Val	Lys	Asn	Gln	Glu	Arg		
				115					120					125			
att	ctc	cgc	gag	gtg	tgc	aga	gtg	ctg	aga	ccg	gga	ggg	gct	ttc	tat	533	
Ile	Leu	Arg	Glu	Val	Cys	Arg	Val	Leu	Arg	Pro	Gly	Gly	Ala	Phe	Tyr		
				130				135					140				
ttc	atg	gag	cat	gtg	gca	gct	gag	tgt	tcg	act	tgg	aat	tac	ttc	tgg	581	
Phe	Met	Glu	His	Val	Ala	Ala	Glu	Cys	Ser	Thr	Trp	Asn	Tyr	Phe	Trp		
				145			150					155					
caa	caa	gtc	ctg	gat	cct	gcc	tgg	cac	ctt	ctg	ttt	gat	ggg	tgc	aac	629	
Gln	Gln	Val	Leu	Asp	Pro	Ala	Trp	His	Leu	Leu	Phe	Asp	Gly	Cys	Asn		
				160		165				170							
ctg	acc	aga	gaq	agc	tgg	aag	gcc	ctg	gag	cgg	gcc	agc	ttc	tct	aag	677	
Leu	Thr	Arg	Glu	Ser	Trp	Lys	Ala	Leu	Glu	Arg	Ala	Ser	Phe	Ser	Lys		
					180				185					190			
ctg	aag	ctg	cag	cac	atc	cag	gcc	cca	ctg	tcc	tgg	gag	ttg	gtg	cgc	725	
Leu	Lys	Leu	Gln	His	Ile	Gln	Ala	Pro	Leu	Ser	Trp	Glu	Leu	Val	Arg		
				195				200						205			
cct	cat	atc	tat	gga	tat	gct	gtg	aaa	tagtgtgagc	tggcagttaa						772	
Pro	His	Ile	Tyr	Gly	Tyr	Ala	Val	Lys									
				210			215										
gagctgaatg	gctcaaagaa	tttaaagctt	cagttttaca	tttaaaatgc	taggtgggtg											832	
cctgtaatcc	caggtacttg	gaaggctgag	gcaggagaat	ctcttgaacc	cagaaggcga											892	
aggttgacgt	gaaccgagat	catgccattg	tactctagcc	tggttgacaa	gagcaagact											952	
ccgtctcaaa	aaaaaataaa	aaaaaaaaaa	aaa													985	

<210> 119

<211> 839

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 185..715

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<222> 185..253

<223> Von Heijne matrix

score 9.49395175807817

seq SLLFICFFGESFC/IC

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cagctcctgg tattttctgc ttcccttcgt agggaattta gttattttat tttattat 120

agctaattta gctattttta aatagctaaa ttttagctac ttttttttca attgacaaag 180

aagg atg tct aat caa aga cta ccg ctg att ttt tct ctg ttg ttt atc 229

Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile

-20

-15

-10

tgc ttc ttc ggg gag agt ttc tgc att tgt gat gga act gtc tgg aca 277

Cys Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr

-5

1

5

aag gtt gga tgg gag att ctt cca gaa gaa gta cat tat tgg aaa gtt 325

Lys	Val	Gly	Trp	Glu	Ile	Leu	Pro	Glu	Glu	Val	His	Tyr	Trp	Lys	Val		
10						15					20						
aag	ggt	tct	cca	tct	cac	tgc	ctg	cct	tat	ctt	ctg	gat	aaa	cta	tgc	373	
Lys	Gly	Ser	Pro	Ser	His	Cys	Leu	Pro	Tyr	Leu	Leu	Asp	Lys	Leu	Cys		
25					30					35				40			
tgc	gac	ttt	gct	aac	atg	gat	ata	ttt	cag	ggt	tgt	tta	tat	ctc	att	421	
Cys	Asp	Phe	Ala	Asn	Met	Asp	Ile	Phe	Gln	Gly	Cys	Leu	Tyr	Leu	Ile		
				45				50						55			
tat	aat	tta	tta	caa	gct	gtc	ttc	ttc	gtc	tta	ttt	ggt	ttg	tct	gtg	469	
Tyr	Asn	Leu	Leu	Gln	Ala	Val	Phe	Phe	Val	Leu	Phe	Val	Leu	Ser	Val		
				60				65					70				
cat	tac	ctg	tgg	aag	aaa	tgg	aag	aaa	cac	caa	aaa	aag	ctg	aaa	aag	517	
His	Tyr	Leu	Trp	Lys	Lys	Trp	Lys	Lys	His	Gln	Lys	Lys	Leu	Lys	Lys		
				75			80					85					
caa	gcc	tcc	tta	gaa	aaa	cct	ggt	aat	gat	cta	gaa	agc	cca	ttg	atc	565	
Gln	Ala	Ser	Leu	Glu	Lys	Pro	Gly	Asn	Asp	Leu	Glu	Ser	Pro	Leu	Ile		
				90			95				100						
aac	aac	att	gac	caa	aca	ctc	cac	aga	gtg	gca	acc	aca	gca	tca	gtg	613	
Asn	Asn	Ile	Asp	Gln	Thr	Leu	His	Arg	Val	Ala	Thr	Thr	Ala	Ser	Val		
105					110					115					120		
ata	tac	aag	atc	tgg	gag	cac	agg	tct	cac	cat	cct	tcc	tct	aag	aaa	661	
Ile	Tyr	Lys	Ile	Trp	Glu	His	Arg	Ser	His	His	Pro	Ser	Ser	Lys	Lys		
				125				130						135			
att	aag	cac	tgc	aaa	tta	aag	aag	aag	agt	aaa	gaa	gaa	gga	gcc	aga	709	
Ile	Lys	His	Cys	Lys	Leu	Lys	Lys	Lys	Ser	Lys	Glu	Glu	Gly	Ala	Arg		
				140				145					150				
aga	tac	taaataaatg	catatgcaaa	tgtagcttac	tcaattatag	atatcacaaa										765	
Arg	Tyr																
agaaatctat	catctaagga	ttaaaaattg	ttctttggaa	acctttataa	aaaaaaaaaga											825	
aaaaaaaaaaaa	aaaaa															839	

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 <213> Homo sapiens

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 <222> 54..527

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 <222> 54..116
 <223> Von Heijne matrix
 score 6.80928714315144
 seq ALXSLNLAPPTVA/AP

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						Met											
gcc	ctg	tgc	gca	ctg	acc	cgc	gct	ctg	ccs	tct	ctg	aac	ctg	gcg	ccc	104	
Ala	Leu	Cys	Ala	Leu	Thr	Arg	Ala	Leu	Pro	Ser	Leu	Asn	Leu	Ala	Pro		
-20					-15					-10					-5		
ccg	acc	gtc	gcc	gcc	cct	gcc	ccg	agt	ctg	ttc	ccc	gcc	gcc	cag	atg	152	
Pro	Thr	Val	Ala	Ala	Pro	Ala	Pro	Ser	Leu	Phe	Pro	Ala	Ala	Gln	Met		
				1			5						10				
atg	aac	aat	ggc	ctc	ctc	caa	cag	ccc	tct	gcc	ttg	atg	ttg	ctc	ccc	200	
Met	Asn	Asn	Gly	Leu	Leu	Gln	Gln	Pro	Ser	Ala	Leu	Met	Leu	Leu	Pro		

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      15      20      25
tgc cgc cca gtt ctt act tct gtg gcc ctt aat gcc aac ttt gtg tcc      248
Cys Arg Pro Val Leu Thr Ser Val Ala Leu Asn Ala Asn Phe Val Ser
      30      35      40
tgg aag agt cgt acc aag tac acc att aca cca gtg aag atg agg aag      296
Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr Pro Val Lys Met Arg Lys
      45      50      55      60
tct ggg ggc cga gac cac aca ggt gct gga aac gtg cgt aga aca gta      344
Ser Gly Gly Arg Asp His Thr Gly Ala Gly Asn Val Arg Arg Thr Val
      65      70      75
ggc cga gta tcc aac gtt gat cat aac aaa cgg gtc att ggc aag gca      392
Gly Arg Val Ser Asn Val Asp His Asn Lys Arg Val Ile Gly Lys Ala
      80      85      90
ggg cgc aac cgc tgg ctg ggc aag agg cct aac agt ggg cgg tgg cac      440
Gly Arg Asn Arg Trp Leu Gly Lys Arg Pro Asn Ser Gly Arg Trp His
      95      100      105
cgc aag ggg ggc tgg gct ggc cga aag att cgg cca cta ccc ccc atg      488
Arg Lys Gly Gly Trp Ala Gly Arg Lys Ile Arg Pro Leu Pro Pro Met
      110      115      120
aag agt tac gtg aag ctg cct tct gct tct gcc caa agc tgatatacct      537
Lys Ser Tyr Val Lys Leu Pro Ser Ala Ser Ala Gln Ser
      125      130      135
gtactcctaataaaaatgcccc cccccctcaaaaaaaaaa aaaaaa      583

<210> 121
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<220>
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<222> 129..686

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<221> sig_peptide
<222> 129..185
<223> Von Heijne matrix
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gcaacgccgg cgtctcttag caaccgcgcg cggcctagggt gggcccccc ggcacccccca      120
gacctgcc atg gcg acc gcg agt cct agc gtc ttt cta ctc atg gtc aac      170
      Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn
      -15      -10
ggg cag gtg gag agc gcc cag ttt cca gag tat gat gac ctc tac tgc      218
Gly Gln Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Leu Tyr Cys
      -5      1      5      10
aag tac tgc ttt gtg tac ggc cag gac tgg gcc ccc aca gcg ggt ctg      266
Lys Tyr Cys Phe Val Tyr Gly Gln Asp Trp Ala Pro Thr Ala Gly Leu
      15      20      25
gag gag ggg atc tca cag atc aca tcc aag agc caa gat gtg cgg caa      314
Glu Glu Gly Ile Ser Gln Ile Thr Ser Lys Ser Gln Asp Val Arg Gln
      30      35      40
gca ctg gtg tgg aac ttc ccc att gat gtc acc ttt aaa agc acc aac      362
Ala Leu Val Trp Asn Phe Pro Ile Asp Val Thr Phe Lys Ser Thr Asn
      45      50      55

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ccc tac ggc tgg cca cag atc gtg ctc agc gtg tat gga cca gat gtg      410
Pro Tyr Gly Trp Pro Gln Ile Val Leu Ser Val Tyr Gly Pro Asp Val
60          65          70          75
ttc ggg aac gat gtg gtt cga ggc tat ggg gcc gtg cac gtg ccc ttc      458
Phe Gly Asn Asp Val Val Arg Gly Tyr Gly Ala Val His Val Pro Phe
80          85          90
tca cct ggc cgg cac aaa agg acc atc ccc atg ttt gtc cca gaa tct      506
Ser Pro Gly Arg His Lys Arg Thr Ile Pro Met Phe Val Pro Glu Ser
95          100          105
acg tct aaa ctg cag aag ttt aca agc tgg ttc atg ggg cgg cgg ccc      554
Thr Ser Lys Leu Gln Lys Phe Thr Ser Trp Phe Met Gly Arg Arg Pro
110          115          120
gag tac aca gac ccc aag gtg gtg gct cag ggt gaa ggc cgg gaa gct      602
Glu Tyr Thr Asp Pro Lys Val Val Ala Gln Gly Glu Gly Arg Glu Ala
125          130          135
atc aca gct ccc cgg aaa gct gtc ttc tct gtc cat ggc ctc acc tca      650
Ile Thr Ala Pro Arg Lys Ala Val Phe Ser Val His Gly Leu Thr Ser
140          145          150          155
ccc agg gca ctg gcc ttg gtc cac atc aag ggg acc tgaagcttcc      696
Pro Arg Ala Leu Ala Leu Val His Ile Lys Gly Thr
160          165
ctgaagcctc tagcctgttg tgtgcacgta caagcctcag gccccatttg tccagcctgt      756
cagcagctgg gaaataactaa gtcaccctct tctgggtatg tttaattttc caatttttct      816
caacattact gaaatgtcta aatgtggaaa agttgacatc attttacagt gaacaccaca      876
taccaccac ctagatttta ccattaccaa tttcctgttc cgtacttgta tattcacata      936
tatccaacta ttcattccctg cttcaatcca tcctattttt attgcatttc aaaataaact      996
gtgaaatcag gaaaaaaaaa aaaaaaaaaa      1024

<210> 122
<211> 760
<212> DNA
<213> Homo sapiens

<220>
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<222> 165..614

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<221> sig_peptide
<222> 165..305
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      seq ALGLALCSTKALS/VG

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gcctctccag gcctcgaagg cttctcctgg gctgatgcga gctggggaac gggagggacg      120
gacgtgggag cgagaacgtc acactggagg cagctgggtg cacg atg ggg gac aga      176
                               Met Gly Asp Arg
                               -45
gtg aaa ggt agc aag tca aga gcc ttc gtg tca cca tgg cca cac acc      224
Val Lys Gly Ser Lys Ser Arg Ala Phe Val Ser Pro Trp Pro His Thr
-40          -35          -30
ccg atg gct tcc ggc ttg agg gac ccc tgg ctg cag ccc aca gcc ctg      272
Pro Met Ala Ser Gly Leu Arg Asp Pro Trp Leu Gln Pro Thr Ala Leu
-25          -20          -15
ggc ctt gca ctg tgc tct acg aag gcc ctg tcc gtg ggc tct gcc cct      320
Gly Leu Ala Leu Cys Ser Thr Lys Ala Leu Ser Val Gly Ser Ala Pro

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-10          -5          1          5
ttg ccc ccg cga aat tcc aac acc atg gcg gcg gct gcc ctg gct gcc      368
Leu Pro Pro Arg Asn Ser Asn Thr Met Ala Ala Ala Leu Ala Ala

          10          15          20
ccc agc ctg ggc ttc gat ggg gtg att ggg gtg ctc gtg gct gat acc      416
Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu Val Ala Asp Thr

          25          30          35
agc ctc acg gac atg cac gtg gtg gat gta gag ctg agc gga ccc cgg      464
Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu Ser Gly Pro Arg

          40          45          50
ggc ccc acg ggc cga agc ttt gct gtg cac acc cgc aga gag aac cct      512
Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg Arg Glu Asn Pro

          55          60          65
gcc gag cca ggc gcg gtc acc ggc tcc gcc acc gtc acg gcc ttc tgg      560
Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val Thr Ala Phe Trp

          70          75          80          85
cgg agc ctc ctg gcc tgc tgc cag ctc ccc tcc agg ccg ggg atc cat      608
Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg Pro Gly Ile His

          90          95          100
ctc tgc tgagaagcct cctccctccc gagacaagat catctgcctg gcctctcacc      664
Leu Cys
accaccatcc caccctgcc ctgccccact tccccagggt ctcccttctg actcagtaaa      724
gatcaccgct gcctccctca aaaaaaaaaa aaaaaa      760

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<210> 123
 <211> 594
 <212> DNA
 <213> Homo sapiens

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 <222> 192..476

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 <222> 192..326
 <223> Von Heijne matrix
 score 6.60884760057354
 seq FILLLLLSGPAEM/SA

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ggagaaggca ggtcctcttt atgttttcgc agctggttca aggggttttg ggttttctat      120
ctaggttaaa gattgcgtaa tacacagctg gagccataga cattaatgca tgtttatcac      180
acgcaacaac g atg ctg cat cat gtg att aca gct ggg cct gtg ctg ctt      230
          Met Leu His His Val Ile Thr Ala Gly Pro Val Leu Leu
          -45          -40          -35
cta cac ctc cct cgc cct gac act tcc acc agg ttg ctc ctc acc tcc      278
Leu His Leu Pro Arg Pro Asp Thr Ser Thr Arg Leu Leu Leu Thr Ser

          -30          -25          -20
gtc tct gct ttt atc ctc tta ctg ctc ctt tca gga cca gca gaa atg      326
Val Ser Ala Phe Ile Leu Leu Leu Leu Ser Gly Pro Ala Glu Met

          -15          -10          -5
tca gct tcc cag gaa tcc ttc cct gga tct ctg cag caa gaa ata gct      374
Ser Ala Ser Gln Glu Ser Phe Pro Gly Ser Leu Gln Gln Glu Ile Ala

          1          5          10          15
tct ctg atc act gta gca ctt ggt tct tta ata tct tta tct tgc tct      422
Ser Leu Ile Thr Val Ala Leu Gly Ser Leu Ile Ser Leu Ser Cys Ser

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                20                25                30
acc ttg tta tat ttt tct tgt gaa ctt aaa att ccc tgt gag gac gta      470
Thr Leu Leu Tyr Phe Ser Cys Glu Leu Lys Ile Pro Cys Glu Asp Val
                35                40                45
aac ctt tgaaggtatg tctcatatct ctgaacctct ttaaaatgcc tagcatccct      526
Asn Leu
                50
gtgtgggtgc caattgcttg tgtattgaat taaattgtga ttgttaactt gaaaaaaaaa      586
aaaaaaaaa      594

<210> 124
<211> 559
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..297

<220>
<221> sig_peptide
<222> 16..93
<223> Von Heijne matrix
      score 6.65836819891491
      seq FCGSACLLAVIRA/FF

<400> 124
ttacacaggg gataa atg gca gca atc gag att gaa gtc aag cct aac cag      51
      Met Ala Ala Ile Glu Ile Glu Val Lys Pro Asn Gln
                -25                -20                -15
ggc ttt tgc ggg agc gca tgc ctt ttg gct gta att cgt gca ttt ttt      99
Gly Phe Cys Gly Ser Ala Cys Leu Leu Ala Val Ile Arg Ala Phe Phe
                -10                -5                1
ttt aag aaa aac gcc tgc ctt ctg cgt gag att ctc cag agc aaa ctg      147
Phe Lys Lys Asn Ala Cys Leu Leu Arg Glu Ile Leu Gln Ser Lys Leu
                5                10                15
ggc ggc atg ggc cct gtg gtc ttt tcg tac aga ggg ctt cct ctt tgg      195
Gly Gly Met Gly Pro Val Val Phe Ser Tyr Arg Gly Leu Pro Leu Trp
                20                25                30
ctc ttt gcc tgg ttg ttt cca aga tgt act gtg cct ctt act ttc ggt      243
Leu Phe Ala Trp Leu Phe Pro Arg Cys Thr Val Pro Leu Thr Phe Gly
                35                40                45                50
ttt gaa aac atg agg ggg ttg ggc gtg gta gct tac gcc tgt aat ccc      291
Phe Glu Asn Met Arg Gly Leu Gly Val Val Ala Tyr Ala Cys Asn Pro
                55                60                65
agc act tagggaggcc gagggcgggag gatggcttga ggtccgtagt tgagaccagc      347
Ser Thr
ctggccaaca tgggtgaagcc tgggtctctac aaaaaaataa taacaaaaat tagccgggtg      407
tgggtggctcg tgccctgtggt cccagctgct cccgtggctg aggcgggagg atctcttgag      467
cttaggcttt tgagctatca tggcgccagt gcactccagc gtgggcaaca gagcgagacc      527
ctgtctctca aaaacaaaaa aaaaaaaaaa aa      559

<210> 125
<211> 744
<212> DNA
<213> Homo sapiens

<220>

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<221> CDS
 <222> 216..635

<220>
 <221> sig_peptide
 <222> 216..335
 <223> Von Heijne matrix
 score 4.38054120608596
 seq ITLVSAAPGKVIC/EM

<400> 125
 gcttcgtcac aagggtgcga tgaaagtcag tgagcaaata gcggaccacc ggggctgcca 60
 gctcgccctga ctcccggcct cttgcgctcc taggggcgga gaagggtgcg ggctcttcgc 120
 cctttgtgtc ctccctcttt cactaacttc tggactttcc agctcttccg aagttcgttc 180
 ttgcgcaaaag cccaaaggct ggaaaaccgt ccacg atg acc agc atg act cag 233
 Met Thr Ser Met Thr Gln
 -40 -35
 tct ctg cgg gag gtg ata aag gcc atg acc aag gct cgc aat ttt gag 281
 Ser Leu Arg Glu Val Ile Lys Ala Met Thr Lys Ala Arg Asn Phe Glu
 -30 -25 -20
 aga gtt ttg gga aag att act ctt gtc tct gct gct cct ggg aaa gtg 329
 Arg Val Leu Gly Lys Ile Thr Leu Val Ser Ala Ala Pro Gly Lys Val
 -15 -10 -5
 att tgt gaa atg aaa gta gaa gaa gag cat acc aat gca ata ggc act 377
 Ile Cys Glu Met Lys Val Glu Glu Glu His Thr Asn Ala Ile Gly Thr
 1 5 10
 ctc cac ggc ggt ttg aca gcc acg tta gta gat aac ata tca aca atg 425
 Leu His Gly Gly Leu Thr Ala Thr Leu Val Asp Asn Ile Ser Thr Met
 15 20 25 30
 gct ctg cta tgc acg gaa agg gga gca ccc gga gtc agt gtc gat atg 473
 Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro Gly Val Ser Val Asp Met
 35 40 45
 aac ata acg tac atg tca cct gca aaa tta gga gaa gat ata gtg att 521
 Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp Ile Val Ile
 50 55 60
 aca gca cat gtt ctg aag caa gga aaa aca ctt gca ttt acc tct gtg 569
 Thr Ala His Val Leu Lys Gln Gly Lys Thr Leu Ala Phe Thr Ser Val
 65 70 75
 gat ctg acc aac aag gcc aca gga aaa tta ata gca caa gga aga cac 617
 Asp Leu Thr Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln Gly Arg His
 80 85 90
 aca aaa cac ctg gga aac tgagagaaca gcagaatgac ctaaagaaac 665
 Thr Lys His Leu Gly Asn
 95 100
 ccaacaatga atatcaagta tagatttgac tcaaacaatt gtaatttttg aaataaacta 725
 gcaaaaaaaaa aaaaaaaaaa 744

<210> 126
 <211> 824
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 164..280

<220>
 <221> sig_peptide

<222> 164..268
 <223> Von Heijne matrix
 score 5.73290676305402
 seq TLPLCPVTSPVWG/WS

<400> 126
 tgtgttcaat cgtgtgaatg gccggcgggc cccctccacg tccccatcct tgcagggggac 60
 ccaggagacc tacacagtgg cccacgagga gaatgtccgc tttgtgtccg aaggtagcga 120
 gcggggccag aggggtgcggc ataggctgct gggtcgcaaa acc atg gac ccg gga 175
 Met Asp Pro Gly
 -35
 tgg ccc cac ttc aag ctg acc cac agc cgc tgc atg gct gtg ctt ttc 223
 Trp Pro His Phe Lys Leu Thr His Ser Arg Cys Met Ala Val Leu Phe
 -30 -25 -20
 ctt ggc act ctg ccc ttg tgt cct gtg acc agc cct gtg tgg ggc tgg 271
 Leu Gly Thr Leu Pro Leu Cys Pro Val Thr Ser Pro Val Trp Gly Trp
 -15 -10 -5 1
 agt cca ggg tgaccatcag gccctgggtg ggcgatgggg tgccctgggac 320
 Ser Pro Gly
 ctggctcagc ccgactgccc tcctcccaca gcctggcagc aggtgcaaca gcagctggat 380
 ggtggcccgag ccggtgaggg cgggccaaag cctgtgcagt acgtggagag gacccccaat 440
 ccccggtgc agaactttgt gccattttac ctagacgagt ggtgggcgca gcagttcctg 500
 gcgagaatca ccagctgttc ctagtggctg ctgggagggg gcgctgctac acggccgacc 560
 tgtcgccagg agagaagcat ggcgccctgc ccaccactg cgccctggctg ggtgccggcc 620
 acacctgaag tgccagcatt tggacttttg cacctttttt tcccttggcc cggctgtccc 680
 aaccaagctg ccatggccaa gggccgaacc cgtctgacct cagccctgct cactgtgccc 740
 agggaccagc gaccagcccc tggggctggc agggaggagc tccaggctaa taaagtggag 800
 aaactgtcaa aaaaaaaaaa aaaa 824

<210> 127
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..301

<220>
 <221> sig_peptide
 <222> 68..190
 <223> Von Heijne matrix
 score 4.68908216483476
 seq AYLLYILLTGALQ/FG

<400> 127
 acatccggtg tggtcgacgg gtcctccaag agtttggggc gcggaccgga gtaccttgcg 60
 tgcagtt atg tgc gcg tgc gta gtg tct gtc att tgc cgg ttc tta gaa 109
 Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu
 -40 -35 -30
 gag tac ttg agc tcc act ccg cag cgt ctg aag ttg ctg gac gcg tac 157
 Glu Tyr Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr
 -25 -20 -15
 ctg ctg tat ata ctg ctg acc ggg gcg ctg cag ttc ggt tac tgt ctc 205
 Leu Leu Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu
 -10 -5 1 5
 ctc gtg ggg acc ttc ccc ttc aac tct ttt ctc tgc ggc ttc atc tct 253
 Leu Val Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser

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          10          15          20
tgt gtg ggg agt ttc atc cta gcg ggt tca ctc ttt gaa ttt cct gga    301
Cys Val Gly Ser Phe Ile Leu Ala Gly Ser Leu Phe Glu Phe Pro Gly
          25          30          35
taagagttct ggagatggca gcttattgga cacatggatt ttcttcagat ttgcacttac    361
tgctagctct gctttttatg caggagaaaa gccagaggtt cactgtgtgt cagaacaact    421
ttctaacaaa catattattaa tccagcctct gcctttcatt aaatgtaacc ttttgccttc    481
caaattaaag aactccatgc cactcctcaa aaaaaaaaaa aaaaa                    526

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<210> 128
 <211> 618
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 179..427

<220>
 <221> sig_peptide
 <222> 179..298
 <223> Von Heijne matrix
 score 7.72883276007822
 seq CLVVVTMATLSLA/RP

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<400> 128
aagcgaagag atgggtctgc actttggagg agcgggacac tgttgacttt cctgatgtga    60
aatctaccca ggaacaaaac accagtgact gcagcagcag cggcagcgcc tcggttctctg    120
agcccaccgc aggctgaagg cattgcgcgt agtccatgcc cgtagaggaa gtgtgcag      178
atg gga tta acg tcc aca tgg aga tat gga aga gga ccg ggg att ggt      226
Met Gly Leu Thr Ser Thr Trp Arg Tyr Gly Arg Gly Pro Gly Ile Gly
-40          -35          -30          -25
acc gta acc atg gtc agc tgg ggt cgt ttc atc tgc ctg gtc gtg gtc      274
Thr Val Thr Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val
          -20          -15          -10
acc atg gca acc ttg tcc ctg gcc cgg ccc tcc ttc agt tta gtt gag      322
Thr Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu
          -5          1          5
gat acc aca tta gag cca gaa gat gcc atc tca tcc gga gat gat gag      370
Asp Thr Thr Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu
          10          15          20
gat gac acc gat ggt gcg gaa gat ttt gtc agt gag aac agt aac aac      418
Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn
          25          30          35          40
aag agt aag taactgccc gctccgatgg tccccgagag aggagcatgg      467
Lys Ser Lys
agggaagttc tgctgtcac ctgtcttctt gtgcactctt ctgcgccatg ctgtgtcccg    527
cggcccttgc ctttccccgc tgtgtctact ttcttgactt tcaaacctga gaataaacca    587
gtgttgctgc acataaaaaa aaaaaaaaaa a                    618

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<210> 129
 <211> 776
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..297


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<220>
<221> sig_peptide
<222> 22..66
<223> Von Heijne matrix
      score 4.68058603039206
      seq VLAGSLLGPTSRS/AA

<400> 129
actgcgggac ccaactgcgga t atg gct gtc ttg gct gga tcc ctg ttg ggc      51
                      Met Ala Val Leu Ala Gly Ser Leu Leu Gly
                      -15                      -10

ccc acg agt agg tgc gca gcg ttg ctg ggt ggc agg tgg ctc cag ccc      99
Pro Thr Ser Arg Ser Ala Ala Leu Leu Gly Gly Arg Trp Leu Gln Pro
-5                      1                      5                      10

cgg gcc tgg ctg ggg ttc cca gac gcc tgg ggc ctc ccc acc ccg cag      147
Arg Ala Trp Leu Gly Phe Pro Asp Ala Trp Gly Leu Pro Thr Pro Gln
                      15                      20                      25

cag gcc cgg ggc aag gct cgc ggg aat gag tat cag ccg agc aat atc      195
Gln Ala Arg Gly Lys Ala Arg Gly Asn Glu Tyr Gln Pro Ser Asn Ile
                      30                      35                      40

aaa cgc aag aac aag cac ggc tgg gtc cgg cgc ctg agc acg ccg gcc      243
Lys Arg Lys Asn Lys His Gly Trp Val Arg Arg Leu Ser Thr Pro Ala
                      45                      50                      55

ggc gtg cag gtc atc ctt cgc cga atg ctc aag ggc cgc aag tgc ctg      291
Gly Val Gln Val Ile Leu Arg Arg Met Leu Lys Gly Arg Lys Ser Leu
60                      65                      70                      75

agc cat tgaggatcgc gacgcagtcg gcgggggaccc tcatggaagc atcgccctcg      347
Ser His

cctcggacct tgcctggcgc tatttttgca gggagctggg gagcaggaac gcctcggacc      407
tgagtgtctt ccatattgtg ggtttgaagt ctggatggga gccttgccaa gtcccttttt      467
aggcttttta attaggaagc atttcgaacc tgcgcaacag accaaagaac agtacaaaga      527
acatccgtgt acccagtacc ctgactaccg actacctaca acccgccctt gccccatcct      587
gagttctttt gaagctgacg tcaggcatcg gattatttct tctgtaaata ttccagaatg      647
tatctctcca agatgagagc tcattaaaaa ataattacaa agcttatcac atccaaaaga      707
attatcaata attttgaaat attattaaac gtgtaataaa tgttcaaagt tcaaaaaaaaa      767
aaaaaaaaaa

<210> 130
<211> 998
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 9..845

<220>
<221> sig_peptide
<222> 9..134
<223> Von Heijne matrix
      score 6.13963522287438
      seq RSLALAAPSSNG/SP

<400> 130
aacgaaaag atg gcg gcg ccc gta agg cgg acg ctg tta ggg gtg gcg ggg      50
      Met Ala Ala Pro Val Arg Arg Thr Leu Leu Gly Val Ala Gly
      -40                      -35                      -30

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<213> Homo sapiens

<220>

<221> CDS

<222> 27..578

<220>

<221> sig_peptide

<222> 27..119

<223> Von Heijne matrix

score 4.50637135496675

seq TALMVGAASLLEG/RP

<400> 131

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atctttctg actggcctg cagagg atg gca tgc acc act act gcc ccc gcc      53
                               Met Ala Cys Thr Thr Thr Ala Pro Ala
                               -30                               -25
cag gaa cac atg ctt ctc acc cct ctc act gct ctg atg gtg ggg gct      101
Gln Glu His Met Leu Leu Thr Pro Leu Thr Ala Leu Met Val Gly Ala
      -20                               -15                               -10
gct tct ctg ctt gag ggc cgg cca cag atc tca gct cca tac tcc cga      149
Ala Ser Leu Leu Glu Gly Arg Pro Gln Ile Ser Ala Pro Tyr Ser Arg
      -5                               1                               5                               10
gct gca tgt tgc agc cct ggg gca ctg gga tgt cct gca gct cgg gtt      197
Ala Ala Cys Cys Ser Pro Gly Ala Leu Gly Cys Pro Ala Ala Arg Val
                               15                               20                               25
ggg att ctg gat ctg atg tat tcc tgg gtt gcc agg aaa gtg ctc agg      245
Gly Ile Leu Asp Leu Met Tyr Ser Trp Val Ala Arg Lys Val Leu Arg
                               30                               35                               40
tgc agc aat act ggg ctg cag ggg ctg cac tgt gca cca gct tat gca      293
Cys Ser Asn Thr Gly Leu Gln Gly Leu His Cys Ala Pro Ala Tyr Ala
      45                               50                               55
gca cag ctt ggt atg gac cct ggg agg ggc caa cga gca gga ggg cct      341
Ala Gln Leu Gly Met Asp Pro Gly Arg Gly Gln Arg Ala Gly Gly Pro
      60                               65                               70
gta gag cag aca tac ttc agt ccc atg ggg aag ctg ccc act ctt tgc      389
Val Glu Gln Thr Tyr Phe Ser Pro Met Gly Lys Leu Pro Thr Leu Ser
      75                               80                               85                               90
tgg ctg gaa ggc tgt aca gca gtc atg acg ctg gca tct gct tgg ctt      437
Trp Leu Glu Gly Cys Thr Ala Val Met Thr Leu Ala Ser Ala Trp Leu
      95                               100                               105
ctg ggg agc cct cgg gaa act tac aat cat gag aag gtg aag gag aag      485
Leu Gly Ser Pro Arg Glu Thr Tyr Asn His Glu Lys Val Lys Glu Lys
      110                               115                               120
cag tgt cca ttc tcc agt atg gtt ttg ggg gag tat ggc ttc cta cct      533
Gln Cys Pro Phe Ser Ser Met Val Leu Gly Glu Tyr Gly Phe Leu Pro
      125                               130                               135
act gtg gac cac ctg tca act ctg ggc tgt aac atg aga gaa ttg      578
Thr Val Asp His Leu Ser Thr Leu Gly Cys Asn Met Arg Glu Leu
      140                               145                               150
tgaactctg tcttgtttga gccatggttt cattctcttt ttcagccatg tagcctgtgc      638
tgtaactcag taccacatta gcaactagt aaagtcaatg tgggtaaatt tgtcattctt      698
caggtagaa catttcttcc ttttattctt gtgtttttgg ctaaataaac tgggaaatta      758
tagtaaaaaa aaaaaaaaaa a      779
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<210> 132

<211> 1025

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 408..710

<220>

<221> sig_peptide

<222> 408..533

<223> Von Heijne matrix

score 5.66440183652506

seq QLCFHLISWLYSWA/SQ

<400> 132

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atggtttgtt gtgagttcca tgtcctcttg gatcagtcac tgtggccatg catgtttggc    60
cacatgatta atccagtctg ggtcatgacc ttttcttcat ccaaaacaag gtgatgggaa    120
gacaaaaaca atagctacta caaacaatag gagtttataa ttatgtgctg atgtattcga    180
agatgtgttg acagtcgtga gtgtgtatcc taggaaaggc gagctggact ctgtctccat    240
ggtggctctc accccagggg cctaggaaca gcctgtcacc acacaattac ttttataacc    300
ctggagatga aaatctcctt gtcctcaaaa tacttccaga agaacaacca gatgggaagg    360
accttggttg ggactctttc cagttcactt ggggcagagg gaattta atg gct cac    416
                                     Met Ala His
                                     -40
gta gct gaa aag gat ggg cta gat tgg gct tca ggc tgc atc cca gga    464
Val Ala Glu Lys Asp Gly Leu Asp Trp Ala Ser Gly Cys Ile Pro Gly
                                     -35          -30          -25
ctc caa aca ggg atc tgt ctc ttt ggc tct cag ctc tgc ttt cat ttg    512
Leu Gln Thr Gly Ile Cys Leu Phe Gly Ser Gln Leu Cys Phe His Leu
                                     -20          -15          -10
agt tgg ctt tat tct tgg gct tca cag tgt ggc ccc aca gca cca gtt    560
Ser Trp Leu Tyr Ser Trp Ala Ser Gln Cys Gly Pro Thr Ala Pro Val
                                     -5          1          5
att gat aaa aag agc tcc cct ttg ctg aca gaa ctg ctg gat ttg gtt    608
Ile Asp Lys Lys Ser Ser Pro Leu Leu Thr Glu Leu Leu Asp Leu Val
10          15          20          25
ctc att ggt cca gac gag gaa ggt atc cag cct caa gtc atc att gtg    656
Leu Ile Gly Pro Asp Glu Glu Gly Ile Gln Pro Gln Val Ile Ile Val
30          35          40
gcc agg aag atg gaa tac acc aaa tgg aca ggc ctg gca tgt acc cac    704
Ala Arg Lys Met Glu Tyr Thr Lys Trp Thr Gly Leu Ala Cys Thr His
45          50          55
aga gac tgagagttgg tgctgggtgg tgtgggtggca gatgatatta cctgaagaag    760
Arg Asp
ggacgaatgg gtgctgggca ggacaaagca tcagctgtcc agttcaggcc tctcctcttt    820
ccctgggtgc ttcattttcc tccgtctccc tgctgtccct taccctctgc ccaatctcat    880
tactcctggg cttgggagtt gccttctgag gatactccac tgggggtacc tgagcctgga    940
ttagagggca gggggaggat attgcctagc caaagtgggt gttcaataaa gaaccatttg   1000
gagatggcaa aaaaaaaaaa aaaaaa                                     1025
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<210> 133

<211> 607

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 247..501

<220>
 <221> sig_peptide
 <222> 247..306
 <223> Von Heijne matrix
 score 6.43040298500966
 seq LLLVTLVASTVPG/NS

<400> 133
 tgttacaaat attccctatg atctctcctt taaatattct tatcaggata ttggaaattc 60
 ttgattttca caactctgct tcagtggcat atgttttagct ttttgtcttc tgaattaatt 120
 gggctttctga tgggtccctag aggtatcagc tactcagtca gaaaacatac atggggaaga 180
 aactgaagtt catgccacaa actgtagcag ctttggaaca gaagggacca gacaacctca 240
 aggaga atg ggc cca aat acc aaa aat tta ctc ttg gtg acc ctt gtt 288
 Met Gly Pro Asn Thr Lys Asn Leu Leu Leu Val Thr Leu Val
 -20 -15 -10
 gct tct act gta cca ggc aac tct ctt ggg cag gat ttt act ttt gca 336
 Ala Ser Thr Val Pro Gly Asn Ser Leu Gly Gln Asp Phe Thr Phe Ala
 -5 1 5 10
 cac tta gaa aga tcc tgc acc agg gaa aat cgg tct cct ggg gag gta 384
 His Leu Glu Arg Ser Cys Thr Arg Glu Asn Arg Ser Pro Gly Glu Val
 15 20 25
 ttc cag caa cca tgc aag tct gga ggc ggg ggg gtt gga gaa cca aat 432
 Phe Gln Gln Pro Cys Lys Ser Gly Gly Gly Gly Val Gly Glu Pro Asn
 30 35 40
 gcc caa ggg cag cta ctt agc cag cac cca cta cct gcc ttc att aat 480
 Ala Gln Gly Gln Leu Leu Ser Gln His Pro Leu Pro Ala Phe Ile Asn
 45 50 55
 tgt tct cac ggg cag gcc ttt tgaaccaccc tggtacagaa caccaaccct 531
 Cys Ser His Gly Gln Ala Phe
 60 65
 ggtgcttttag gctgtctgtg ccattttctag gcaatgaacg agtagttact gtaccaaccc 591
 aaaaaaaaaa aaaaaa 607

<210> 134
 <211> 774
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 333..602

<220>
 <221> sig_peptide
 <222> 333..416
 <223> Von Heijne matrix
 score 4.79986448293481
 seq VPALPLLSSLCMA/MV

<400> 134
 ctcttcagtc cggggccttg ttgaacggac tcaccaggaa acgtgacttt cgtgtccgac 60
 ctctgtgta tcaggattcg attcttgggtg ttaaacaaga caacgctgaa ggctcgggtgc 120
 agcagccctg caaaggtttt tccagcgtc ttgggagggtg ggctgtgccc tgcctggccc 180
 acctggccca cctggcccac cattacctga agggaagcat gaacagcctt tgacgtggga 240
 gtggcgactg ctgagaggga actgtctgta cacaagcaat gtagccttat gggacctgag 300
 tggagcccca acccacgcag ggcgtgktct tc atg gct ttt cct ggc caa tct 353
 Met Ala Phe Pro Gly Gln Ser
 -25

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gat acc aag atg cag tgg cca gaa gta cct gca ctt cca ctc ctg tca      401
Asp Thr Lys Met Gln Trp Pro Glu Val Pro Ala Leu Pro Leu Leu Ser
-20 -15 -10
agt ctc tgc atg gct atg gtg agg aag agc tct gca ctg ggc aag gaa      449
Ser Leu Cys Met Ala Met Val Arg Lys Ser Ser Ala Leu Gly Lys Glu
-5 1 5 10
gtt ggc cgt cga gtg aag gaa atg gtg atg ctg gtg gcc cct ttc cgg      497
Val Gly Arg Arg Val Lys Glu Met Val Met Leu Val Ala Pro Phe Arg
15 20 25
cag tca agt tcc cta tca agg aca ttc agt tct cgg aaa gtg gtg aag      545
Gln Ser Ser Ser Leu Ser Arg Thr Phe Ser Ser Arg Lys Val Val Lys
30 35 40
gca cat gct tcc ctg cat ggt gcc cgc ctc tct cca ctc tct aga aat      593
Ala His Ala Ser Leu His Gly Ala Arg Leu Ser Pro Leu Ser Arg Asn
45 50 55
att aga ggc taggctgctg ctgtatgtca gggctagtcc ctcttctatg      642
Ile Arg Gly
60
aatccagaat aactctgaag aagccgagta acagggcatga agtgaagaga aatcgctgta      702
acaggaagac agcaaagcag atgctaataga ccacactatt taacgaactg gaaccaacaa      762
aaaaaaaaaa aa      774

<210> 135
<211> 611
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 110..376

<220>
<221> sig_peptide
<222> 110..208
<223> Von Heijne matrix
      score 3.64796206065748
      seq LVPHSPLPGALSS/AP

<220>
<221> misc_feature
<222> 347
<223> n=a, g, c or t

<400> 135
tcttgtcaac actgccact cagcgaggaa gcagccgcga cgccacact tcctgttgga      60
gcctgcgag agccagaggg ctcagaagcc acaggaacat ggctaggc atg gct cag      118
                               Met Ala Gln
cca gca gcc ccc tcc ctg acg cgg ccc ttc ctg gca gag gcc ccg aca      166
Pro Ala Ala Pro Ser Leu Thr Arg Pro Phe Leu Ala Glu Ala Pro Thr
-30 -25 -20 -15
gca ctg gtc cca cac agc ccc ctg cct ggg gcc ctg tca agc gcc cct      214
Ala Leu Val Pro His Ser Pro Leu Pro Gly Ala Leu Ser Ser Ala Pro
-10 -5 1
ggc ccg aag cag ccc ccg acg gca agc aca ggc ccg gag ctg ctg ctg      262
Gly Pro Lys Gln Pro Pro Thr Ala Ser Thr Gly Pro Glu Leu Leu Leu
5 10 15
ctg cct ctt tcc tcc ttc atg ccc tgc ggg gcg gct gca cca gcc agg      310
Leu Pro Leu Ser Ser Phe Met Pro Cys Gly Ala Ala Ala Pro Ala Arg

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      20              25              30
gtg tca tca cag cgg gct act cct agg gat aag ccc ncc ggt ccc ctc      358
Val Ser Ser Gln Arg Ala Thr Pro Arg Asp Lys Pro Xaa Gly Pro Leu
35              40              45              50
atc cct ggc cag tgt ccc tgacccccat ctactccttc ctgggggactt      406
Ile Pro Gly Gln Cys Pro
      55
ctcagcgcca gccattggc gcctgcgttg cccgcattcca ggccctgcgg caggccctgt      466
gctagcgtgt tcgcaccagg aacgcaggtg ctgggctgtc ggggaggcct caggccacct      526
ccaggaacag aacacagttt taagtttgat tttttttatt tcaaaatgct ttgcaattaa      586
atgaattact gttcaaaaaa aaaaaa      611

<210> 136
<211> 925
<212> DNA
<213> Homo sapiens

<220>
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<222> 22..417

<220>
<221> sig_peptide
<222> 22..66
<223> Von Heijne matrix
      score 5.47092708754574
      seq RVLCPAAGAVRA/LR

<400> 136
agtcgaggag tcaaggcagc a atg aat cgt gtc ttg tgt gcc ccg gcg gcc      51
                        Met Asn Arg Val Leu Cys Ala Pro Ala Ala
                        -15                        -10
ggg gcc gtc cgg gcg ctg agg ctc ata ggc tgg gct tcc cga agc ctt      99
Gly Ala Val Arg Ala Leu Arg Leu Ile Gly Trp Ala Ser Arg Ser Leu
-5              1              5              10
cat ccg ttg ccc ggt tcc cgg gat cgg gcc cac cct gcc gcc gag gaa      147
His Pro Leu Pro Gly Ser Arg Asp Arg Ala His Pro Ala Ala Glu Glu
      15              20              25
gag gac gac cct gac cgc ccc att gag ttt tcc tcc agc aaa gcc aac      195
Glu Asp Asp Pro Asp Arg Pro Ile Glu Phe Ser Ser Ser Lys Ala Asn
      30              35              40
cct cac cgc tgg tgc gtg ggc cat acc atg gga aag gga cat cag cgg      243
Pro His Arg Trp Ser Val Gly His Thr Met Gly Lys Gly His Gln Arg
      45              50              55
ccc tgg tgg aag gtg ctg ccc ctc agc tgc ttc ctc gtg gcg ctg atc      291
Pro Trp Trp Lys Val Leu Pro Leu Ser Cys Phe Leu Val Ala Leu Ile
      60              65              70              75
atc tgg tgc tac ctg agg gag gag agc gag gcg gac cag tgg ttg aga      339
Ile Trp Cys Tyr Leu Arg Glu Glu Ser Glu Ala Asp Gln Trp Leu Arg
      80              85              90
cag gtg tgg gga gag gtg cca gag ccc agt gat cgt tct gag gag cct      387
Gln Val Trp Gly Glu Val Pro Glu Pro Ser Asp Arg Ser Glu Glu Pro
      95              100              105
gag act cca gct gcc tac aga gcg aga act tgacgggggtg cccgtgagg      437
Glu Thr Pro Ala Ala Tyr Arg Ala Arg Thr
      110              115
ctggcaggaa gggagccgac agccgccctt cggatttgat gtcacgtttg cccgtgactg      497
tcctggctat gcgtgcgtcc tcagcactga aggacttggc tggtggatgg ggcacttggc      557

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tatgctgatt	cgcgtgaagg	cggagcagaa	tctcagcaga	tcggaaactg	ctcctcgcct	617
ggctcttgat	gtccaaggat	tccatcggca	agactttctca	gatccttggg	gaaggtttca	677
gttgactgt	atgctgttgg	atttgccaag	tctttgtata	acataatcat	gtttccaaag	737
cacttctggt	gacacttgtc	atccagtgtt	agtttgcagg	taatttgctt	tctgagatag	797
aatatctggc	agaagtgtga	aactgtattg	catgctgcgg	cctgtgcaag	gaacacttcc	857
acatgtgagt	tttacacaac	aacaaatgaa	aataaatttt	aattttataa	taaaaaaaaa	917
aaaaaaaa						925

<210> 137
 <211> 674
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..367

<220>
 <221> sig_peptide
 <222> 62..103
 <223> Von Heijne matrix
 score 4.49063834776683
 seq FLTALLWRGRIPG/RQ

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acgccacggc gtctgctggc ggccgcggag acgcagagtc ttgagcagcg cggcaggcac	60
c atg ttc ctg act gcg ctc ctc tgg cgc ggc cgc att ccc ggc cgt cag	109
Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln	
-10 -5 1	
tgg atc ggg aag cac cgg cgg ccg cgg ttc gtg tgc ttg cgc gcc aag	157
Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys	
5 10 15	
cag aac atg atc cgc cgc ctg gag atc gat gcg gag aac cat tac tgg	205
Gln Asn Met Ile Arg Arg Leu Glu Ile Asp Ala Glu Asn His Tyr Trp	
20 25 30	
ctg agc atg ccc tac atg acc cgg gag cag gag cgc ggc cac gcc gsg	253
Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Xaa	
35 40 45 50	
dtg cgc agg agg gag gcc ttc gag gcc ata aag gcg gcc gcc act tcc	301
Xaa Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser	
55 60 65	
aag ttc ccc ccg cat aga ttc att gcg gac cag ctc gac cat ctc aat	349
Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn	
70 75 80	
gtc acc aag aaa tgg tcc taatcctgag tagtcaccct tggattttat	397
Val Thr Lys Lys Trp Ser	
85	
ggatcacgga gctgaccatc ttacactggt cctggaactg aaaaactgta gcttgtgtga	457
aaatgagcct ttggaccagt ctttattaaa acaaacaac atgagtagtc tgcataatcga	517
atatctagag ctctaaaccc cccaataactt aaaagtctaa ttgctgtcct gtggtttcat	577
tagtctgata ggaagatagg gatttctctca gtcacagatg atattttgaa ggaaagctgc	637
aataaagcca caatgattcg aaaaaaaaaa aaaaaaa	674

<210> 138
 <211> 1725
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 107..1618

<220>
 <221> sig_peptide
 <222> 107..178
 <223> Von Heijne matrix
 score 6.19650168602189
 seq LGLYSLVLSGALA/YA

<400> 138
 agagctcagc cggtcgcacg gacggacagt tggaagccgg accccagagc ctgaggtggg 60
 cagtgtgccca ggggtcccttg cggcctcctc aagccctgtc caggct atg ggc atc 115
 Met Gly Ile
 aag aca gca ttg ccg gcg gct gag ctg ggc ctc tac tct ctg gtg ctg 163
 Lys Thr Ala Leu Pro Ala Glu Leu Gly Leu Tyr Ser Leu Val Leu
 -20 -15 -10
 agt ggg gcc ctg gcc tat gct ggc cgg ggc ctc ctt gag gct tca caa 211
 Ser Gly Ala Leu Ala Tyr Ala Gly Arg Gly Leu Leu Glu Ala Ser Gln
 -5 1 5 10
 gat ggg gcc cac agg aag gcc ttc cgg gag tct gtg cga cct ggc tgg 259
 Asp Gly Ala His Arg Lys Ala Phe Arg Glu Ser Val Arg Pro Gly Trp
 15 20 25
 gag tac att ggc cgg aag atg gat gtg gct gac ttc gag tgg gtg atg 307
 Glu Tyr Ile Gly Arg Lys Met Asp Val Ala Asp Phe Glu Trp Val Met
 30 35 40
 tgg ttc acc tcc ttt cgc aac gtc atc atc ttt gcc ctc tcc gga cat 355
 Trp Phe Thr Ser Phe Arg Asn Val Ile Ile Phe Ala Leu Ser Gly His
 45 50 55
 gtg ctg ttt gct aaa ctc tgc acg atg gtt gcc cca aag ctc cgc tcc 403
 Val Leu Phe Ala Lys Leu Cys Thr Met Val Ala Pro Lys Leu Arg Ser
 60 65 70 75
 tgg atg tat gct gtg tac ggg gcc ttg gct gtg atg ggc aca atg ggc 451
 Trp Met Tyr Ala Val Tyr Gly Ala Leu Ala Val Met Gly Thr Met Gly
 80 85 90
 cct tgg tac ctg ctg ctg ctg ctt ggt cac tgt gtg ggc ctc tat gtg 499
 Pro Trp Tyr Leu Leu Leu Leu Leu His Cys Val Gly Leu Tyr Val
 95 100 105
 gcc tcg ctt ttg ggc cag ccc tgg ctc tgt ctt ggc ctt ggc ttg gcc 547
 Ala Ser Leu Leu Gly Gln Pro Trp Leu Cys Leu Gly Leu Gly Leu Ala
 110 115 120
 agc ctg gcc tcc ttc aag atg gac ccc cta atc tct tgg cag agc ggg 595
 Ser Leu Ala Ser Phe Lys Met Asp Pro Leu Ile Ser Trp Gln Ser Gly
 125 130 135
 ttt gta aca ggc act ttt gat ctt caa gag gtg ctg ttt cat ggg ggc 643
 Phe Val Thr Gly Thr Phe Asp Leu Gln Glu Val Leu Phe His Gly Gly
 140 145 150 155
 agc agc ttc aca gtg ctg cgt tgc acc agc ttt gca ctg gag agc tgt 691
 Ser Ser Phe Thr Val Leu Arg Cys Thr Ser Phe Ala Leu Glu Ser Cys
 160 165 170
 gcc cac cct gac cgc cac tac tcc tta gct gac ctg ctc aag tac agc 739
 Ala His Pro Asp Arg His Tyr Ser Leu Ala Asp Leu Leu Lys Tyr Ser
 175 180 185
 ttc tac ctg ccc ttc ttc ttc ttc ggg ccc atc atg acc ttt gat cgc 787
 Phe Tyr Leu Pro Phe Phe Phe Phe Gly Pro Ile Met Thr Phe Asp Arg
 190 195 200
 ttc cat gct cag gtg agc cag gtg gag cca gtg aga cgc gag ggt gag 835

Phe	His	Ala	Gln	Val	Ser	Gln	Val	Glu	Pro	Val	Arg	Arg	Glu	Gly	Glu		
205						210							215				
ctg	tgg	cac	atc	cga	gcc	cag	gca	ggc	cta	agc	gtg	gtg	gcc	atc	atg	883	
Leu	Trp	His	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Ser	Val	Val	Ala	Ile	Met		
220					225					230					235		
gcc	gtc	gac	atc	ttt	cac	ttc	ttc	tac	atc	ctc	act	atc	ccc	agc		931	
Ala	Val	Asp	Ile	Phe	Phe	His	Phe	Phe	Tyr	Ile	Leu	Thr	Ile	Pro	Ser		
				240					245					250			
gac	ctc	aag	ttc	gcc	aac	cgc	ctc	cca	gac	att	gcc	ctc	gct	ggc	cta	979	
Asp	Leu	Lys	Phe	Ala	Asn	Arg	Leu	Pro	Asp	Ile	Ala	Leu	Ala	Gly	Leu		
			255					260					265				
gcc	tat	tca	aac	ctg	gtg	tat	gac	tgg	gtg	aag	gcg	gcc	gtc	ctc	ttt	1027	
Ala	Tyr	Ser	Asn	Leu	Val	Tyr	Asp	Trp	Val	Lys	Ala	Ala	Val	Leu	Phe		
			270					275					280				
ggg	gtt	gtc	aac	act	gtg	gca	tgc	ctc	gac	cac	ctg	gac	cca	ccc	cag	1075	
Gly	Val	Val	Asn	Thr	Val	Ala	Cys	Leu	Asp	His	Leu	Asp	Pro	Pro	Gln		
			285				290						295				
cct	ccc	aag	tgc	atc	acc	gca	ctc	tac	gtc	ttt	gcg	gaa	acg	cac	ttt	1123	
Pro	Pro	Lys	Cys	Ile	Thr	Ala	Leu	Tyr	Val	Phe	Ala	Glu	Thr	His	Phe		
300					305					310					315		
gac	cgt	ggc	atc	aac	gac	tgg	ctt	tgc	aaa	tat	gtg	tat	aac	cac	att	1171	
Asp	Arg	Gly	Ile	Asn	Asp	Trp	Leu	Cys	Lys	Tyr	Val	Tyr	Asn	His	Ile		
				320					325					330			
ggg	ggg	gag	cat	tcc	gct	gtg	atc	cca	gag	ctg	gca	gcc	aca	gtg	gcc	1219	
Gly	Gly	Glu	His	Ser	Ala	Val	Ile	Pro	Glu	Leu	Ala	Ala	Thr	Val	Ala		
			335					340					345				
aca	ttt	gcc	atc	acc	aca	ctg	tgg	ctt	ggg	cct	tgt	gac	att	gtc	tac	1267	
Thr	Phe	Ala	Ile	Thr	Thr	Leu	Trp	Leu	Gly	Pro	Cys	Asp	Ile	Val	Tyr		
			350				355					360					
ctg	tgg	tca	ttc	ctt	aac	tgc	ttt	ggc	ctc	aac	ttt	gag	ctc	tgg	atg	1315	
Leu	Trp	Ser	Phe	Leu	Asn	Cys	Phe	Gly	Leu	Asn	Phe	Glu	Leu	Trp	Met		
			365				370					375					
caa	aaa	ctg	gca	gag	tgg	ggg	ccc	cta	gca	cga	att	gag	gcc	tct	ctg	1363	
Gln	Lys	Leu	Ala	Glu	Trp	Gly	Pro	Leu	Ala	Arg	Ile	Glu	Ala	Ser	Leu		
380					385					390					395		
tca	gtg	cag	atg	tcc	cgt	agg	gtc	cgg	gcc	ctg	ttt	gga	gcc	atg	aac	1411	
Ser	Val	Gln	Met	Ser	Arg	Arg	Val	Arg	Ala								

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..471

<220>
<221> sig_peptide
<222> 16..93
<223> Von Heijne matrix
score 5.809301698725
seq FCVVCVIAIGVVQA/LI

<400> 139
tacacgtttt cgtta atg gtg acc ttc cct gat gtg cct ctg ggc atc ttc 51
Met Val Thr Phe Pro Asp Val Pro Leu Gly Ile Phe
-25 -20 -15
ttg ttc tgt gtg tgt gtg atc gcc atc ggg gtc gtg cag gca ctg att 99
Leu Phe Cys Val Cys Val Ile Ala Ile Gly Val Val Gln Ala Leu Ile
-10 -5 1
gta ggg tac gca ttc cac ttc ccg cac ctg ctg agc ccg cag atc cag 147
Val Gly Tyr Ala Phe His Phe Pro His Leu Leu Ser Pro Gln Ile Gln
5 10 15
cgc tct gcc cac agg gct ctg tac cga cga cac gtc ctg ggc atc gtc 195
Arg Ser Ala His Arg Ala Leu Tyr Arg Arg His Val Leu Gly Ile Val
20 25 30
ctc caa ggc ccg gcc ctg tgc ttt gca gcg gcc atc ttc tct ctc ttc 243
Leu Gln Gly Pro Ala Leu Cys Phe Ala Ala Ala Ile Phe Ser Leu Phe
35 40 45 50
ttt gtc ccc ttg tct tac ctg ctg atg gtg act gtc atc ctc ctc ccc 291
Phe Val Pro Leu Ser Tyr Leu Leu Met Val Thr Val Ile Leu Leu Pro
55 60 65
tat gtc agc aag gtc acc ggc tgg tgc aga gac agg ctc ctg ggc cac 339
Tyr Val Ser Lys Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His
70 75 80
agg gag ccc tcg gct cac cca gtg gaa gtc ttc tcg ttt gac ctc cac 387
Arg Glu Pro Ser Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His
85 90 95
gag cca ctc agc aag gag cgc gtg gaa gcc ttc agc gac gga gtc tac 435
Glu Pro Leu Ser Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr
100 105 110
gcc atc gtg gcc acg ctt ctc atc ctg gac atc tgg tgaggacccc 481
Ala Ile Val Ala Thr Leu Leu Ile Leu Asp Ile Trp
115 120 125
gcgtcacctg cccagctat caggtggcca atgtgtcttg agtccctggc gtctcactct 541
ggaaacccca gaaaggcaca ggggtcttgg ctccaccctc ctctggatgc cttagagttt 601
gtgtgaggtc agggcagccc ccacttcagg gaggacaacc ttcccggcgg cccctccctt 661
cccagcggcc cctcccttcc cagaggctcc caccccaagc acagccgagg atgggggtgcc 721
agggtgaggt cagcaccagc agccaactgc tctcctcact cctctcagag gggctcagca 781
gccatgggta tccccctgcc ccaggcctca cccctgcccc aacaccagcc cctcctagtc 841
cctagtcctt cccattccct ccggtccct cccagtgcct cccatcgctt cgcagccctt 901
tctgtccctt ttggtggct gttgcttccct tccagcgtct gtcctcctgc ggcctcatct 961
gcctcttcgt ctggttagagc gcgcgtctcg tctcagtcgt cacgtttttg gtttttgtgg 1021
ggtttttttt tttttttttt tttgagacag tctgtctgtg tcgcccaggc tggagtatag 1081
tggctcaagc tcagctcact gcaacctccg cctcccaggt tcaagcaatt ctccctgcctc 1141
agcctcccaa gtagttggga ttacaagcac ccaccacat gccagctaa ctttttgcctc 1201
ttttaataga gatgaggttt caccaagttg gccaggctgg tcttgaactc ctgacctcag 1261

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gtgatctgcc cacctcggcc tcccaaagtg ctgggattac aggtgtaagc caccgtgccc 1321
ggccatcgta atgtttgaat ttgctttttt acatcttcca tccttttgga gtgtcttggt 1381
ccctcgatcat agttcagcac tgtgaccacc ttgggggttag acactatggt tttatatacct 1441
gtacttgata ttctccaaaa aaaaaaaaaa aaa 1474

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<210> 140
<211> 653
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 222..374

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<220>
<221> sig_peptide
<222> 222..299
<223> Von Heijne matrix
      score 4.28353322771141
      seq ILFKFSLCPYAAA/LS

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<400> 140
taataatggt gttaaattat tgcctttctca tctgcgtgtc tcttatgttc tgcttaaaga 60
gattgtcagt ttgttcaagc tcttttttagt tgttgctcct ccagtgccta gctttgagct 120
ttgtacacgg tagttattga gttgagtaac atagtttggt ctgagtcatt tgttccacat 180
gcttgaagac ttggcttaac ctagtagata ataggaaaga a atg gaa atg ctc ttt 236
                                         Met Glu Met Leu Phe
                                         -25
gat gaa aga gcc cct ctc tta ttc atc ctt ttt aaa ttt tct ttg tgc 284
Asp Glu Arg Ala Pro Leu Leu Phe Ile Leu Phe Lys Phe Ser Leu Cys
-20 -15 -10
cca tat gca gca gct ctc agc aaa cct ata ttt ggc agt gtg gcc tgt 332
Pro Tyr Ala Ala Ala Leu Ser Lys Pro Ile Phe Gly Ser Val Ala Cys
-5 1 5 10
atg act aaa gaa atc ctg gcc agg cac ggt ggc tca cgc ctg 374
Met Thr Lys Glu Ile Leu Ala Arg His Gly Gly Ser Arg Leu
15 20 25
taatcccagc actttgggag gccgaggcgg gtggattacg aggtcaggag attgagacca 434
tcctggctaa catggcgaaa ccccatctct acgaaaaata caaaaaaaaaa aattagccgg 494
gcatcatggc gggcgccctgt agtcttagct actcaggagg ctgaggcagg agaatggcgt 554
gaacccggga ggcggagctt gcagtgaacc gagattgcgc cactgcactc cagcctgggg 614
caacagagca agactccgtc tcaaaaaaaaa aaaaaaaaaa 653

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<210> 141
<211> 1490
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 59..274

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<220>
<221> sig_peptide
<222> 59..127
<223> Von Heijne matrix
      score 7.37647149292058
      seq LGLCSLLVGAEAE/PS

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<400> 141
agacagaggc agggccttgcg acggaagtgg cctctctgct tctgcagggc tggggaag      58
atg ctg cgt cca gcg tta ccg tgg ctg tac ctt ggc ctc tgc agc ctc      106
Met Leu Arg Pro Ala Leu Pro Trp Leu Tyr Leu Gly Leu Cys Ser Leu
      -20      -15      -10
ctg gtg ggg gag gca gag gcc ccg agc ccc gtg gat ccg ctg gag cgg      154
Leu Val Gly Glu Ala Glu Ala Pro Ser Pro Val Asp Pro Leu Glu Arg
      -5      1      5
agc cgg ccg tac gcg gtg ctg cga ggg cag aac ctg gtg ttg atg gga      202
Ser Arg Pro Tyr Ala Val Leu Arg Gly Gln Asn Leu Val Leu Met Gly
10      15      20      25
acc att ttc agc atc ctg ctg gtg act gtc atc ctt atg gca ttt tgt      250
Thr Ile Phe Ser Ile Leu Leu Val Thr Val Ile Leu Met Ala Phe Cys
      30      35      40
gtc tac aag ccc att cgg cgt cgg tgacagccag acaagttctt caatgagtat      304
Val Tyr Lys Pro Ile Arg Arg Arg
      45
ttgggaatag gataagttgt gttgcacaca ggccagtgga gaagttggaa ccaaaaacttt      364
cctacttggg aatgaccttt ggtctggaca gttggtaaat gctaaatgaa ttagaagaaa      424
acatgtacta gacattatth tttcctaaca ctgtagcgca aataattggc ccctgagtcc      484
gcttctcagt gtttctgact gtacttgta aaagtaagac ctgaaagctc caaaggctcag      544
tgtaaagatg gagtgttcat gagaaagaaa acatggtaac cttgtgagtg cctgtaagaa      604
ccacactgta aagaactcat cattaatgct tgaataatgtt attaagaagg agacttacca      664
tgacagacatt ccctatttaa gaaccatttg gttacagtgg gttaagaatc acagattttt      724
ttttttaatc tcacctgagt tagcctagaa tgcgctgggt gcaaagtggg gtcagctgtg      784
gggatcttgg gccctcgttc ctcacctgca tcctgccctg cactcagggtg ctccccctga      844
agtcagggtc acatcaggta gacctgttac tatatgcacc tttggcctgg aatgctctga      904
agttggactg gaaatgttac taggttgccc tgttacaaaa aggaccccat cctgcttaaa      964
cacattgata tcccttgccc tgcatttgag tctttctagc ccacgggtctg aaacttgagg      1024
cagctttcca gatttggaat gtaaaaggct cagtgggcac tctgttcac cctgggtggg      1084
gagggcccag ccaacagaag tgcattgtcca ctgtgcgggc cagtgtgtgt ttacacaaat      1144
ttcatctcag ctttgaaaat gctgctatta gtttccactg ttggtgaact ggattttttc      1204
ctcctattga aatgatactt tcatacttat aaagctgtcg tcaatattta tttcaagggtg      1264
ctagatttaa ttttgttatt aaattgaaat gcttatcttg tgttcaagca cagcactgat      1324
tttaacaacc tgcatttaac gtgaagtaac cgaagtagga tactgtaact gtgtaaggat      1384
tttgtttgta atcttgtaac attgaacat tgaaatgttc agttctttgc ttttgagcaa      1444
aacgtcaatt aaaactaaag taaaatctta aaaaaaaaaa aaaaaa      1490

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<210> 142
<211> 661
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 158..442

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<220>
<221> sig_peptide
<222> 158..301
<223> Von Heijne matrix
      score 7.53908709538105
      seq FVILLLFIFTVVS/LV

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<400> 142
aaaaacagac gataccatcg cttcagcagc atcctctcag acaagagcca ctattttctga      60
ttcagatcac ctgtcatcga agtttaaaga aggggaaaca ggagacagaa atacactgaa      120

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ccaaaaagat tcaaaagagc aagtgggaatc tctaaga atg gct tcc agc cac tgg 175
Met Ala Ser Ser His Trp

-45
aat gaa acc act acc tct gtt tat cag tac ctt ggt ttt caa gtt caa 223
Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr Leu Gly Phe Gln Val Gln

-40 -35 -30
aaa att tac cct ttc cat gac aac tgg aac act gcc tgc ttt gtc atc 271
Lys Ile Tyr Pro Phe His Asp Asn Trp Asn Thr Ala Cys Phe Val Ile

-25 -20 -15
ctg ctt tta ttt ata ttt aca gtg gta tct tta gtg gtg ctg gct ttc 319
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Leu Tyr Glu Val Leu Asp Cys Cys Cys Cys Val Lys Asn Lys Thr Val

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Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu Arg Ser Met Met Asp Asn

25 30 35
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Ile Arg Lys Arg Glu Thr Glu Val Val

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Arg Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala

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Ile Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg

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 Glu Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val
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 Phe Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro
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 Met Pro Thr Cys Arg Val Tyr Gly Thr Val Ala His Gln Asp Gly His
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Ser	Cys	Ser	Ser	Leu	Gln	Ala	Gly	Pro	Arg	Leu	Phe	Val	Ile	Gly	Gly	
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Arg	Trp	Gly	Ala	Lys	Arg	Leu	Gly	Val	Ala	Ser	Thr	Glu	Ala	Gln	Arg	
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Gly	Val	Ser	Phe	Lys	Leu	Glu	Lys	Thr	Ala	His	Ser	Ser	Leu	Ala		
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Pro	Thr	Lys	Val	Ala	Leu	Asn	Val	Glu	Arg	Phe	Arg	Glu	Trp	Ala	Val	
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Met	Ser	Arg	Asp	Ser	Cys	Ile	Gly	Val	Asp	Asp	Arg	Ser	Trp	Val	Phe	
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Thr	Tyr	Ala	Gln	Arg	Lys	Trp	Tyr	Thr	Met	Leu	Ala	Asn	Glu	Lys	Ala	
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Pro	Val	Glu	Gly	Ile	Gly	Gln	Pro	Glu	Lys	Val	Gly	Leu	Leu	Leu	Glu	
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Val His Thr Leu Gln Thr Asp Phe Arg Gly Pro Val Val Pro Ala Phe						
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gct ctc tgg gat ggg gag ctg ctg acc cat tca ggg ctt gag gtg ccc						626
Ala Leu Trp Asp Gly Glu Leu Leu Thr His Ser Gly Leu Glu Val Pro						
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gag ggc ctc tagtatgtcc attactggag tccctaataca cgcctttggc						675
Glu Gly Leu						
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Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg Phe Ser Val						
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Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala Val Ala Ile						
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Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala Pro Ala Pro						
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att ggg gag ctg gcc cct ggc agc ttc ctg gcg gct gtg gtg gat gcc						405
Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val Val Asp Ala						
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Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu Ser Gly Met						
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tac tcc ctg ccc ttc ctc acg gcc cct ggc tcc cag ctc ccg ggc ttt						501
Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu Pro Gly Phe						
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gtg cca gtg gcc ccc atc tgc act gac aaa atc aat gct gcc aac tat						549

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 <221> CDS
 <222> 21..1145

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Cys	Pro	Leu	Leu	Leu	Pro	Gln	Asn	Arg	Ser	Lys	Thr	Val	Tyr	Glu	Gly	
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ttc	atc	tcg	gct	cag	gga	aga	gac	ttc	cac	ctt	agg	ata	gtg	ttg	cct	149
Phe	Ile	Ser	Ala	Gln	Gly	Arg	Asp	Phe	His	Leu	Arg	Ile	Val	Leu	Pro	
		30				35					40					
gaa	gat	tta	caa	ctg	aag	aat	gca	aga	tta	tta	tgt	att	tgg	cag	ctg	197
Glu	Asp	Leu	Gln	Leu	Lys	Asn	Ala	Arg	Leu	Leu	Cys	Ile	Trp	Gln	Leu	
	45				50				55							
aga	aca	ata	ctt	agt	gga	tac	cat	cga	ata	gta	caa	cag	aga	atg	cag	245
Arg	Thr	Ile	Leu	Ser	Gly	Tyr	His	Arg	Ile	Val	Gln	Gln	Arg	Met	Gln	
	60				65				70							
cac	tct	cct	gat	cta	atg	agc	ttt	atg	atg	gag	ttg	aag	atg	ctt	ttg	293
His	Ser	Pro	Asp	Leu	Met	Ser	Phe	Met	Met	Glu	Leu	Lys	Met	Leu	Leu	

80										85					90					
gaa	ggt	gcc	ttt	aag	aat	aga	caa	gag	ctg	tat	gca	cta	cct	cct	cct		341			
Glu	Val	Ala	Leu	Lys	Asn	Arg	Gln	Glu	Leu	Tyr	Ala	Leu	Pro	Pro	Pro					
			95					100					105							
ccc	cag	ttc	tac	tca	agc	ctt	att	gaa	gag	ata	gga	act	ctt	ggg	tgg		389			
Pro	Gln	Phe	Tyr	Ser	Ser	Leu	Ile	Glu	Glu	Ile	Gly	Thr	Leu	Gly	Trp					
		110					115					120								
gat	aaa	ctt	gtg	tat	gcg	gat	acc	tgc	ttc	agt	acc	atc	aag	tta	aaa		437			
Asp	Lys	Leu	Val	Tyr	Ala	Asp	Thr	Cys	Phe	Ser	Thr	Ile	Lys	Leu	Lys					
		125				130					135									
gca	gaa	gat	gct	tct	ggg	aga	gag	cat	tta	atc	act	ctc	aag	ttg	aag		485			
Ala	Glu	Asp	Ala	Ser	Gly	Arg	Glu	His	Leu	Ile	Thr	Leu	Lys	Leu	Lys					
		140			145				150						155					
gca	aag	tat	cct	gca	gaa	tca	cca	gat	tat	ttt	gtg	gat	ttt	cct	ggt		533			
Ala	Lys	Tyr	Pro	Ala	Glu	Ser	Pro	Asp	Tyr	Phe	Val	Asp	Phe	Pro	Val					
			160						165					170						
cca	ttt	tgt	gcc	tcc	tgg	aca	cct	cag	agc	tcc	tta	ata	agc	att	tat		581			
Pro	Phe	Cys	Ala	Ser	Trp	Thr	Pro	Gln	Ser	Ser	Leu	Ile	Ser	Ile	Tyr					
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agt	cag	ttt	ttg	gca	gca	ata	gaa	tca	cta	aag	gca	ttc	tgg	gat	ggt		629			
Ser	Gln	Phe	Leu	Ala	Ala	Ile	Glu	Ser	Leu	Lys	Ala	Phe	Trp	Asp	Val					
		190				195						200								
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Met	Asp	Glu	Ile	Asp	Glu	Lys	Thr	Trp	Val	Leu	Glu	Pro	Glu	Lys	Pro					
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cca	cgg	agt	gca	aca	gca	cgc	aga	att	gca	tta	ggg	aat	aat	ggt	tcc		725			
Pro	Arg	Ser	Ala	Thr	Ala	Arg	Arg	Ile	Ala	Leu	Gly	Asn	Asn	Val	Ser					
		220			225				230						235					
ata	aat	ata	gag	gta	gac	ccc	agg	cat	cct	act	atg	ctt	cct	gag	tgc		773			
Ile	Asn	Ile	Glu	Val	Asp	Pro	Arg	His	Pro	Thr	Met	Leu	Pro	Glu	Cys					
			240					245						250						
ttc	ttt	ctt	gga	gct	gac	cat	gtg	gta	aaa	ccc	ctg	gga	att	aag	ctg		821			
Phe	Phe	Leu	Gly	Ala	Asp	His	Val	Val	Lys	Pro	Leu	Gly	Ile	Lys	Leu					
		255					260						265							
agc	agg	aac	ata	cat	ttg	tgg	gat	cca	gaa	aat	agt	gtg	tta	caa	aat		869			
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Leu	Lys	Asp	Val	Leu	Glu	Ile	Asp	Phe	Pro	Ala	Arg	Ala	Ile	Leu	Glu					
		285				290					295									
aaa	tct	gat	ttt	act	atg	gat	tgt	gga	att	tgt	tat	gct	tat	caa	ctt		965			
Lys	Ser	Asp	Phe	Thr	Met	Asp	Cys	Gly	Ile	Cys	Tyr	Ala	Tyr	Gln	Leu					
		300			305			310						315						
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Asp	Gly	Thr	Ile	Pro	Asp	Gln	Val	Cys	Asp	Asn	Ser	Gln	Cys	Gly	Gln					
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cct	ttc	cat	caa	ata	tgc	tta	tat	gag	tgg	ctg	aga	gga	cta	cta	act		1061			
Pro	Phe	His	Gln	Ile	Cys	Leu	Tyr	Glu	Trp	Leu	Arg	Gly	Leu	Leu	Thr					
		335						340					345							
agt	aga	cag	agt	ttt	aac	atc	ata	ttt	ggg	gaa	tgt	cca	tat	tgt	agt		1109			
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Lys	Pro	Ile	Thr	Leu	Lys	Met	Ser	Gly	Arg	Lys	His									
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gataataata	aacatctgcg	tttgtctctt	cactaagagt	aaactgggaa	attgtaggcc												1335			

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tcaaagggtc ttgagactct tgatatttct gtcttctcct tgtgctttcc tatggaaaaa 1575
atacatatat agtttagttt gttagacgtg agttatccaa gtattttattt tgtgtagtgt 1635
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<220>
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Met Ala Ala Ile Gly Val His Leu Gly Cys Thr Ser Ala Cys
      1             5             10
gtg gcc gtc tat aag gat ggc cgg gct ggt gtg gtt gca aat gat gcc 159
Val Ala Val Tyr Lys Asp Gly Arg Ala Gly Val Val Ala Asn Asp Ala
15             20             25             30
ggt gac cga gtt act cca gct gtt gtt gct tac tca gaa aat gaa gag 207
Gly Asp Arg Val Thr Pro Ala Val Val Ala Tyr Ser Glu Asn Glu Glu
      35             40             45
att gtt gga ttg gca gca aaa caa agt aga ata aga aat att tca aat 255
Ile Val Gly Leu Ala Ala Lys Gln Ser Arg Ile Arg Asn Ile Ser Asn
      50             55             60
aca gta atg aaa gta aag cag atc ctg ggc aga agc tcc agt gat cca 303
Thr Val Met Lys Val Lys Gln Ile Leu Gly Arg Ser Ser Ser Asp Pro
      65             70             75
caa gct cag aaa tac atc gcg gaa agt aaa tgt tta gtc att gaa aaa 351
Gln Ala Gln Lys Tyr Ile Ala Glu Ser Lys Cys Leu Val Ile Glu Lys
      80             85             90
aat ggg aaa tta cga tat gaa ata gat act gga gaa gaa aca aaa ttt 399
Asn Gly Lys Leu Arg Tyr Glu Ile Asp Thr Gly Glu Glu Thr Lys Phe
      95             100            105            110
gtt aac cca gaa gat gtt gcc aga ctg ata ttt agt aaa atg aaa gaa 447
Val Asn Pro Glu Asp Val Ala Arg Leu Ile Phe Ser Lys Met Lys Glu
      115            120            125
acg gca cat tct gta ttg ggc tca gat gca aat gat gta gtt att act 495
Thr Ala His Ser Val Leu Gly Ser Asp Ala Asn Asp Val Val Ile Thr
      130            135            140
gtc ccg ttt gat ttt gga gaa aag caa aaa aat gct ctt gga gaa gca 543
Val Pro Phe Asp Phe Gly Glu Lys Gln Lys Asn Ala Leu Gly Glu Ala
      145            150            155
gct aga gct gct gga ttt aat gtt ttg cga tta att cac gaa ccg tct 591
Ala Arg Ala Ala Gly Phe Asn Val Leu Arg Leu Ile His Glu Pro Ser
      160            165            170
gca gct ctt ctt gct tat gga att gga caa gac tcc cct act gga aaa 639
Ala Ala Leu Leu Ala Tyr Gly Ile Gly Gln Asp Ser Pro Thr Gly Lys
      175            180            185            190
agc aat att ttg gtg ttt aag ctt gga gga aca tcc tta tct ctc agc 687
Ser Asn Ile Leu Val Phe Lys Leu Gly Gly Thr Ser Leu Ser Leu Ser
      195            200            205
gtc atg gaa gtt aac agt gga ata tat cgg gtt ctt tca aca aac act 735

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Asp	Asp	Asn	Ile	Gly	Gly	Ala	His	Phe	Thr	Glu	Thr	Leu	Ala	Gln	Tyr	
		225					230					235				
cta	gct	tct	gag	ttc	caa	aga	tcc	ttc	aaa	cat	gat	gtg	aga	gga	aat	831
Leu	Ala	Ser	Glu	Phe	Gln	Arg	Ser	Phe	Lys	His	Asp	Val	Arg	Gly	Asn	
	240					245					250					
gcg	cga	gcc	atg	atg	aaa	tta	acg	aac	agt	gct	gaa	gta	gcg	aaa	cat	879
Ala	Arg	Ala	Met	Met	Lys	Leu	Thr	Asn	Ser	Ala	Glu	Val	Ala	Lys	His	
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Ser	Leu	Ser	Thr	Leu	Gly	Ser	Ala	Asn	Cys	Phe	Leu	Asp	Ser	Leu	Tyr	
			275						280						285	
gaa	ggg	caa	gat	ttt	gat	tgc	aat	gtg	tcc	aga	gca	aga	ttt	gaa	ctt	975
Glu	Gly	Gln	Asp	Phe	Asp	Cys	Asn	Val	Ser	Arg	Ala	Arg	Phe	Glu	Leu	
			290					295					300			
ctt	tgt	tct	cca	ctt	ttt	aat	aag	tgt	ata	gaa	gca	atc	aga	gga	ctc	1023
Leu	Cys	Ser	Pro	Leu	Phe	Asn	Lys	Cys	Ile	Glu	Ala	Ile	Arg	Gly	Leu	
		305					310					315				
tta	gat	caa	aat	gga	ttt	aca	aca	gat	gat	atc	aac	aag	gtt	gtc	ctt	1071
Leu	Asp	Gln	Asn	Gly	Phe	Thr	Thr	Asp	Asp	Ile	Asn	Lys	Val	Val	Leu	
	320					325					330					
tgt	gga	ggg	tct	tct	cga	atc	cca	aag	cta	cag	caa	ctg	att	aaa	gat	1119
Cys	Gly	Gly	Ser	Ser	Arg	Ile	Pro	Lys	Leu	Gln	Gln	Leu	Ile	Lys	Asp	
335					340					345					350	
ctt	ttc	cca	gct	gtt	gag	ctt	ctc	aat	tct	atc	cct	cct	gat	gaa	gtg	1167
Leu	Phe	Pro	Ala	Val	Glu	Leu	Leu	Asn	Ser	Ile	Pro	Pro	Asp	Glu	Val	
				355					360						365	
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Ile	Pro	Ile	Gly	Ala	Ala	Ile	Glu	Ala	Gly	Ile	Leu	Ile	Gly	Lys	Glu	
			370					375					380			
aac	ctg	ttg	gtg	gaa	gac	tct	ctt	atg	ata	gag	tgt	tca	gcc	aga	gat	1263
Asn	Leu	Leu	Val	Glu	Asp	Ser	Leu	Met	Ile	Glu	Cys	Ser	Ala	Arg	Asp	
		385					390					395				
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Ile	Leu	Val	Lys	Gly	Val	Asp	Glu	Ser	Gly	Ala	Ser	Arg	Phe	Thr	Val	
	400					405					410					
ctg	ttt	cca	tca	ggg	act	cct	ttg	cca	gct	cga	aga	caa	cac	aca	ttg	1359
Leu	Phe	Pro	Ser	Gly	Thr	Pro	Leu	Pro	Ala	Arg	Arg	Gln	His	Thr	Leu	
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Gln	Ala	Pro	Gly	Ser	Ile	Ser	Ser	Val	Cys	Leu	Glu	Leu	Tyr	Glu	Ser	
				435					440						445	
gat	ggg	aag	aac	tct	gcc	aaa	gag	gaa	acc	aag	ttt	gca	cag	gtt	gta	1455
Asp	Gly	Lys	Asn	Ser	Ala	Lys	Glu	Glu	Thr	Lys	Phe	Ala	Gln	Val	Val	
		450						455					460			
ctc	cag	gat	tta	gat	aaa	aaa	gaa	aat	gga	tta	cgt	gat	ata	tta	gct	1503
Leu	Gln	Asp	Leu	Asp	Lys	Lys	Glu	Asn	Gly	Leu	Arg	Asp	Ile	Leu	Ala	
		465					470					475				
gtt	ctt	act	atg	aaa	agg	gat	gga	tct	tta	cat	gtg	aca	tgc	aca	gat	1551
Val	Leu	Thr	Met	Lys	Arg	Asp	Gly	Ser	Leu	His	Val	Thr	Cys	Thr	Asp	
	480					485					490					
caa	gaa	act	gga	aaa	tgt	gaa	gca	atc	tct	att	gag	ata	gca	tct		1596
Gln	Glu	Thr	Gly	Lys	Cys	Glu	Ala	Ile	Ser	Ile	Glu	Ile	Ala	Ser		
495					500					505						
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1747

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<211> 658

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 129..362

<400> 149

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gtggggacc atg tac aac act gga aga cac gta tcc ctt cgc ctg gac aag 170

Met Tyr Asn Thr Gly Arg His Val Ser Leu Arg Leu Asp Lys

1 5 10

gag cac ttg gtc aac ata tct gga ggg ccc atg aca lac agc cac cgg 218

Glu His Leu Val Asn Ile Ser Gly Gly Pro Met Thr Tyr Ser His Arg

15 20 25 30

ctg gag gag atc cga cta cac ttt ggg agt gag gac agc caa ggg tcg 266

Leu Glu Glu Ile Arg Leu His Phe Gly Ser Glu Asp Ser Gln Gly Ser

35 40 45

gag cac ctc ctc aat gga cag gcc ttc tct ggg gag ctt caa gag agg 314

Glu His Leu Leu Asn Gly Gln Ala Phe Ser Gly Glu Leu Gln Glu Arg

50 55 60

gat ttg ttc atc ttg ttg act tct gta tca gga cat ctg ccc gat aca 362

Asp Leu Phe Ile Leu Leu Thr Ser Val Ser Gly His Leu Pro Asp Thr

65 70 75

tagaaaaagt ctgctgaccc ctgaattaca gtatgagcca ttcggaatgc atttctcttt 422

aaaagttctc gcctcattca gtgtctggaa cacagtgggt gctccccaat aggtgacacc 482

ttcctcaagt ttccttggga gaacagactc aatgtcggat ccacaaagga gacctgcaca 542

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<213> Homo sapiens

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Met Ala Thr

1

cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg gtg 165

His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met Val

5 10 15

ggc aca gtg gct gtc act gtc atg cct cag tgg ata gtg tcg gcc ttc 213

Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Ile Val Ser Ala Phe

20 25 30 35

att gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg tgg 261

Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu Gly Leu Trp

40 45 50

atg aat tgc gtg agg cag gct aac atc agg atg cag tgc aaa atc tat	309
Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile Tyr	
55 60 65	
gat tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga ctg	357
Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly Leu	
70 75 80	
atg tgt gct gct tcc gtg atg tcc ttc ttg gct ttc atg atg gcc atc	405
Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala Ile	
85 90 95	
ctt ggc atg aaa tgc acc agg tgc acg ggg gac aat gag aag gtg aag	453
Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val Lys	
100 105 110 115	
gct cac att ctg ctg acg gct gga atc atc ttc atc atc acg ggc atg	501
Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met	
120 125 130	
gtg gtg ctc atc cct gtg agc tgg gtt gcc aat gcc atc atc aga gat	549
Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp	
135 140 145	
ttc tat aac cca ata gtg aat gtt gcc caa aaa cgt gag ctt gga	594
Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly	
150 155 160	
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ccaaaaaac aacaacaaaa aaagttgtcc tttgagaact tcacctgctc ctatgtgggt	1794
acctgagtc aattgtcat tttgttctg tgaaaaataa atttccttct tgtaccattt	1854
ctgttttagtt ttactaaaaat ctgtaaatac tgtatttttc tgtttattcc aaatttgatg	1914
aaactgacaa tccaatttga aagtttgtgt cgacgtctgt ctagcttaaa tgaatgtgtt	1974
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aaaaaaaaa a	2045

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 150..587

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gacatttcac aaatccaaaa ttgccgtgg atg aac tct tta ctt cac ttc ggg	173
Met Asn Ser Leu Leu His Phe Gly	
1 5	
ata ttg ctg gag ctg agt ctc ctg aaa cag ttt aag tct gta tat gtt	221
Ile Leu Leu Glu Leu Ser Leu Leu Lys Gln Phe Lys Ser Val Tyr Val	
10 15 20	
cct gga aat cat acc cac cag gca tct tat aag cca ttg ttg aag caa	269
Pro Gly Asn His Thr His Gln Ala Ser Tyr Lys Pro Leu Leu Lys Gln	
25 30 35 40	
gtt gtg gag gaa ata ttt cat ccc gag agg cca gat tcc gtt gat att	317
Val Val Glu Glu Ile Phe His Pro Glu Arg Pro Asp Ser Val Asp Ile	
45 50 55	
gaa cac atg tct tca ggc ctc act gat ctc ctt aaa act gga ttt agc	365
Glu His Met Ser Ser Gly Leu Thr Asp Leu Leu Lys Thr Gly Phe Ser	
60 65 70	
atg ttc atg aag gtg agc cgg cct cat cct agt gac tac ccc ctc ctg	413
Met Phe Met Lys Val Ser Arg Pro His Pro Ser Asp Tyr Pro Leu Leu	
75 80 85	
atc ctc ttt gtg gta ggt ggg gtc aca gtc tct gaa gtg aaa atg gtc	461
Ile Leu Phe Val Val Gly Gly Val Thr Val Ser Glu Val Lys Met Val	
90 95 100	
aaa gat ctt gtg gca tcg ttg aag cca gga acc cag gta atc gtg ctg	509
Lys Asp Leu Val Ala Ser Leu Lys Pro Gly Thr Gln Val Ile Val Leu	
105 110 115 120	
tcc aca cga ctc ctg aag cca ctt aac att cct gag ctg tta ttt gca	557
Ser Thr Arg Leu Leu Lys Pro Leu Asn Ile Pro Glu Leu Leu Phe Ala	
125 130 135	
act gac cga ctg cat cca gac ctt ggc ttc tgagcatccg ctaagaagat	607
Thr Asp Arg Leu His Pro Asp Leu Gly Phe	
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cacaaccagc gtccctgtca ctaattgcga gaatgatgga attctgcctg aagggtcttg	727
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gcagaagtag cagttccgga gtccagctgg ctaaaactca tcccagagga ta atg gca	178
Met Ala	
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acc cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg	226
Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met	
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Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val Ser Ala	
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                               Met Arg Leu Gln Asp
                               1           5

cgc atc gcc acg ttc ttc ttc cca aaa ggc atg atg ctc acc acg gct      162
Arg Ile Ala Thr Phe Phe Phe Pro Lys Gly Met Met Leu Thr Thr Ala
                10           15           20

gcg ctg atg ctc ttc ttc tta cac ctg ggc atc ttc atc aga gac gtg      210
Ala Leu Met Leu Phe Phe Leu His Leu Gly Ile Phe Ile Arg Asp Val
                25           30           35

cac aac ttc tgc atc acc tac cac tat gac cac atg agc ttt cac tac      258
His Asn Phe Cys Ile Thr Tyr His Tyr Asp His Met Ser Phe His Tyr
                40           45           50

acg gtc gtc ctg atg ttc tcc cag gtg atc agc atc tgc tgg gct gcc      306
Thr Val Val Leu Met Phe Ser Gln Val Ile Ser Ile Cys Trp Ala Ala
                55           60           65

atg ggg tca ctc tat gct gag atg aca gaa aac aat gct caa cgg agc      354
Met Gly Ser Leu Tyr Ala Glu Met Thr Glu Asn Asn Ala Gln Arg Ser
                70           75           80           85

cat gtt ctt caa ccg cct gtc ctt gga gtt tct ggc cat cga gta ccg      402
His Val Leu Gln Pro Pro Val Leu Gly Val Ser Gly His Arg Val Pro
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gga gga gca cca ctg agg cct ggg gag tcg gaa cag ggc taaggagggg      451
Gly Gly Ala Pro Leu Arg Pro Gly Glu Ser Glu Gln Gly
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aaa                                                                    514
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acc ccc acc aac tgc agc tgg tgg ccc atc tcc gcg ctg gag agc gat      100
Thr Pro Thr Asn Cys Ser Trp Trp Pro Ile Ser Ala Leu Glu Ser Asp
                10           15           20

gcg gcc aag cca gcg gag gcc ccc gac gct ccc gag gcg gcc agc ccc      148
Ala Ala Lys Pro Ala Glu Ala Pro Asp Ala Pro Glu Ala Ala Ser Pro
                25           30           35

gcc cat tgg ccc agg gag agc ctg gtt ctg tac cac tgg acc cag tcc      196
Ala His Trp Pro Arg Glu Ser Leu Val Leu Tyr His Trp Thr Gln Ser
                40           45           50           55

ttc agc tcg cag aag gtg cgg ctg gtg atc gcc gag aag ggc ctg gtg      244
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Phe	Ser	Ser	Gln	Lys	Val	Arg	Leu	Val	Ile	Ala	Glu	Lys	Gly	Leu	Val		
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tgc	gag	gag	cgg	gac	gtg	agc	ctg	cca	cag	agc	gag	cac	aag	gag	ccc		292
Cys	Glu	Glu	Arg	Asp	Val	Ser	Leu	Pro	Gln	Ser	Glu	His	Lys	Glu	Pro		
			75					80					85				
tgg	ttc	atg	cgg	ctc	aac	ctg	ggc	gag	gag	gtg	ccc	gtc	atc	atc	cac		340
Trp	Phe	Met	Arg	Leu	Asn	Leu	Gly	Glu	Glu	Val	Pro	Val	Ile	Ile	His		
		90					95					100					
cgc	gac	aac	atc	atc	agt	gac	tat	gac	cag	atc	att	gac	tat	gtg	gag		388
Arg	Asp	Asn	Ile	Ile	Ser	Asp	Tyr	Asp	Gln	Ile	Ile	Asp	Tyr	Val	Glu		
	105					110					115						
cgc	acc	ttc	aca	gga	gag	cac	gtg	gtg	gcc	ctg	atg	ccc	gag	gtg	ggc		436
Arg	Thr	Phe	Thr	Gly	Glu	His	Val	Val	Ala	Leu	Met	Pro	Glu	Val	Gly		
	120					125					130				135		
agc	ctg	cag	cac	gca	cgg	gtg	ctg	cag	tac	cgg	gag	ctg	ctg	gac	gca		484
Ser	Leu	Gln	His	Ala	Arg	Val	Leu	Gln	Tyr	Arg	Glu	Leu	Leu	Asp	Ala		
				140					145					150			
ctg	ccc	atg	gat	gcc	tac	acg	cat	ggc	tgc	atc	ctg	cat	ccc	gag	ctc		532
Leu	Pro	Met	Asp	Ala	Tyr	Thr	His	Gly	Cys	Ile	Leu	His	Pro	Glu	Leu		
			155					160					165				
acc	acc	gac	tcc	atg	atc	ccc	aag	tac	gcc	acg	gcc	gag	atc	cgc	aga		580
Thr	Thr	Asp	Ser	Met	Ile	Pro	Lys	Tyr	Ala	Thr	Ala	Glu	Ile	Arg	Arg		
		170					175					180					
cat	tta	gcc	aat	gcc	acc	acg	gac	ctc	atg	aaa	ctg	gac	cat	gaa	gag		628
His	Leu	Ala	Asn	Ala	Thr	Thr	Asp	Leu	Met	Lys	Leu	Asp	His	Glu	Glu		
	185					190					195						
gag	ccc	cag	ctc	tcc	gag	ccc	tac	ctt	tct	aaa	caa	aag	aag	ctc	atg		676
Glu	Pro	Gln	Leu	Ser	Glu	Pro	Tyr	Leu	Ser	Lys	Gln	Lys	Lys	Leu	Met		
	200				205					210					215		
gtc	aag	atc	ttg	gag	cat	gat	gat	gtg	agc	tac	ctg	aag	aag	atc	ctc		724
Val	Lys	Ile	Leu	Glu	His	Asp	Asp	Val	Ser	Tyr	Leu	Lys	Lys	Ile	Leu		
				220					225					230			
ggg	gaa	ctg	gcc	atg	gtg	ctg	gac	cag	att	gag	gag	gag	ctg	gag	aag		772
Gly	Glu	Leu	Ala	Met	Val	Leu	Asp	Gln	Ile	Glu	Ala	Glu	Leu	Glu	Lys		
			235				240					245					
agg	aag	ctg	gag	aac	gag	ggg	cag	aaa	tgc	gag	ctg	tgg	ctc	tgt	ggc		820
Arg	Lys	Leu	Glu	Asn	Glu	Gly	Gln	Lys	Cys	Glu	Leu	Trp	Leu	Cys	Gly		
		250				255						260					
tgt	gcc	ttc	acc	ctc	gct	gat	gtc	ctc	ctg	gga	gcc	acc	ctg	cac	cgc		868
Cys	Ala	Phe	Thr	Leu	Ala	Asp	Val	Leu	Leu	Gly	Ala	Thr	Leu	His	Arg		
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ctc	aag	ttc	ctg	gga	ctg	tcc	aag	aaa	tac	tgg	gaa	gat	ggc	agc	cgg		916
Leu	Lys	Phe	Leu	Gly	Leu	Ser	Lys	Lys	Tyr	Trp	Glu	Asp	Gly	Ser	Arg		
	280				285					290					295		
ccc	aac	ctg	cag	tcc	ttc	ttt	gag	agg	gtc	cag	aga	cgc	ttt	gcc	ttc		964
Pro	Asn	Leu	Gln	Ser	Phe	Phe	Glu	Arg	Val	Gln	Arg	Arg	Phe	Ala	Phe		
				300					305					310			
cgg	aaa	gtc	ctg	ggt	gac	atc	cac	acc	ctg	ctg	tcg	gcc	gtc	atc			1012
Arg	Lys	Val	Leu	Gly	Asp	Ile	His	Thr	Leu	Leu	Ser	Ala	Val	Ile			
			315					320					325				
ccc	aat	gct	ttc	cgg	ctg	gtc	aag	agg	aaa	ccc	cca	tcc	ttc	ttc	ggg		1060
Pro	Asn	Ala	Phe	Arg	Leu	Val	Lys	Arg	Lys	Pro	Pro	Ser	Phe	Phe	Gly		
		330					335					340					
gcg	tcc	ttc	ctc	atg	ggc	tcc	ctg	ggt	ggg	atg	ggc	tac	ttt	gcc	tac		1108
Ala	Ser	Phe	Leu	Met	Gly	Ser	Leu	Gly	Gly	Met	Gly	Tyr	Phe	Ala	Tyr		
		345				350					355						
tgg	tac	ctc	aag	aaa	aaa	tac	atc	tagggccagg	cctggggcctt	ggtgtctgac							1162
Trp	Tyr	Leu	Lys	Lys	Lys	Tyr	Ile										

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1183

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tatgcaccg tgctgtggcg tgcccgtcgt ctgtgtggc atg cct gtc tgt gca 174
Met Pro Val Cys Ala
1 5
ccc gtg ctg tgg cgt gcc cgt cgt ctg tgt ggc atg cct gtc tgt gca 222
Pro Val Leu Trp Arg Ala Arg Arg Leu Cys Gly Met Pro Val Cys Ala
10 20
ccc gtg ccg tgg cgt gcc cgt cgt ctg tgc acc cgt gct gtg gtg tgc 270
Pro Val Pro Trp Arg Ala Arg Arg Leu Cys Thr Arg Ala Val Val Cys
25 30 35
cct tcg tct gtt cct ttt att gcc ggg cag ggt tgc acc cac atg tgc 318
Pro Ser Ser Val Pro Phe Ile Ala Gly Gln Gly Cys Thr His Met Cys
40 45 50
aag cca gcg acg gac ccc agg ttc acc cgt tca ccg ctg gct gga ggc 366
Lys Pro Ala Thr Asp Pro Arg Phe Thr Arg Ser Pro Leu Ala Gly Gly
55 60 65
gtg atc ctg ggt gtg gcc ctg tgg ctc cgc cat gac ccg cag acc acc 414
Val Ile Leu Gly Val Ala Leu Trp Leu Arg His Asp Pro Gln Thr Thr
70 75 80 85
aac ctc ctg tat ctg gag ctg gga gac aag ccc gcg ccc aac acc ttc 462
Asn Leu Leu Tyr Leu Glu Leu Gly Asp Lys Pro Ala Pro Asn Thr Phe
90 95 100
tat gta ggc atc tac atc ctc atc gct gtg ggc gct gtc atg atg ttc 510
Tyr Val Gly Ile Tyr Ile Leu Ile Ala Val Gly Ala Val Met Met Phe
105 110 115
gtt ggc ttc ctg ggc tgc tac ggg gcc atc cag gaa tcc cag tgc ctg 558
Val Gly Phe Leu Gly Cys Tyr Gly Ala Ile Gln Glu Ser Gln Cys Leu
120 125 130
ctg ggg acg ttc ttc act tgc ctg gtc atc ctg ttt gcc tgt gag gtg 606
Leu Gly Thr Phe Phe Thr Cys Leu Val Ile Leu Phe Ala Cys Glu Val
135 140 145
gcc gcc ggc atc tgg ggc ttt gtc aac aag gac cag atc gcc aag gat 654
Ala Ala Gly Ile Trp Gly Phe Val Asn Lys Asp Gln Ile Ala Lys Asp
150 155 160 165
gtg aag cag ttc tat gac cag gcc cta cag cag gcc gtg gtg gat gat 702
Val Lys Gln Phe Tyr Asp Gln Ala Leu Gln Gln Ala Val Val Asp Asp
170 175 180
gac gcc aac aac gcc aag gct gtg gtg aag acc ttc cac gag acg ctt 750
Asp Ala Asn Asn Ala Lys Ala Val Val Lys Thr Phe His Glu Thr Leu
185 190 195
gac tgc tgt ggc tcc agc aca ctg act gct ttg acc acc tca gtg ctc 798
Asp Cys Cys Gly Ser Ser Thr Leu Thr Ala Leu Thr Thr Ser Val Leu
200 205 210
aag aac aat ttg tgt ccc tcg ggc agc aac atc atc agc aac ctc ttc 846

Lys Asn Asn Leu Cys Pro Ser Gly Ser Asn Ile Ile Ser Asn Leu Phe
 215 220 225
 aag gag gac tgc cac cag aag atc gat gac ctc ttc tcc ggg aag ctg 894
 Lys Glu Asp Cys His Gln Lys Ile Asp Asp Leu Phe Ser Gly Lys Leu
 230 235 240 245
 tac ctc atc ggc att gct gcc atc gtg gtc gct gtg atc atg atc ttc 942
 Tyr Leu Ile Gly Ile Ala Ala Ile Val Val Ala Val Ile Met Ile Phe
 250 255 260
 gag atg atc ctg agc atg gtg ctg tgc tgt ggc atc cgg aac agc tcc 990
 Glu Met Ile Leu Ser Met Val Leu Cys Cys Gly Ile Arg Asn Ser Ser
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 Val Tyr
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 Leu Leu Val Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly
 15 20 25
 gac ctg ggg gag ccg ccc ccg aca cgg ccc acg gtg ggc acc aat ctt 145
 Asp Leu Gly Glu Pro Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu
 30 35 40 45
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 Thr Asp Ile Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly
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 Cys Met Gly Pro Ile Trp Ser Ser Tyr Gly Asn Cys Arg Ser Leu
 65 70 75
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 Leu Phe Val Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Ser Cys
 80 85 90
 gtg cag ctc tta ggt ctc ctt tct gca gaa caa ctt gca gaa gca tgc 337
 Val Gln Leu Leu Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser
 95 100 105
 gtg ctg ata ctc ttc aat aaa atc gac cta ccc tgt tac atg tcc acg 385
 Val Leu Ile Leu Phe Asn Lys Ile Asp Leu Pro Cys Tyr Met Ser Thr
 110 115 120 125
 gag gag atg aag tca tta atc agg ctt cca gac atc att gct tgt gcc 433

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Lys	Gln	Asn	Ile	Thr	Thr	Ala	Glu	Ile	Ser	Ala	Arg	Glu	Gly	Thr	Gly		
			145					150					155				
tta	gca	ggg	gtg	ctg	gcc	tgg	ctc	cag	gcc	acc	cac	aga	gcc	aac	gat		529
Leu	Ala	Gly	Val	Leu	Ala	Trp	Leu	Gln	Ala	Thr	His	Arg	Ala	Asn	Asp		
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gctttgctgc	caatagtttc	ttctcacagg	ggcagaataa	cccaaagtaa	ccctacatga												649
tggggctctg	tgctgggatg	caatgatgtg	taaactgagg	catgtggaga	tggaagttga												709
catctggcct	ctgaaaaaag	tgtccccagg	ggctaggcat	ggtggctcac	acctgtaatc												769
ccagcacttt	gagaggccga	ggcgggtgta	tcacctgagg	tcgggagttc	gagactagcc												829
tgaccaacat	ggagaaaccc	tgtctctact	aaaaatacaa	aattagctgg	gtgtgctggt												889
gcatgcctgt	aatctcagct	acttgggagg	ctgagacagg	agaatccctt	gaacctggga												949
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	Met	Ala	Ala	Ala	Arg	Pro	Ser	Leu	Gly	Arg	Val	Leu					
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Pro	Gly	Ser	Ser	Val	Leu	Phe	Leu	Cys	Asp	Met	Gln	Glu	Lys	Phe	Arg		
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cac	aac	atc	gcc	tac	ttc	cca	cag	atc	gtc	tca	gtg	gct	gcc	cgc	atg		266
His	Asn	Ile	Ala	Tyr	Phe	Pro	Gln	Ile	Val	Ser	Val	Ala	Ala	Arg	Met		
	30				35					40							
ctc	aag	gtg	gcc	cgg	ctg	ctt	gag	gtg	cca	gtc	atg	ctg	acg	gag	cag		314
Leu	Lys	Val	Ala	Arg	Leu	Leu	Glu	Val	Pro	Val	Met	Leu	Thr	Glu	Gln		
	45				50					55					60		
tac	cca	caa	ggc	ctg	ggc	ccc	acg	gtg	ccc	gag	ctg	ggg	act	gag	ggc		362
Tyr	Pro	Gln	Gly	Leu	Gly	Pro	Thr	Val	Pro	Glu	Leu	Gly	Thr	Glu	Gly		
		65						70						75			
ctt	cgg	ccg	ctg	gcc	aag	acc	tgc	ttc	agc	atg	gtg	cct	gcc	ctg	cag		410
Leu	Arg	Pro	Leu	Ala	Lys	Thr	Cys	Phe	Ser	Met	Val	Pro	Ala	Leu	Gln		
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Gln	Glu	Leu	Asp	Ser	Arg	Pro	Gln	Leu	Arg	Ser	Val	Leu	Leu	Cys	Gly		
	95					100					105						
att	gag	gca	cag	gcc	tgc	atc	ttg	aac	acg	acc	ctg	gac	ctc	cta	gac		506
Ile	Glu	Ala	Gln	Ala	Cys	Ile	Leu	Asn	Thr	Thr	Leu	Asp	Leu	Leu	Asp		
	110					115					120						
cgg	ggg	ctg	cag	gtc	cat	gtg	gtg	gtg	gac	gcc	tgc	tcc	tca	cgc	agc		554
Arg	Gly	Leu	Gln	Val	His	Val	Val	Val	Asp	Ala	Cys	Ser	Ser	Arg	Ser		
	125				130				135					140			
cag	gtg	gac	cgt	ctg	gtg	gct	ctg	gcc	cgc	atg	aga	cag	agt	ggt	gcc		602

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Phe Leu Ser Thr Ser Glu Gly Leu Ile Leu Gln Leu Val Gly Asp Ala	
160 165 170	
gtc cac ccc cag ttc aag gag atc cag aaa ctc atc aag gag ccc gcc	698
Val His Pro Gln Phe Lys Glu Ile Gln Lys Leu Ile Lys Glu Pro Ala	
175 180 185	
cca gac agc gga ctg ctg ggc ctc ttc caa ggc cag aac tcc ctc ctc	746
Pro Asp Ser Gly Leu Leu Gly Leu Phe Gln Gly Gln Asn Ser Leu Leu	
190 195 200	
cac tgaactccaa ccctgccttg aggggaagacc accctcctgt caccgagacc	799
His	
205	
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Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr Lys Pro Met Phe Val Ile	
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Ala Phe Leu Ser Pro Leu Ser Leu Ile Phe Leu Ala Lys Phe Leu Lys	
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Lys Ala Asp Thr Arg Asp Ser Arg Gln Ala Cys Leu Ala Ala Ser Leu	
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Ala Leu Ala Leu Asn Gly Val Phe Thr Asn Thr Ile Lys Leu Ile Val	
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Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe Pro Asp Gly Leu	
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Gly Arg Lys Ser Phe Pro Ser Gly His Ser Ser Phe Ala Phe Ala Gly	
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Leu Ala Phe Ala Ser Phe Tyr Leu Ala Gly Lys Leu His Cys Phe Thr	
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Lys Tyr Glu Pro Lys Asp Ser Leu Gly Pro Glu Met Thr Phe Val Ala
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gat gct gcc aga ggc ccc ctg tta tcc tcc ctg gac tct cca gct aac    379
Asp Ala Ala Arg Gly Pro Leu Leu Ser Ser Leu Asp Ser Pro Ala Asn
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Leu Met Ser Thr Ala Ser Val Cys Ile Ser Leu Pro Glu Gly Cys Ser
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Gly Gly Arg Ser Pro Cys Tyr Ser Gln Lys Trp Pro Pro Glu Val Pro
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gaa aaa tta acc tcc ctt ggc cag cag tcc tca acc agc tcc ctc act    523
Glu Lys Leu Thr Ser Leu Gly Gln Gln Ser Ser Thr Ser Ser Leu Thr
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gac act gat gtg cag gtg tct cct atg ctg gtt gct gga gtc aac cac    571
Asp Thr Asp Val Gln Val Ser Pro Met Leu Val Ala Gly Val Asn His
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agc agc agc ctt ctt gac aac ata ccc ttc act ggc tgc ctt cct ttc    619
Ser Ser Ser Leu Leu Asp Asn Ile Pro Phe Thr Gly Cys Leu Pro Phe
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cat ctc tct tct tca ctc ccc tac cta tgt ctc cta ggc tct ccc ttc    667
His Leu Ser Ser Ser Leu Pro Tyr Leu Cys Leu Leu Gly Ser Pro Phe
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 Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser
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 Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly Ala Pro Lys Cys
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 Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe Gln Glu Arg His
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 gcc cta atc acc cac cag cgc agc cac ggt cca gcc gcc aag ccc acc 464
 Ala Leu Ile Thr His Gln Arg Ser His Gly Pro Ala Ala Lys Pro Thr
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 Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser
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 Pro Gln Pro Arg Arg Gln His Leu Pro Pro Gly Gly Pro Glu Val His
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 Pro Leu Pro His His Leu Arg Arg Phe Gln Val Pro Gly Ala Ser His
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 Glu Ala Gly Ala Pro Ser Gly Leu Arg Gly Pro Glu Ala Ala Gly Gly
 55 60 65
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 Pro Leu His Leu Leu His Leu Arg Pro Leu Leu Pro Leu Leu Gln Ser
 70 75 80
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 Pro Asn His Pro Pro Ala Gln His Gly Pro Ala Ala Lys Pro Thr Leu
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Lys	Pro	Ala	Glu	Ala	Pro	Asp	Ala	Pro	Glu	Ala	Ala	Ser	Pro	Ala	His	
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Trp	Pro	Arg	Glu	Ser	Leu	Val	Leu	Tyr	His	Trp	Thr	Gln	Ser	Phe	Ser	
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Glu	Arg	Asp	Val	Ser	Leu	Pro	Gln	Ser	Glu	His	Lys	Glu	Pro	Trp	Phe	
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Met	Arg	Leu	Asn	Leu	Gly	Glu	Glu	Val	Pro	Val	Ile	Ile	His	Arg	Asp	
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Phe	Thr	Gly	Glu	His	Val	Val	Ala	Leu	Met	Pro	Glu	Val	Gly	Ser	Leu	
		125					130						135			
cag	cac	gca	cgg	gtg	ctg	cag	tac	cgg	gag	ctg	ctg	gac	gca	ctg	ccc	486
Gln	His	Ala	Arg	Val	Leu	Gln	Tyr	Arg	Glu	Leu	Leu	Asp	Ala	Leu	Pro	
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Met	Asp	Ala	Tyr	Thr	His	Gly	Cys	Ile	Leu	His	Leu	Glu	Leu	Thr	Thr	
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Asp	Ser	Met	Ile	Pro	Lys	Tyr	Ala	Thr	Ala	Glu	Ile	Arg	Arg	His	Leu	
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Ala	Asn	Ala	Thr	Thr	Asp	Leu	Met	Lys	Leu	Asp	His	Glu	Glu	Glu	Pro	
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cag	ctc	tcc	gag	ccc	tac	ctt	tct	aaa	caa	aag	aag	ctc	atg	gcc	aag	678
Gln	Leu	Ser	Glu	Pro	Tyr	Leu	Ser	Lys	Gln	Lys	Lys	Leu	Met	Ala	Lys	
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Leu	Ala	Met	Val	Leu	Asp	Gln	Ile	Glu	Ala	Glu	Leu	Glu	Lys	Arg	Lys	
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Phe	Thr	Leu	Ala	Asp	Val	Leu	Leu	Gly	Ala	Thr	Leu	His	Arg	Leu	Lys	
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Ala Phe Arg Leu Val Lys Arg Lys Pro Pro Ser Phe Phe Gly Ala Ser				
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Phe Leu Met Gly Ser Leu Gly Gly Met Gly Tyr Phe Ala Tyr Trp Tyr				
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Pro Gly Ser Ser Pro Val Pro Val	
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aagcatctac tctttttatc atttacttca aaatgacatt gctaaagact gcattattct      1147
actactgtaa tttctccacg acatagcatt atgtacatag atgagtgtaa catttatatc      1207
tcacatagag acatgcttat atggttttat ttaaaatgaa atgccagtcc attacactga      1267

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ataaatagaa ctcaactatt gcttttcagg gaaatcatgg ataggggttga agaagggttac 1327
tattaattgt ttaaaaacag cttatggatt aatgtcctcc atttataatg aagattaaaaa 1387
tgaaggcttt aatcagcatt gtaaaggaaa ttgaatggct ttctgatatg ctgttttttta 1447
gcctaggagt tagaaatcct aacttccttta tcctcttctc ccagaggctt tttttttctt 1507
gtgtattaaa ttaacatttt taaaaagcag atattttgtc aaggggcttt gcattcaaac 1567
tgcttttcca gggctatact cagaagaaag ataaaagtgt gatctaagaa aaagtgatgg 1627
ttttaggaaa gtgaaaatat ttttgttttt gtatttgaaag aagaatgatg cattttgaca 1687
agaaatcata tatgtatgta tatatttttaa taagtatttg agtacagact ttgagggtttc 1747
atcaatataa ataaaagagc agaaaagtaa aaaaaaaaaa aaaaaa 1793

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<210> 165
<211> 1849
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 8..1141

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<220>
<221> misc_feature
<222> 1707
<223> n=a, g, c or t

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cgttgcc atg gat cct ggg gac gac tgg ctg gtg gaa tcc ttg cgc ttg 49
      Met Asp Pro Gly Asp Asp Trp Leu Val Glu Ser Leu Arg Leu
      1          5          10
tac cag gat ttc tat gca ttc gac ctg tca gga gcc act cga gtc ctt 97
Tyr Gln Asp Phe Tyr Ala Phe Asp Leu Ser Gly Ala Thr Arg Val Leu
15          20          25          30
gaa tgg att gat gac aaa gga gtc ttt gtt gct ggc tat gaa agc ctg 145
Glu Trp Ile Asp Asp Lys Gly Val Phe Val Ala Gly Tyr Glu Ser Leu
      35          40          45
aaa aag aat gaa att ctt cat ctg aaa tta cct ctc aga ctt tct gta 193
Lys Lys Asn Glu Ile Leu His Leu Lys Leu Pro Leu Arg Leu Ser Val
      50          55          60
aag gaa aac aag ggc tta ttc cca gaa aga gat ttc aaa gtg cgc cat 241
Lys Glu Asn Lys Gly Leu Phe Pro Glu Arg Asp Phe Lys Val Arg His
      65          70          75
gga gga ttt tca gac agg tct atc ttt gat cta aag cat gtg cca cat 289
Gly Gly Phe Ser Asp Arg Ser Ile Phe Asp Leu Lys His Val Pro His
      80          85          90
acc aga ttg ctg gtt acc agt ggc ctt cca ggt tgt tat ctg cag gtg 337
Thr Arg Leu Leu Val Thr Ser Gly Leu Pro Gly Cys Tyr Leu Gln Val
95          100          105          110
tgg cag gtt gca gag gac agt gat gtc att aaa gct gtc agc acc att 385
Trp Gln Val Ala Glu Asp Ser Asp Val Ile Lys Ala Val Ser Thr Ile
      115          120          125
gct gtg cat gag aaa gag gag agt ctc tgg cct agg gtg gcc gtc ttc 433
Ala Val His Glu Lys Glu Glu Ser Leu Trp Pro Arg Val Ala Val Phe
      130          135          140
tcc aca ttg gca ccc gga gtc ctc cat ggg gcg agg ctc cga agt ctg 481
Ser Thr Leu Ala Pro Gly Val Leu His Gly Ala Arg Leu Arg Ser Leu
      145          150          155
cag gtc gtt gat ctg gag tcc cgg aag acc acg tac acc tca gat gtc 529
Gln Val Val Asp Leu Glu Ser Arg Lys Thr Thr Tyr Thr Ser Asp Val
      160          165          170

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agt gac agt gag gag ctg agt agc ctg cag gtc cta gat gcg gac acc	577
Ser Asp Ser Glu Glu Leu Ser Ser Leu Gln Val Leu Asp Ala Asp Thr	
175 180 185 190	
ttt gcc ttc tgc tgt gct tcg ggc cgg ctg ggg ctt gtt gac acc cgg	625
Phe Ala Phe Cys Cys Ala Ser Gly Arg Leu Gly Leu Val Asp Thr Arg	
195 200 205	
cag aag tgg gca ccg ttg gag aat cgc agc cct ggc cct ggg tct ggt	673
Gln Lys Trp Ala Pro Leu Glu Asn Arg Ser Pro Gly Pro Gly Ser Gly	
210 215 220	
gga gag aga tgg tgt gct gaa gtt ggg agc tgg ggc cag ggc cct ggg	721
Gly Glu Arg Trp Cys Ala Glu Val Gly Ser Trp Gly Gln Gly Pro Gly	
225 230 235	
ccc agc att gcc agc ctt agc tca gat ggg cgt ctt tgt ctt ctt gac	769
Pro Ser Ile Ala Ser Leu Ser Ser Asp Gly Arg Leu Cys Leu Leu Asp	
240 245 250	
ccc cgg gat ctc tgc cat cct gtg agc tca gtc cag tgc cca gta tcc	817
Pro Arg Asp Leu Cys His Pro Val Ser Ser Val Gln Cys Pro Val Ser	
255 260 265 270	
gta cct agc cct gac cca gag ctg ctg cga gtg act tgg gcc cca ggc	865
Val Pro Ser Pro Asp Pro Glu Leu Leu Arg Val Thr Trp Ala Pro Gly	
275 280 285	
ctg aag aat tgc ttg gcc atc tca ggt ttt gat ggt aca gtc cag gtc	913
Leu Lys Asn Cys Leu Ala Ile Ser Gly Phe Asp Gly Thr Val Gln Val	
290 295 300	
tat gat gcc aca tct tgg gat gga aca cgg agc caa gat gga aca cgg	961
Tyr Asp Ala Thr Ser Trp Asp Gly Thr Arg Ser Gln Asp Gly Thr Arg	
305 310 315	
agc caa gta gaa cct ctc ttc act cac aga ggt cac atc ttc cta gat	1009
Ser Gln Val Glu Pro Leu Phe Thr His Arg Gly His Ile Phe Leu Asp	
320 325 330	
gga aat ggg atg gac cct gct cct ttg gtc acc acc cac acc tgg cat	1057
Gly Asn Gly Met Asp Pro Ala Pro Leu Val Thr Thr His Thr Trp His	
335 340 345 350	
ccc tgc aga cca agg act ttg tta tca gca aca aat gat gcc tct ctg	1105
Pro Cys Arg Pro Arg Thr Leu Leu Ser Ala Thr Asn Asp Ala Ser Leu	
355 360 365	
cat gtg tgg gac tgg gtg gac ctt tgt gcc ccc cgc tgacaccagc	1151
His Val Trp Asp Trp Val Asp Leu Cys Ala Pro Arg	
370 375	
atctttccat ctaggcctct agaaagggga ggagctgctg tagtagcaag ggtgctgatg	1211
taggactcaa gtgactacca gtccctgtta ccagctgtgt ggccttgggc aagtctgcca	1271
gcgtcactta gcctcagttt ccttatctgt aaaatgagga tagtaagaac tacctcgtag	1331
tgatattgcg aagggttagaa gaaacgcatg gcataattac ttggtagcta ttgttagatc	1391
tgggagtgtg aaatggtagc gtttttgtccc tgtcttcaca ctatcatagg gagaatcaaa	1451
agagctaaca aatataaaca tgctttgtga atttttttaa agaaaaaaat gtaggggggc	1511
caataaacat gaaaaaatcc cagccctagt agcaattaag gaaatagcaa aacaggattt	1571
ctgctcctct tgaggggggtc tcatgggaac acaggtgcac tttcccacac ttgtccccc	1631
agggtgactag gttcaagaga catttgcttt tggtggcccc acaaacattt ccttttgagg	1691
gcccatagtg aatatntaaa gtgtgctgga catggtggct catgcctgta atcccagcac	1751
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catagcaaga tcccttcccc aaaaaaaaaa aaaaaaaaaa	1849

<210> 166
 <211> 1748
 <212> DNA
 <213> Homo sapiens

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<221> CDS
<222> 136..264

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ggcacagaga accctgcttc aaagcagaag tagcagttcc ggagtcagc tggctaaaac 120
tcattccaga ggata atg gca acc cat gcc tta gaa atc gct ggg ctg ttt 171
Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe
1 5 10
ctt ggt ggt gtt gga atg gtg ggc aca gtg gct gtc act gtc atg cct 219
Leu Gly Gly Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro
15 20 25
cag tgg aga gtg tcg gcc ttc att gaa aac aac atc gtg gtt ttt 264
Gln Trp Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe
30 35 40
taaaacttct gggaaggact gtggatgaat tgcgtgaggc aggctaacat caggatgcag 324
tgcaaaatct atgattccct gctggctctt tctccggacc tacaggcagc cagaggactg 384
atgtgtgctg ctcccgtagt gtccttcttg gctttcatga tggccatcct tggcatgaaa 444
tgcaccagggt gcacggggga caatgagaag gtgaaggctc acattctgct gacggctgga 504
atcatcttca tcatcacggg catggtggtg ctcacccctg tgagctgggt tgccaatgcc 564
atcatcagag atttctataa ctcaatagtg aatggtgccc aaaaacgtga gcttggagaa 624
gctctctact taggatggac cacggcactg gtgctgattg ttggaggagc tctgttctgc 684
tgcggtttttt gttgcaacga aaagagcagt agctacagat actcgatacc ttcccatcgc 744
acaacccaaa aaagttatca caccggaaaag aagtcaccga gcgtctactc cagaagtcag 804
tatgtgtagt tgtgtatgtt tttttaactt tactataaag ccatgcaaat gacaaaaatc 864
tatattactt tctcaaaatg gaccccaaaag aaactttgat ttactgttct taactgccta 924
atcttaatta caggaactgt gcatcagcta tttatgattc tataagctat ttcagcagaa 984
tgagatatta aaccgaatgc tttgattggt ctagaaagta tagtaatttg ttttctaagg 1044
tggktcaagc atctactctt tttatcattt acttcaaaat gacattgcta aagactgcat 1104
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cactgaataa atagaactca actattgctt ttcagggaag tcatggatag ggttgaagaa 1284
ggttactatt aattgtttta aaacagctta gggattaatg tcttccattt ataatgaaga 1344
ttaaataaataa ggctttaatc agcattgtaa aggaaattga atggctttct gatatgctgt 1404
tttttagcct aggagttaga aatcctaact tctttatcct cttctcccag aggcctttttt 1464
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tcaaactgct tttccagggc tatactcaga agaaagataa aagtgtgatc taagaaaaag 1584
tgatggttttt aggaaagtga aaatatTTTT gtttttgtat ttgaagaaga atgatgcatt 1644
ttgacaagaa atcatatatg tatggatata ttttaataag tatttgagta cagactttga 1704
ggtttcatca atataaataa aagagcaaaa aaaaaaaaaa aaaa 1748

<210> 167
<211> 1275
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 14..1048

<400> 167
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1 5 10
tgc ggc cag gcg tgg ggt gcg tcg gtg ggc ggc cgc agc tgc gag gag 97
Cys Gly Gln Ala Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu
15 20 25
ctc act gcg gtc cta acc ccg ccg cag ctc ctc gga cgc agg ttt aac 145

Leu	Thr	Ala	Val	Leu	Thr	Pro	Pro	Gln	Leu	Leu	Gly	Arg	Arg	Phe	Asn	
30						35					40					
ttc	ttt	att	caa	caa	aaa	tgc	gga	ttc	aga	aaa	gca	ccc	agg	aag	gtt	193
Phe	Phe	Ile	Gln	Gln	Lys	Cys	Gly	Phe	Arg	Lys	Ala	Pro	Arg	Lys	Val	
45					50					55					60	
gaa	cct	cga	aga	tca	gac	cca	ggg	aca	agt	ggg	gaa	gca	tac	aag	aga	241
Glu	Pro	Arg	Arg	Ser	Asp	Pro	Gly	Thr	Ser	Gly	Glu	Ala	Tyr	Lys	Arg	
				65					70						75	
agt	gct	ttg	att	cct	cct	gtg	gaa	gaa	aca	gtc	ttt	tat	cct	tct	ccc	289
Ser	Ala	Leu	Ile	Pro	Pro	Val	Glu	Glu	Thr	Val	Phe	Tyr	Pro	Ser	Pro	
			80				85						90			
tat	cct	ata	agg	agt	ctc	ata	aaa	cct	tta	ttt	ttt	act	gtt	ggg	ttt	337
Tyr	Pro	Ile	Arg	Ser	Leu	Ile	Lys	Pro	Leu	Phe	Phe	Thr	Val	Gly	Phe	
		95					100					105				
aca	ggc	tgt	gca	ttt	gga	tca	gct	att	tgg	caa	tat	gaa	tca	ctg		385
Thr	Gly	Cys	Ala	Phe	Gly	Ser	Ala	Ala	Ile	Trp	Gln	Tyr	Glu	Ser	Leu	
	110					115					120					
aaa	tcc	agg	gtc	cag	agt	tat	ttt	gat	ggg	ata	aaa	gct	gat	tgg	ttg	433
Lys	Ser	Arg	Val	Gln	Ser	Tyr	Phe	Asp	Gly	Ile	Lys	Ala	Asp	Trp	Leu	
125					130					135					140	
gat	agc	ata	aga	cca	caa	aaa	gaa	gga	gac	ttc	aga	aag	gag	att	aac	481
Asp	Ser	Ile	Arg	Pro	Gln	Lys	Glu	Gly	Asp	Phe	Arg	Lys	Glu	Ile	Asn	
				145					150					155		
aag	tgg	tgg	aat	aac	cta	agt	gat	ggc	cag	cgg	act	gtg	aca	ggg	att	529
Lys	Trp	Trp	Asn	Asn	Leu	Ser	Asp	Gly	Gln	Arg	Thr	Val	Thr	Gly	Ile	
			160					165					170			
ata	gct	gca	aat	gtc	ctt	gta	ttc	tgt	tta	tgg	aga	gta	cct	tct	ctg	577
Ile	Ala	Ala	Asn	Val	Leu	Val	Phe	Cys	Leu	Trp	Arg	Val	Pro	Ser	Leu	
		175					180					185				
cag	cgg	aca	atg	atc	aga	tat	ttc	aca	tcg	aat	cca	gcc	tca	aag	gtc	625
Gln	Arg	Thr	Met	Ile	Arg	Tyr	Phe	Thr	Ser	Asn	Pro	Ala	Ser	Lys	Val	
	190					195					200					
ctt	tgt	tct	cca	atg	ttg	ctg	tca	aca	ttc	agt	cat	ttc	tcc	tta	ttt	673
Leu	Cys	Ser	Pro	Met	Leu	Leu	Ser	Thr	Phe	Ser	His	Phe	Ser	Leu	Phe	
205					210					215					220	
cac	atg	gca	gca	aat	atg	tat	gtt	ttg	tgg	agc	ttc	tct	tcc	agc	ata	721
His	Met	Ala	Ala	Asn	Met	Tyr	Val	Leu	Trp	Ser	Phe	Ser	Ser	Ser	Ile	
				225					230					235		
gtg	aac	att	ctg	ggg	caa	gag	cag	ttc	atg	gca	gtg	tac	cta	tct	gca	769
Val	Asn	Ile	Leu	Gly	Gln	Glu	Gln	Phe	Met	Ala	Val	Tyr	Leu	Ser	Ala	
			240				245					250				
ggg	gtt	att	tcc	aat	ttt	gtc	agt	tac	gtg	ggg	aaa	gtt	gcc	aca	gga	817
Gly	Val	Ile	Ser	Asn	Phe	Val	Ser	Tyr	Val	Gly	Lys	Val	Ala	Thr	Gly	
		255					260					265				
aga	tat	gga	cca	tca	ctt	ggg	gca	gcc	ctg	aaa	gcc	att	atc	gcc	atg	865
Arg	Tyr	Gly	Pro	Ser	Leu	Gly	Ala	Ala	Leu	Lys	Ala	Ile	Ile	Ala	Met	
		270				275					280					
gat	aca	gca	gga	atg	atc	ctg	gga	tgg	aaa	ttt	ttt	gat	cat	gcg	gca	913
Asp	Thr	Ala	Gly	Met	Ile	Leu	Gly	Trp	Lys	Phe	Phe	Asp	His	Ala	Ala	
		285			290					295					300	
cat	ctt	ggg	gga	gct	ctt	ttt	gga	ata	tgg	tat	gtt	act	tac	ggg	cat	961
His	Leu	Gly	Gly	Ala	Leu	Phe	Gly	Ile	Trp	Tyr	Val	Thr	Tyr	Gly	His	
				305					310					315		
gaa	ctg	att	tgg	aag	aac	agg	gag	ccg	cta	gtg	aaa	atc	tgg	cat	gaa	1009
Glu	Leu	Ile	Trp	Lys	Asn	Arg	Glu	Pro	Leu	Val	Lys	Ile	Trp	His	Glu	
			320				325						330			
ata	agg	act	aat	ggc	ccc	aaa	aaa	gga	ggg	ggc	tct	aag	taaaa	actggg		1058
Ile	Arg	Thr	Asn	Gly	Pro	Lys	Lys	Gly	Gly	Gly	Ser	Lys				

335	340	345	
attggacagt	agtgggtgcat	ctgggtccttg	cgcgctgaga
gagtgaccat	ggctatgctc	ccgtctggaa	gatgccagca
agctgtgtcc	cccagtcctg	gtcttttttag	aatgtgaatg
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1118
1178
1238
1275

<210> 168
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<212> DNA
<213> Homo sapiens

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<222> 70..777

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Met Lys Arg Ser Gly Asn Pro Gly Ala Glu Val Thr Asn Ser	
1 5 10	
tcg gtg gca ggg cct gac tgc tgc gga ggc ctc ggc aat att gat ttt	159
Ser Val Ala Gly Pro Asp Cys Cys Gly Gly Leu Gly Asn Ile Asp Phe	
15 20 25 30	
aga cag gca gac ttc tgc gtt atg acc cgg ctg ctg ggc tac gtg gac	207
Arg Gln Ala Asp Phe Cys Val Met Thr Arg Leu Leu Gly Tyr Val Asp	
35 40 45	
ccc ctg gat ccc agc ttt gtg gct gcc gtc atc acc atc acc ttc aat	255
Pro Leu Asp Pro Ser Phe Val Ala Ala Val Ile Thr Ile Thr Phe Asn	
50 55 60	
ccg ctc tac tgg aat gtg gtt gca cga tgg gaa cac aag acc cgc aag	303
Pro Leu Tyr Trp Asn Val Val Ala Arg Trp Glu His Lys Thr Arg Lys	
65 70 75	
ctg agc agg gcc ttc gga tcc ccc tac ctg gcc tgc tac tct cta agc	351
Leu Ser Arg Ala Phe Gly Ser Pro Tyr Leu Ala Cys Tyr Ser Leu Ser	
80 85 90	
atc acc atc ctg ctc ctg aac ttc ctg cgc tgc cac tgc ttc acg cag	399
Ile Thr Ile Leu Leu Asn Phe Leu Arg Ser His Cys Phe Thr Gln	
95 100 105 110	
gcc atg ctg agc cag ccc agg atg gag agc ctg gac acc ccc gcg gcc	447
Ala Met Leu Ser Gln Pro Arg Met Glu Ser Leu Asp Thr Pro Ala Ala	
115 120 125	
tac agc ctg gtc ctc gca ctc ctg gga ctg ggc gtc gtg ctc gtg ctc	495
Tyr Ser Leu Val Leu Ala Leu Leu Gly Leu Gly Val Val Leu Val Leu	
130 135 140	
tcc agc ttc ttt gca ctg ggg ttc gct gga act ttc cta ggt gat tac	543
Ser Ser Phe Phe Ala Leu Gly Phe Ala Gly Thr Phe Leu Gly Asp Tyr	
145 150 155	
ttc ggg atc ctc aag gag gcg aga gtg acc gtg ttc ccc ttc aac atc	591
Phe Gly Ile Leu Lys Glu Ala Arg Val Thr Val Phe Pro Phe Asn Ile	
160 165 170	
ctg gac aac ccc atg tac tgg gga agc aca gcc aac tac ctg ggc tgg	639
Leu Asp Asn Pro Met Tyr Trp Gly Ser Thr Ala Asn Tyr Leu Gly Trp	
175 180 185 190	
gcc atc atg cac gcc agc ccc acg ggc ctg ctc ctg acg gtg ctg gtg	687
Ala Ile Met His Ala Ser Pro Thr Gly Leu Leu Leu Thr Val Leu Val	
195 200 205	
gcc ctc acc tac ata gtg gct ctc cta tac gaa gag ccc ttc acc gct	735
Ala Leu Thr Tyr Ile Val Ala Leu Leu Tyr Glu Glu Pro Phe Thr Ala	

	210		215		220	
	gag atc tac cgg cag aaa gcc tcc ggg tcc cac aag agg agc					777
	Glu Ile Tyr Arg Gln Lys Ala Ser Gly Ser His Lys Arg Ser					
	225		230		235	
	tgattgagct gcaacagctt tgctgaaggc ctggccagcc tectggcctg ccccaagtgg					837
	caggccctgc gcagggcgag aatggtgcct gctgctcagg gctcgcccc ggctgtgggt					897
	gccccagtgc cttggaacct gctgccttgg ggacctgga cgtgccgaca tatggccatt					957
	gagctccaac ccacacattc ccattcacca ataaaggcac cctgacctca aaaaaaaaaa					1017
	aaaaaa					1023

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 <211> 1085
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..400

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	caa cag ctt ctc cat cac gcc aga aat ggc aat gct gaa gaa gta aga	103
	Gln Gln Leu Leu His His Ala Arg Asn Gly Asn Ala Glu Glu Val Arg	
	10 15 20	
	caa cta tta gag acc atg gcg agt aat gaa gtg att gct gac att aat	151
	Gln Leu Leu Glu Thr Met Ala Ser Asn Glu Val Ile Ala Asp Ile Asn	
	25 30 35	
	tgc aaa gga aga agt aag tct aac ttg ggc tgg aca ccc cta cat ctg	199
	Cys Lys Gly Arg Ser Lys Ser Asn Leu Gly Trp Thr Pro Leu His Leu	
	40 45 50	
	gca tgc tat ttt gga cac aga caa gtg gtc cag gat ctg ttg aag gct	247
	Ala Cys Tyr Phe Gly His Arg Gln Val Val Gln Asp Leu Leu Lys Ala	
	55 60 65 70	
	ggt gca gaa gtg aat gtg ttg aat gac atg gga gac acg ccg ctt cat	295
	Gly Ala Glu Val Asn Val Leu Asn Asp Met Gly Asp Thr Pro Leu His	
	75 80 85	
	cga gct gcc ttt aca gga cga aag gtg aaa atc att cta tgt tca atg	343
	Arg Ala Ala Phe Thr Gly Arg Lys Val Lys Ile Ile Leu Cys Ser Met	
	90 95 100	
	ttt gta agt gag gta ttt gga gga gta gtt acc att gtt ttc tct gtt	391
	Phe Val Ser Glu Val Phe Gly Gly Val Val Thr Ile Val Phe Ser Val	
	105 110 115	
	ata acc atc tgaccagcaa ccgaagaaag ccacacaaaa aaatgtatac	440
	Ile Thr Ile	
	120	
	accagcactt tgggtcaaaa ggccacagga tcttttgagt ctgacagtga ggtccagtac	500
	taagggtcatg gagaccccca ctctgtagca tccctgtgag gagatcattc cgtttctgct	560
	tgtgtactcc agcaatgggg aactcctgat tattcttttt ttttaaaaaa aaatagcttc	620
	attgaggtat aacttacatt gcataaactt cacctgtgat attgtgaaat atatatattgg	680
	tctttgacct tgtacactaa agatgtacaa aaagatgact ggcaaccctt ggcttcagga	740
	tgggggctgg tcaccagaaa gaccaaggca ggactagggg gttgggactt tcagccgaac	800
	tttgcaacct ccagggaggg tagaggggct gaaggggaaa tggctcgcta atggccagtg	860
	gtttcatcaa tcatgcctat ttaatggaac ctccataaaa acctgaaagg acagggttct	920
	aggagctcct gggtagctga acacgtggag gttcttgaat gatcacaccc agggagggca	980
	tgggtgctct gtgcccttcc tccatgcctt gctttatgta tctcttcac tgtatccttt	1040
	gtaataaagc agtaaacatg ttttcttgaa aaaaaaaaaa aaaaa	1085

<210> 170
 <211> 776
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..572

<400> 170
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 ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
 1 5 10 15
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
 20 25 30
 gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
 35 40 45
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
 50 55 60
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
 Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
 65 70 75
 ctt ggc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
 Leu Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
 80 85 90 95
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
 100 105 110
 ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
 Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
 115 120 125
 aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
 Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
 130 135 140
 gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
 Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
 145 150 155
 gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
 Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 160 165 170
 gaggagggac gccccaggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggtt 652
 caccccaatg ggaccaccct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712
 aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagcaaaaaa 772
 aaaa 776

<210> 171
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 <212> DNA
 <213> Homo sapiens

<220>
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<400> 171

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ggtttccgga ggacagccaa caagcgatgc tgccgccgcc gtttcctgat tggttgtggg      120
tggctacctc ttcgttctga ttggccgcta gtgagcaag atg ctg agc aag ggt      174
                               Met Leu Ser Lys Gly
                               1       5

ctg aag cgg aaa cgg gag gag gag gag gag aag gaa cct ctg gca gtc      222
Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys Glu Pro Leu Ala Val
                               10       15       20

gac tcc tgg tgg cta gat cct ggc cac aca gcg gtg gca cag gca ccc      270
Asp Ser Trp Trp Leu Asp Pro Gly His Thr Ala Val Ala Gln Ala Pro
                               25       30       35

ccg gcc gtg gcc tct agc tcc ctc ttt gac ctc tca gtg ctc aag ctc      318
Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu Ser Val Leu Lys Leu
                               40       45       50

cac cac agc ctg cag cag agt gag ccg gac ctg cgg cac ctg gtg ctg      366
His His Ser Leu Gln Gln Ser Glu Pro Asp Leu Arg His Leu Val Leu
                               55       60       65

gtc gtg aac act ctg cgg cgc atc cag gcg tcc atg gca ccc gcg gct      414
Val Val Asn Thr Leu Arg Arg Ile Gln Ala Ser Met Ala Pro Ala Ala
70                               75       80       85

gcc ctg cca cct gtg cct agc cca cct gca gcc ccc agt gtg gct gac      462
Ala Leu Pro Pro Val Pro Ser Pro Pro Ala Ala Pro Ser Val Ala Asp
                               90       95       100

aac tta ctg gca agc tcg gac gct gcc ctt tca gcc tcc atg gcc agc      510
Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser Ala Ser Met Ala Ser
                               105       110       115

ctc ctg gag gac ctc agc cac att gag ggc ctg agt cag gct ccc caa      558
Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu Ser Gln Ala Pro Gln
120                               125       130

ccc ttg gca gac gag ggg cca cca ggc cgt agc atc ggg gga gca gcg      606
Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser Ile Gly Gly Ala Ala
135                               140       145

ccc agc ctg ggt gcc ttg gac ctg ctg ggc cca gcc act ggc tgt cta      654
Pro Ser Leu Gly Ala Leu Asp Leu Leu Gly Pro Ala Thr Gly Cys Leu
150                               155       160       165

ctg gac gat ggg ctt gag ggc ctg ttt gag gat att gac acc tct atg      702
Leu Asp Asp Gly Leu Glu Gly Leu Phe Glu Asp Ile Asp Thr Ser Met
170                               175       180

tat gac aat gaa ctt tgg gca cca gcc tct gag ggc ctc aaa cca ggc      750
Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu Gly Leu Lys Pro Gly
185                               190       195

cct gag gat ggg ccg ggc aag gag gaa gct ccg gag ctg gac gag gcc      798
Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro Glu Leu Asp Glu Ala
200                               205       210

gaa ttg gac tac ctc atg gat gtg ctg gtg ggc aca cag gca ctg gag      846
Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly Thr Gln Ala Leu Glu
215                               220       225

cga ccg ccg ggg cca ggg cgc tgagccctcg tgctggaatg gttgtctggt      897
Arg Pro Pro Gly Pro Gly Arg
230                               235

atctgaactg agcctgctgg ctggaccaac tgtcctcgaa aagacacagc tggcttcctt      957
agtacagaga acagggcttg ggccactttg gagagacaga atctagtcct gggcaacttc      1017
acatccgtcc tctgtctca gggctggcag ggggagcctg gaattacccc ctagtgatgg      1077
aatgacaggg tctgggtggg acttaattcc ctggccctgg ggtcatagct tgggctgttc      1137
cttctctgat acgggaagag acctccaatca gatttttcaa attaaagcca gtccctgggaa      1197
atctcaaaaa aaaaaaaaaa aa      1219

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<210> 172
 <211> 1487
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..640

<400> 172
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 ggtgact atg aaa ggc tta tat ttc caa cag agt tcc aca gat gaa gaa 109
 Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu
 1 5 10
 ata aca ttt gta ttt caa gaa aag gaa gat ctt cct gtt aca gag gat 157
 Ile Thr Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp
 15 20 25 30
 aac ttt gtg aaa ctt caa gtt aaa gct tgt gct ctg agc cag ata aat 205
 Asn Phe Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn
 35 40 45
 aca aag ctt ctg gca gaa atg aag atg aaa aag gat tta ttt cct gtt 253
 Thr Lys Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val
 50 55 60
 ggg aga gaa att gct gga att gta tta gat gtt gga agc aag gta tca 301
 Gly Arg Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser
 65 70 75
 ttc ttt caa cca gat gat gaa gta gtt gga att ttg ccc ctg gac tct 349
 Phe Phe Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser
 80 85 90
 gaa gac cct gga ctt tgt gaa gtt gtt aga gta cat gag cat tac ttg 397
 Glu Asp Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu
 95 100 105 110
 gtt cat aaa cca gaa aag gtc aca tgg acg gaa gca gca gga agc att 445
 Val His Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile
 115 120 125
 cgg gat gga gtg cgt gcc tat aca gct ctg cat tat ctt tct cat ctc 493
 Arg Asp Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu
 130 135 140
 tct cct gga aaa tca gtg ctg ata atg gat gga gca agt gca ttt ggt 541
 Ser Pro Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly
 145 150 155
 aca ata gct att cag tta gca cat cat aga gga gcc aaa gta ttt caa 589
 Thr Ile Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Phe Gln
 160 165 170
 cag cat gca gcc ttg aag ata agc agt gcc ttg aaa gat tca gac ctc 637
 Gln His Ala Ala Leu Lys Ile Ser Ser Ala Leu Lys Asp Ser Asp Leu
 175 180 185 190
 cca tagcccgagt gattgatgta tctaattggga aagttcatgt tgctgaaagc 690
 Pro
 tgttttggaag aaacagggtgg cctgggagta gatattgtcc tagatgctgg agtgagatta 750
 tatagtaaag atgatgaacc agctgtaaaa ctacaactac taccacataa acatgatatc 810
 atcacacttc ttggtgttgg aggccactgg gtaacaacag aagaaaaacct tcagttggat 870
 cctccagata gccactgcct tttcctcaag ggagcaacgt tagctttcct gaatgatgaa 930
 gtttgggaatt tgtcaaatgt acaacaggga aaatatcttt gtatcttaaa ggatgtgatg 990
 gagaagtatt caactgggtgt ttccagacct cagttggatg aacccattcc actgtatgag 1050
 gcaaaagttt ccatggaagc tgttcagaaa aatcaaggaa gaaaaaagca agttgttcaa 1110
 ttttaatttt cttctttctc agacctcagt cggatgaaca tattccagta tttgaagcca 1170

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gaatttttctt tggaaattgt tgagaaaaac caaggaagat aaaacaagtt gcattttttaa 1230
gcacgtttct ctgctaagac aagatgctca gttgacacat ttgaaaagt tttgaaaaat 1290
tcttgtgcaa atgatcaaga taattctata attaacatct taagggaatt tttctaaaaa 1350
ccttttcatt gtttctatat attttgccc tgctataaaa ttccttccat gaagaaaact 1410
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aaaaaaaaaa aaaaaaa 1487

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<210> 173
<211> 1915
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 132..1298

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tgacggggaca cagtgggttg tgacggggaca gagcggtcgg tgacagcctc aagggttca 120
gcaccgcgcc c atg gca gag cca gac ccc tct cac cct ctg gag acc cag 170
          Met Ala Glu Pro Asp Pro Ser His Pro Leu Glu Thr Gln
          1          5          10
gca ggg aag gtg cag gag gct cag gac tca gat tca gac tct gag gga 218
Ala Gly Lys Val Gln Glu Ala Gln Asp Ser Asp Ser Asp Ser Glu Gly
          15          20          25
gga gcc gct ggt gga gaa gca gac atg gac ttc ctg cgg aac tta ttc 266
Gly Ala Ala Gly Gly Glu Ala Asp Met Asp Phe Leu Arg Asn Leu Phe
          30          35          40          45
tcc cag acg ctc agc ctg ggc agc cag aag gag cgt ctg ctg gac gag 314
Ser Gln Thr Leu Ser Leu Gly Ser Gln Lys Glu Arg Leu Leu Asp Glu
          50          55          60
ctg acc ttg gaa ggg gtg gcc cgg tac atg cag agc gaa cgc tgt cgc 362
Leu Thr Leu Glu Gly Val Ala Arg Tyr Met Gln Ser Glu Arg Cys Arg
          65          70          75
aga gtc atc tgt ttg gtg gga gct gga atc tcc aca tcc gca ggc atc 410
Arg Val Ile Cys Leu Val Gly Ala Gly Ile Ser Thr Ser Ala Gly Ile
          80          85          90
ccc gac ttt cgc tct cca tcc acc ggc ctc tat gac aac cta gag aag 458
Pro Asp Phe Arg Ser Pro Thr Gly Leu Tyr Asp Asn Leu Glu Lys
          95          100          105
tac cat ctt ccc tac cca gag gcc atc ttt gag atc agc tat ttc aag 506
Tyr His Leu Pro Tyr Pro Glu Ala Ile Phe Glu Ile Ser Tyr Phe Lys
          110          115          120          125
aaa cat ccg gaa ccc ttc ttc gcc ctc gcc aag gaa ctc tat cct ggg 554
Lys His Pro Glu Pro Phe Phe Ala Leu Ala Lys Glu Leu Tyr Pro Gly
          130          135          140
cag ttc aag cca acc atc tgt cac tac ttc atg cgc ctg ctg aag gac 602
Gln Phe Lys Pro Thr Ile Cys His Tyr Phe Met Arg Leu Leu Lys Asp
          145          150          155
aag ggg cta ctc ctg cgc tgc tac acg cag aac ata gat acc ctg gag 650
Lys Gly Leu Leu Leu Arg Cys Tyr Thr Gln Asn Ile Asp Thr Leu Glu
          160          165          170
cga ata gcc ggg ctg gaa cag gag gac ttg gtg gag gcg cac ggc acc 698
Arg Ile Ala Gly Leu Glu Gln Glu Asp Leu Val Glu Ala His Gly Thr
          175          180          185
ttc tac aca tca cac tgc gtc agc gcc agc tgc cgg cac gaa tac ccg 746
Phe Tyr Thr Ser His Cys Val Ser Ala Ser Cys Arg His Glu Tyr Pro
          190          195          200          205

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cta agc tgg atg aaa gag aag atc ttc tct gag gtg acg ccc aag tgt	794
Leu Ser Trp Met Lys Glu Lys Ile Phe Ser Glu Val Thr Pro Lys Cys	
210 215 220	
gaa gac tgt cag agc ctg gtg aag cct gat atc gtc ttt ttt ggt gag	842
Glu Asp Cys Gln Ser Leu Val Lys Pro Asp Ile Val Phe Phe Gly Glu	
225 230 235	
agc ctc cca gcg cgt ttc ttc tcc tgt atg cag tca gac ttc ctg aag	890
Ser Leu Pro Ala Arg Phe Phe Ser Cys Met Gln Ser Asp Phe Leu Lys	
240 245 250	
gtg gac ctc ctc ctg gtc atg ggt acc tcc ttg cag gtg cag ccc ttt	938
Val Asp Leu Leu Leu Val Met Gly Thr Ser Leu Gln Val Gln Pro Phe	
255 260 265	
gcc tcc ctc atc agc aag gca ccc ctc tcc acc cct cgc ctg ctc atc	986
Ala Ser Leu Ile Ser Lys Ala Pro Leu Ser Thr Pro Arg Leu Leu Ile	
270 275 280 285	
aac aag gag aaa gct ggc cag tcg gac cct ttc ctg ggg atg att atg	1034
Asn Lys Glu Lys Ala Gly Gln Ser Asp Pro Phe Leu Gly Met Ile Met	
290 295 300	
ggc ctc gga gga ggc atg gac ttt gac tcc aag aag gcc tac agg gac	1082
Gly Leu Gly Gly Met Asp Phe Asp Ser Lys Lys Ala Tyr Arg Asp	
305 310 315	
gtg gcc tgg ctg ggt gaa tgc gac cag ggc tgc ctg gcc ctt gct gag	1130
Val Ala Trp Leu Gly Glu Cys Asp Gln Gly Cys Leu Ala Leu Ala Glu	
320 325 330	
ctc ctt gga tgg aag aag gag ctg gag gac ctt gtc cgg agg gag cac	1178
Leu Leu Gly Trp Lys Lys Glu Leu Glu Asp Leu Val Arg Arg Glu His	
335 340 345	
gcc agc ata gat gcc cag tcg ggc ggc ggc gtc ccc aac ccc agc act	1226
Ala Ser Ile Asp Ala Gln Ser Gly Ala Gly Val Pro Asn Pro Ser Thr	
350 355 360 365	
tca gct tcc ccc aag aag tcc ccg cca cct gcc aag gac gag gcc agg	1274
Ser Ala Ser Pro Lys Lys Ser Pro Pro Pro Ala Lys Asp Glu Ala Arg	
370 375 380	
aca aca gag agg gag aaa ccc cag tgacagctgc atctcccagg cgggatgccg	1328
Thr Thr Glu Arg Glu Lys Pro Gln	
385	
agctcctcag ggacagctga gcccacaccg ggccctggccc cctcttaacc agcagttctt	1388
gtctgaggag ctccagaacat cccccaatct cttacagctc cctcccaaaa actggggtcc	1448
cagcaaccct ggcccccaac cccagcaaatt ctctaaccac tcctagaggc caaggcttaa	1508
acaggcatct ctaccagccc cactgtctct aaccactcct gggctaagga gtaacctccc	1568
tcattctctaa ctgccccccac gggggccagggt ctaccccaga actttttaact cttccaggac	1628
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tacctaacct accccagtgt ggggtgtgggc ctctgaatct aaccacacac cagcgtaggg	1748
ggagtctgag ccgggagggc tcccagatct ctgccttcag ctcccaaagt ggggtgtggg	1808
cccccttcac gtgggaccca cttcccatgc tggatgggca gaagacattg cttattggag	1868
acaaattaaa aacaaaaaca actaacaag aaaaaaaaaa aaaaaaa	1915

<210> 174
 <211> 1990
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 259..1701

<400> 174
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tatctgtctg	agcagtggaa	tgtgccagga	aagaaggagc	aaccactgac	tgatgaacct	180
ttgccagtct	cccttccaag	agggatgcca	gagccttctg	taagctcctc	agatgtcact	240
ggtatctagg	caacaggg	atg agc ctg aac ctc cct	gag gcc agc tta ctt			291
		Met Ser Leu Asn Leu Pro	Glu Ala Ser Leu Leu			
		1	5	10		
agc aga gca tcc tgg	cca gaa caa gcc aag gag	cca aga cga gag gga				339
Ser Arg Ala Ser Trp	Pro Glu Gln Ala Lys Glu Pro	Arg Arg Glu Gly				
	15	20	25			
cac acg gac aaa caa cag	aca gaa gac gta ctg gcc	gct gga ctc cgc				387
His Thr Asp Lys Gln Gln Thr	Glu Asp Val Leu Ala Ala Gly	Leu Arg				
	30	35	40			
tgc ctc ccc cat ctc ccc	gcc atc tgc gcc cgg agg	atg agc cca gcc				435
Cys Leu Pro His Leu Pro	Ala Ile Cys Ala Arg Arg	Met Ser Pro Ala				
	45	50	55			
ttc agg gcc atg gat gtg	gag ccc cgc gca aaa ggc	gtc ctt ctg gag				483
Phe Arg Ala Met Asp Val	Glu Pro Arg Ala Lys Gly	Val Leu Leu Glu				
	60	65	70	75		
ccc ttt gtc cac cag gtc	ggg ggg cac tca tgc	gtg ctc cgc ttc aat				531
Pro Phe Val His Gln Val	Gly Gly His Ser Cys Val	Leu Arg Phe Asn				
	80	85	90			
gag aca acc ctg tgc aag	ccc ctg gtc cca agg	gaa cat cag ttc tac				579
Glu Thr Thr Leu Cys Lys	Pro Leu Val Pro Arg	Glu His Gln Phe Tyr				
	95	100	105			
gag acc ctc cct gct gag	atg cgc aaa ttc act	ccc cag tac aaa ggt				627
Glu Thr Leu Pro Ala Glu	Met Arg Lys Phe Thr	Pro Gln Tyr Lys Gly				
	110	115	120			
gtg gta tct gtg cgc ttt	gaa gaa gat gaa gac	agg aac ttg tgt cta				675
Val Val Ser Val Arg Phe	Glu Glu Asp Glu Asp	Asn Leu Cys Leu				
	125	130	135			
ata gca tat cca ttg aaa	ggg gac cat gga att	gtg gac att gta gat				723
Ile Ala Tyr Pro Leu Lys	Gly Asp His Gly Ile	Val Asp Ile Val Asp				
	140	145	150	155		
aat tca gac tgt gaa cca	aaa agt aag ctc cta	agg tgg aca aca aac				771
Asn Ser Asp Cys Glu Pro	Lys Ser Lys Leu Leu	Arg Trp Thr Thr Asn				
	160	165	170			
aaa aaa cat cat gtc tta	gaa aca gaa aag acc	cct aag gac tgg gtg				819
Lys Lys His His Val Leu	Glu Thr Glu Lys Thr	Pro Lys Asp Trp Val				
	175	180	185			
cgt cag cac cgt aaa gag	gag aaa atg aag agc	cat aag tta gaa gaa				867
Arg Gln His Arg Lys Glu	Glu Glu Lys Met Lys	Ser His Lys Leu Glu Glu				
	190	195	200			
gaa ttt gag tgg cta aag	aaa tct gaa gtc ttg	tac tac act gta gag				915
Glu Phe Glu Trp Leu Lys	Ser Glu Val Leu Tyr	Tyr Thr Val Glu				
	205	210	215			
aag aag ggg aat ata agt	tcc cag ctt aaa cac	tat aac cct tgg agc				963
Lys Lys Gly Asn Ile Ser	Ser Ser Gln Leu Lys	His Tyr Asn Pro Trp Ser				
	220	225	230	235		
atg aaa tgt cac cag caa	cag tta cag aga atg	aag gag aat gca aag				1011
Met Lys Cys His Gln Gln	Gln Leu Gln Arg Met	Lys Glu Asn Ala Lys				
	240	245	250			
cat cgg aac cag tac aaa	ttt atc tta ctg gaa	aac ctg act tcc cgc				1059
His Arg Asn Gln Tyr Lys	Phe Ile Leu Leu Glu	Asn Leu Thr Ser Arg				
	255	260	265			
tat gag gtg cct tgt gtc	ctt gac ctc aag atg	ggc aca cga caa cat				1107
Tyr Glu Val Pro Cys Val	Leu Asp Leu Lys Met	Gly Thr Arg Gln His				
	270	275	280			
ggt gat gat gct tca gag	gag aag gca gcc aac	cag atc cga aaa tgt				1155

Gly	Asp	Asp	Ala	Ser	Glu	Glu	Lys	Ala	Ala	Asn	Gln	Ile	Arg	Lys	Cys	
	285					290					295					
cag	cag	agc	aca	tct	gca	gtc	att	ggg	gtg	cgt	gtg	tgt	ggc	atg	cag	1203
Gln	Gln	Ser	Thr	Ser	Ala	Val	Ile	Gly	Val	Arg	Val	Cys	Gly	Met	Gln	
300					305					310					315	
gtg	tac	caa	gca	ggc	agt	ggg	cag	ctc	atg	ttc	atg	aac	aag	tac	cat	1251
Val	Tyr	Gln	Ala	Gly	Ser	Gly	Gln	Leu	Met	Phe	Met	Asn	Lys	Tyr	His	
				320					325					330		
gga	cgg	aag	cta	tcg	gtg	cag	ggc	ttc	aag	gag	gca	ctt	ttc	cag	ttc	1299
Gly	Arg	Lys	Leu	Ser	Val	Gln	Gly	Phe	Lys	Glu	Ala	Leu	Phe	Gln	Phe	
			335					340				345				
ttc	cac	aat	ggg	cgg	tac	ctg	cgc	cgt	gaa	ctc	ctg	ggc	cct	gtg	ctc	1347
Phe	His	Asn	Gly	Arg	Tyr	Leu	Arg	Arg	Glu	Leu	Leu	Gly	Pro	Val	Leu	
		350					355					360				
aag	aag	ctg	act	gag	ctc	aag	gca	gtg	ttg	gag	cga	cag	gag	tcc	tac	1395
Lys	Lys	Leu	Thr	Glu	Leu	Lys	Ala	Val	Leu	Glu	Arg	Gln	Glu	Ser	Tyr	
	365					370				375						
cgc	ttc	tac	tca	agc	tcc	ctg	ctg	gtc	att	tat	gat	ggc	aag	gag	cgg	1443
Arg	Phe	Tyr	Ser	Ser	Ser	Leu	Leu	Val	Ile	Tyr	Asp	Gly	Lys	Glu	Arg	
380					385					390					395	
ccc	gaa	gtg	gtc	ctg	gac	tca	gat	gct	gag	gat	ttg	gag	gac	ctg	tca	1491
Pro	Glu	Val	Val	Leu	Asp	Ser	Asp	Ala	Glu	Asp	Leu	Glu	Asp	Leu	Ser	
				400					405					410		
gag	gaa	tca	gct	gat	gag	tct	gct	ggg	gcc	tat	gcc	tac	aaa	ccc	atc	1539
Glu	Glu	Ser	Ala	Asp	Glu	Ser	Ala	Gly	Ala	Tyr	Ala	Tyr	Lys	Pro	Ile	
			415					420				425				
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Cys	Arg	Leu	Tyr	Gly	Glu	Asp	Thr	Val	Val	His	Glu	Gly	Gln	Asp	Ala	
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Ser	Glu	Glu	Ser	Gly	Glu											
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Gln	Pro	Gly	Pro	His	Asn	Phe	Tyr	Ser	Arg	Pro	His	Phe	Val	Asn	Thr		
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Ala Val Glu Ala Leu Cys Leu Arg Asp Gly Val						
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1 5 10	
ata aca ttt gta ttt caa taaaaggaag atcttcctgt tacagaggat	157
Ile Thr Phe Val Phe Gln	
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aactttgtga aacttcaagt taaagcttgt gctctgagcc agataaatac aaagcttctg	217
gcagaaatga agatgaaaaa ggattttattt cctgttgaggga gagaaattgc tggaattgtg	277
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gttcataaac cagaaaaagg cacaatggacg gaagcagcag gaagcattcg ggatggagtg	457
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Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile																
1 5 10 15																
aca	ttt	gta	ttt	caa	gaa	aag	gaa	gat	ctt	cct	ggt	aca	gag	gat	aac	157
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Lys	Leu	Leu	Ala	Glu	Met	Lys	Met	Lys	Lys	Asp	Leu	Phe	Pro	Val	Gly	
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Arg	Glu	Ile	Ala	Gly	Ile	Val	Leu	Asp	Val	Gly	Ser	Lys	Val	Ser	Phe	
65 70 75																
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Phe	Gln	Pro	Asp	Asp	Glu	Val	Val	Gly	Ile	Leu	Pro	Leu	Asp	Ser	Glu	
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Asp	Pro	Gly	Leu	Cys	Glu	Val	Val	Arg	Val	His	Glu	His	Tyr	Leu	Val	
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His	Lys	Pro	Glu	Lys	Val	Thr	Trp	Thr	Glu	Ala	Ala	Gly	Ser	Ile	Arg	
115 120 125																
gat	gga	gtg	cgt	gcc	tat	aca	gct	ctg	cat	tat	ctt	tct	cat	ctc	tct	493
Asp	Gly	Val	Arg	Ala	Tyr	Thr	Ala	Leu	His	Tyr	Leu	Ser	His	Leu	Ser	
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Pro	Gly	Lys	Ser	Val	Leu	Ile	Met	Asp	Gly	Ala	Ser	Ala	Phe	Gly	Thr	
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Ile	Ala	Ile	Gln	Leu	Ala	His	His	Arg	Gly	Ala	Lys	Val	Ile	Ser	Thr	
160 165 170 175																
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Ala	Cys	Ser	Leu	Glu	Asp	Lys	Gln	Cys	Leu	Glu	Arg	Phe	Arg	Pro	Pro	
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195 200 205																

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Ser Cys Leu Glu Glu Thr Gly Gly Leu Gly Val Asp Ile Val Leu Asp
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gct gga gtg aga tta tat agt aaa gat gat gaa cca gct gta aaa cta      781
Ala Gly Val Arg Leu Tyr Ser Lys Asp Asp Glu Pro Ala Val Lys Leu
      225                      230                      235
caa cta cta cca cat aaa cat gat atc atc aca ctt ctt ggt gtt gga      829
Gln Leu Leu Pro His Lys His Asp Ile Ile Thr Leu Leu Gly Val Gly
      240                      245                      250                      255
ggc cac tgg gta aca aca gaa gaa aac ctt cag ttg gat cct cca gat      877
Gly His Trp Val Thr Thr Glu Glu Asn Leu Gln Leu Asp Pro Pro Asp
      260                      265                      270
agc cac tgc ctt ttc ctc aag gga gca acg tta gct ttc ctg aat gat      925
Ser His Cys Leu Phe Leu Lys Gly Ala Thr Leu Ala Phe Leu Asn Asp
      275                      280                      285
gaa gtt tgg aat ttg tca aat gta caa cag gga aaa tat ctt tat ctt      973
Glu Val Trp Asn Leu Ser Asn Val Gln Gln Gly Lys Tyr Leu Tyr Leu
      290                      295                      300
aaa gga tgt gat gga gaa gtt atc aac tgg tgt ttt cag acc tca gtc      1021
Lys Gly Cys Asp Gly Glu Val Ile Asn Trp Cys Phe Gln Thr Ser Val
      305                      310                      315
gga tgaacatatt ccagtatttg aagccagaat tttctttgga aattgttgag      1074
Gly
320
aaaaaccaag gaagataaaa caagttgcat ttttaagcac gtttctctgc taagacaaga      1134
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tcccttttct ctcccttgaaa gtccagcaca ccattcttgt ccttccccag tttcctcgcc      1254
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 <213> Homo sapiens

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 <221> CDS
 <222> 109..585

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                                   Met Glu Lys
                                   1
ctg cgg cga gtc ctg agc ggc cag gac gac gag gag cag ggc ctg act      165
Leu Arg Arg Val Leu Ser Gly Gln Asp Asp Glu Glu Gln Gly Leu Thr
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gcg cag gtc ctg gat gcc tca tcc ctt agt ttc aac acc aga ttg aaa      213
Ala Gln Val Leu Asp Ala Ser Ser Leu Ser Phe Asn Thr Arg Leu Lys
      20                      25                      30                      35
tgg ttt gcc atc tgc ttc gta tgt ggc gtt ttc ttt tct att ctt gga      261
Trp Phe Ala Ile Cys Phe Val Cys Gly Val Phe Phe Ser Ile Leu Gly
      40                      45                      50
act gga ttg ctg tgg ctt ccg ggc ggc ata aag ctt ttt gca gtg ttt      309
Thr Gly Leu Leu Trp Leu Pro Gly Gly Ile Lys Leu Phe Ala Val Phe
      55                      60                      65
tat acc ctc ggc aat ctt gct gcg tta gcc agt aca tgc ttt tta atg      357
Tyr Thr Leu Gly Asn Leu Ala Ala Leu Ala Ser Thr Cys Phe Leu Met

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      85      90      95
gca aca att gtt atg ctt ttg tgt ttc ata ttt acc ctg tgt gct gct      453
Ala Thr Ile Val Met Leu Leu Cys Phe Ile Phe Thr Leu Cys Ala Ala
100      105      110      115
ctt tgg tgg cat aag aag gga ctg gct gtg tta ttc tgc ata ttg cag      501
Leu Trp Trp His Lys Lys Gly Leu Ala Val Leu Phe Cys Ile Leu Gln
      120      125      130
ttc ttg tca atg acc tgg tat agc ctg tgc tac atc cca tat gca agg      549
Phe Leu Ser Met Thr Trp Tyr Ser Leu Ser Tyr Ile Pro Tyr Ala Arg
      135      140      145
gat gca gtt att aaa tgc tgt tct ctc cta agt tgaaaatcag      595
Asp Ala Val Ile Lys Cys Cys Ser Ser Leu Leu Ser
      150      155
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ctcattttgt atactggtaa aaactacatg cttgattaaa ccattaaatg cttgtaactt      775
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<213> Homo sapiens

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<222> 29..577

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cgg gcg gcg cgg aaa cgg gcg ggt ctg gcg gcc caa ccc cct gct gcc      100
Arg Ala Ala Arg Lys Arg Ala Gly Leu Ala Ala Gln Pro Pro Ala Ala
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agt cag ggc gca caa acc cca gga gag aag gcg gaa gca gca gcg act      148
Ser Gln Gly Ala Gln Thr Pro Gly Glu Lys Ala Glu Ala Ala Ala Thr
      25      30      35      40
cta aag gca gcc cca ggc tgg cta aag cgg ttc ctg gta tgg aaa cct      196
Leu Lys Ala Ala Pro Gly Trp Leu Lys Arg Phe Leu Val Trp Lys Pro
      45      50      55
agg ccc gcg agt gcc cgg gcc cag ccc ggc cta gtt cag gaa gcg gct      244
Arg Pro Ala Ser Ala Arg Ala Gln Pro Gly Leu Val Gln Glu Ala Ala
      60      65      70
cag ccc cag ggc agc aca tca gag aca cca tgg aac aca gcc att cct      292
Gln Pro Gln Gly Ser Thr Ser Glu Thr Pro Trp Asn Thr Ala Ile Pro
      75      80      85
ctg ccg tgc tgc tgg gac cag tct ttc ctg acc aat atc acc ttc ttg      340
Leu Pro Ser Cys Trp Asp Gln Ser Phe Leu Thr Asn Ile Thr Phe Leu
      90      95      100
aag gtt ctt ctc tgg ttg gtc ctg ctg gga ctg ttt gtg gaa ctg gaa      388

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Lys	Val	Leu	Leu	Trp	Leu	Val	Leu	Leu	Gly	Leu	Phe	Val	Glu	Leu	Glu		
105					110					115				120			
ttt	ggc	ctg	gca	tat	ttt	gtc	ctg	tcc	ttg	ttc	tat	tgg	atg	tac	gtc		436
Phe	Gly	Leu	Ala	Tyr	Phe	Val	Leu	Ser	Leu	Phe	Tyr	Trp	Met	Tyr	Val		
				125					130					135			
ggg	aca	cga	ggc	cct	gaa	gag	aag	aaa	gag	gga	gag	aag	agc	gcc	tac		484
Gly	Thr	Arg	Gly	Pro	Glu	Glu	Lys	Lys	Glu	Gly	Glu	Lys	Ser	Ala	Tyr		
			140					145					150				
tct	gtg	ttc	aat	cca	ggc	tgt	gaa	gcc	atc	cag	ggc	acc	ctg	act	gca		532
Ser	Val	Phe	Asn	Pro	Gly	Cys	Glu	Ala	Ile	Gln	Gly	Thr	Leu	Thr	Ala		
		155				160						165					
gag	cag	ttg	gag	cgc	gag	tta	cag	ttg	aga	ccc	ctg	gca	ggg	aga			577
Glu	Gln	Leu	Glu	Arg	Glu	Leu	Gln	Leu	Arg	Pro	Leu	Ala	Gly	Arg			
	170				175					180							
taggacccag	ctgtgctgtc	atgcagctaa	cctctgatgt	ggctcttcctc	accattggct												637
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<211> 1443

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 23..451

<400> 180

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		Met	Ala	Ala	Pro	Arg	Arg	Gly	Arg	Gly	Ser						
		1				5					10						
tcc	aca	gtg	ctc	tct	tca	gtt	ccc	ctt	caa	atg	ctg	ttt	tat	ctc	agc		100
Ser	Thr	Val	Leu	Ser	Ser	Val	Pro	Leu	Gln	Met	Leu	Phe	Tyr	Leu	Ser		
			15				20					25					
gga	acg	tac	tac	gcc	ctg	tat	ttc	ctc	gcc	acg	ctc	ctg	atg	atc	acg		148
Gly	Thr	Tyr	Tyr	Ala	Leu	Tyr	Phe	Leu	Ala	Thr	Leu	Leu	Met	Ile	Thr		
			30				35					40					

tat aaa agt cag gtg ttc agc tat cct cac cgc tac ctg gtc ctc gat 196
 Tyr Lys Ser Gln Val Phe Ser Tyr Pro His Arg Tyr Leu Val Leu Asp
 45 50 55
 ctt gct ctg ctg ttt ctg atg ggg att cta gaa gca gtt cgg tta tac 244
 Leu Ala Leu Leu Phe Leu Met Gly Ile Leu Glu Ala Val Arg Leu Tyr
 60 65 70
 ctg ggc acc agg ggc aac ctg aca gag gct gag agg ccg ctg gcc gcc 292
 Leu Gly Thr Arg Gly Asn Leu Thr Glu Ala Glu Arg Pro Leu Ala Ala
 75 80 85 90
 agc ctg gcc ctc acg gct ggc acc gcc ctc ctc tct gcc cac ttc ctg 340
 Ser Leu Ala Leu Thr Ala Gly Thr Ala Leu Leu Ser Ala His Phe Leu
 95 100 105
 ctt tgg cag gcc cta gtg ttg tgg gcg gac tgg gcc ctc agc gcc acg 388
 Leu Trp Gln Ala Leu Val Leu Trp Ala Asp Trp Ala Leu Ser Ala Thr
 110 115 120
 ctc ctg gcc ctt cac ggc ctg gag gcc gtc ctg cag gtg gtt gcc atc 436
 Leu Leu Ala Leu His Gly Leu Glu Ala Val Leu Gln Val Val Ala Ile
 125 130 135
 gcg gcc ttc acc agg tagctacgga caccgaggat accccacact ggggccctcc 491
 Ala Ala Phe Thr Arg
 140
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 ttcctagtga ctggccatag atgggttttg atggttccat ctgttctggc aggagtggga 611
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 ctattgtgtg ttttctatgt ttggaataat tacacccaaa tatctagata ttttctcttc 1391
 accgcatttt gtaaataaag agatgtgtat gcctcaaaaa aaaaaaaaaa aa 1443

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 <213> Homo sapiens

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 <222> 232..450

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 ccaaaactta caggcttaaaa acaacaaaca tgtatcattt cttatgattc tgtgggttgg 180
 ctgggtgggt cttctagctg aggcaggatg gtctaggata gctacatcca c atg tct 237
 Met Ser
 1
 ggg gtc cca gct gag atg act ggg gct gtt gag gcc ttt ctc cct gtg 285
 Gly Val Pro Ala Glu Met Thr Gly Ala Val Glu Ala Phe Leu Pro Val
 5 10 15
 gtg tca tcc tcc aga agg ctg ccc aga ttt gtc cat atg gta gca gga 333

Val	Ser	Ser	Ser	Arg	Arg	Leu	Pro	Arg	Phe	Val	His	Met	Val	Ala	Gly	
	20					25				30						
ggt	tcc	tcg	aag	caa	gag	agg	gca	aga	tcc	aac	aca	gaa	gca	ctt	ttc	381
Val	Ser	Ser	Lys	Gln	Glu	Arg	Ala	Arg	Ser	Asn	Thr	Glu	Ala	Leu	Phe	
35				40					45					50		
aag	ctc	tgt	ttc	cat	cac	att	tgc	caa	tgt	ctc	act	gat	gaa	cac	aag	429
Lys	Leu	Cys	Phe	His	His	Ile	Cys	Gln	Cys	Leu	Thr	Asp	Glu	His	Lys	
			55				60						65			
ttc	cat	ggc	caa	gtc	cag	ttt	taagaaatgg	agaaataggg	cttgggtcag							480
Phe	His	Gly	Gln	Val	Gln	Phe										
			70													
tggtctcatgt	ctgtaatccc	agcacttttg	gaggccaagg	catgcggatc	atttgaggtc											540
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aaaaa																605

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<211> 1724

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 758..1183

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ccagcccccc	accatggtaa	gtccttcaag	ggtgggatct	ggaagaggaa	agaggaggga	180
caccagccag	gtggagggtg	cctaaaaatg	accatcagaa	attgggggtga	ggggaggggc	240
atgggtggact	tctgtggggg	tgggggtgtc	ctcagtgtag	ctcaggtggt	tccagcatcc	300
cttaccagggt	agcaagctcc	catctgtagg	tgggtggggat	gccaggggtg	tatccctgga	360
tccaaggata	gggcaggacc	tggaagacag	aaggtggccc	agggagaatc	acagagtctg	420
cagggacaag	gacatagcct	cctttgcttg	caaattaagg	gagccctttc	ccagtccagc	480
ccagtctctc	gtctccctgt	gtagccttgg	gctagtcact	tcccctctct	tggccccggt	540
tcccacagat	gtcatatttg	gaaatccgtc	tagatgcgga	agttgtctct	caggggtctt	600
tcagttgcaa	cattctcaag	gtctgtgggt	tctgccacag	agtcctcggc	tgagatggga	660
agctatgtct	aacaagcgat	gggggtgatt	gacgcctcc	ctgtgccggg	gacgggcggg	720
atggctgcag	cagaggcagg	agaggctgaa	tacgtcc	atg	cca ccc ttt ggt ggg	775

Met Pro Pro Phe Gly Gly

1 5

cat	ccc	tta	tcc	caa	gag	gag	gat	ggc	agc	cag	agg	tgt	tgc	tgc	ctg	823
His	Pro	Leu	Ser	Gln	Glu	Glu	Asp	Gly	Ser	Gln	Arg	Cys	Cys	Cys	Leu	

10

15

20

tca	agt	ctg	agg	tct	gtc	gat	gat	agc	aac	ggg	gag	act	gtc	gtg	atc	871
Ser	Ser	Leu	Arg	Ser	Val	Asp	Asp	Ser	Asn	Gly	Glu	Thr	Val	Val	Ile	

25

30

35

atg	gcg	cta	ttc	cta	gca	gta	tcg	tac	cac	cat	aag	acg	caa	agt	aag	919
Met	Ala	Leu	Phe	Leu	Ala	Val	Ser	Tyr	His	His	Lys	Thr	Gln	Ser	Lys	

40

45

50

agg	tgg	cca	ggg	ctg	acc	cca	ccc	cac	agc	tct	ctg	ctg	tgt	aga	cca	967
Arg	Trp	Pro	Gly	Leu	Thr	Pro	Pro	His	Ser	Ser	Leu	Leu	Cys	Arg	Pro	

55

60

65

70

ctt	cag	ctt	tca	ttt	ctc	gtc	att	cag	tca	gtg	agg	atg	aga	gca	tgt	1015
Leu	Gln	Leu	Ser	Phe	Leu	Val	Ile	Gln	Ser	Val	Arg	Met	Arg	Ala	Cys	

75

80

85

ggc	tgt	gac	agc	ggc	cac	tgc	agg	att	ctt	ggc	agg	tac	agc	tta	cta	1063
Gly	Cys	Asp	Ser	Gly	His	Cys	Arg	Ile	Leu	Gly	Arg	Tyr	Ser	Leu	Leu	

90

95

100

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ggg tgg agt cag gga cat agg gca aga ggc aga ggt ggt gtt agt ctg      1111
Gly Trp Ser Gln Gly His Arg Ala Arg Gly Arg Gly Gly Val Ser Leu
      105                      110                      115
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Arg Asp Asn Thr Phe Phe Gln Glu Ala Ser Glu Gly Gln Gly Gln Trp
      120                      125                      130
ctc atg cct gta atc cca gca ttt taggaggctg agacaggtag atcacttgag      1213
Leu Met Pro Val Ile Pro Ala Phe
      135                      140
gtcaggtggt cgagaccagc ctggccaacg tgggtgaaacc tcgtctctac taaaaaatac      1273
aaaaaattaa ctgggcgtgg tggcacacgc ctgtaatccc agctacatat gaggctgagg      1333
caagagaata acttgaaccc aggaggcgga ggggtgcagtg agctgagatc ctgccgctgc      1393
actccagcct ggggtgacaga gcacactccg tctcaaaaaa ggaaagctga tgagaaattg      1453
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ttacggaacc tagtctccgt tctgtccatg gccttcttct ggacactgct aggatccaga      480
agagt atg tta tca att ctc aag cct agg aga agt cag gag tgg aga aca      530
      Met Leu Ser Ile Leu Lys Pro Arg Arg Ser Gln Glu Trp Arg Thr
      1          5          10          15
gct ctg aga aga tac tgt tgt cca act gat ctc cag gca cca cgg agt      578
Ala Leu Arg Arg Tyr Cys Cys Pro Thr Asp Leu Gln Ala Pro Arg Ser
      20          25          30
ccg gtc cct cca atc agg aag gtc gga atc tct gat gtc atc gtt cat      626
Pro Val Pro Pro Ile Arg Lys Val Gly Ile Ser Asp Val Ile Val His
      35          40          45
gcc aac ctg gca acc agt ttg aaa aaa aac aca tgt aac tgc cag gct      674
Ala Asn Leu Ala Thr Ser Leu Lys Lys Asn Thr Cys Asn Cys Gln Ala
      50          55          60
gat ctc ttg tcc tgg aga tcc tgg gtg aat ggt atc tcc tgc cac tgt      722
Asp Leu Leu Ser Trp Arg Ser Trp Val Asn Gly Ile Ser Cys His Cys
      65          70          75
ccc aac ctc aga cca ttg tcc aaa agc atc ttc agg gac tcc aca tcc      770
Pro Asn Leu Arg Pro Leu Ser Lys Ser Ile Phe Arg Asp Ser Thr Ser
      80          85          90          95
ctc tgt tcc ctg tcc cag cag agg ctg tgt cct ctc cac tca aag cct      818
Leu Cys Ser Leu Ser Gln Gln Arg Leu Cys Pro Leu His Ser Lys Pro
      100          105          110

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gaa gca tgt tgg ggt ctc ttt gtc tct gta cat gcc cat ttc aga gtc 866
Glu Ala Cys Trp Gly Leu Phe Val Ser Val His Ala His Phe Arg Val
115 120 125
cag gct ggt ggg aga ggg aac aga gtg gga aag aaa act agg gta agc 914
Gln Ala Gly Gly Arg Gly Asn Arg Val Gly Lys Lys Thr Arg Val Ser
130 135 140
aga aac gat gaa acc tta taagagtgag attatcatgt gcaagagtga 962
Arg Asn Asp Glu Thr Leu
145
gattatcatg tacaagagat cccaggaaat actgactttg atgaaaaagt cacatcagag 1022
cactcagttt tggcagagct ttttctgccc aatgtttact cacattcact gtccgagatt 1082
ctatactggg ggtacacacg tcctctgccc taaggcaatt ttgagtccaa gagacatttt 1142
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agactcatgt gacaggaaga tcacttgagc ccgggggtta gaggctgcag tgagctatga 1622
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aaaa 1686

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<213> Homo sapiens

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<222> 80..304

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ccattagatc atttcacaa atg tat ctg cca cca aac agg tca gag ctt tgc 112
Met Tyr Leu Pro Pro Asn Arg Ser Glu Leu Cys
1 5 10
aac ttt gct ttg tct ctt aac ctc tat ggc aaa ggg ttt ttt agc ctg 160
Asn Phe Ala Leu Ser Leu Asn Leu Tyr Gly Lys Gly Phe Phe Ser Leu
15 20 25
gtg gaa aag cat aac agc agg gat tta gaa gat aga gct agt tct ggc 208
Val Glu Lys His Asn Ser Arg Asp Leu Glu Asp Arg Ala Ser Ser Gly
30 35 40
cca tca ctt tca tct cca tca cac ccg gac tgg ggt tat ata gtt ctg 256
Pro Ser Leu Ser Ser Pro Ser His Pro Asp Trp Gly Tyr Ile Val Leu
45 50 55
att tta gtg gca acc ctg ggg gaa ctt gat acc cag gta ggt ggt cac 304
Ile Leu Val Ala Thr Leu Gly Glu Leu Asp Thr Gln Val Gly Gly His
60 65 70 75
tgatcagtag ttgggagagg taggaattgg tgagtacagg taattagagg aaagtcttgt 364
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ttatcaatta cagtctaaat ccaaaagaaa aaaaaaaaaa 463

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 aaaggactct ggattggttg gcagtctgct ttttttttc caaggtgatc actttactgt 180
 agaagaa atg agg tta aca gaa aag agt gag gga gaa caa caa ctc aag 229
 Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys
 1 5 10
 ccc aac aac tct aat gca ccc aat gaa gat caa gaa gaa gaa atc caa 277
 Pro Asn Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Glu Ile Gln
 15 20 25 30
 cag tca gaa cag cat act cca gca agg cag cga aca caa aga gca gac 325
 Gln Ser Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp
 35 40 45
 aca cag cca tcc aga tgt cga ttg cct tca cgt agg aca cct aca aca 373
 Thr Gln Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr
 50 55 60
 tcc agc gac aga acg atc aac ctt ctt gaa gtc ctt ccg tgg cct act 421
 Ser Ser Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr
 65 70 75
 gag tgg att ttc aac ccc tat cga ttg cct gct ctt ttt gag ctt tat 469
 Glu Trp Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr
 80 85 90
 cct gaa ttt ctt ctg gtg ttt aaa gaa gcc ttc cat gac ata tcc cat 517
 Pro Glu Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His
 95 100 105 110
 tgt ctg aaa gcc cag atg gaa aag atc gga ctg ccc atc ata ctc cac 565
 Cys Leu Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His
 115 120 125
 ctc ttc gca ctc tcc acc ctc tac ttc tac aag ttt ttc ctt cct aca 613
 Leu Phe Ala Leu Ser Thr Leu Tyr Phe Tyr Lys Phe Phe Leu Pro Thr
 130 135 140
 att ctt tcc ctt tct ttc ttt att ctt ctt gta ctt ctg ctt ctg ctt 661
 Ile Leu Ser Leu Ser Phe Phe Ile Leu Leu Val Leu Leu Leu Leu Leu
 145 150 155
 ttt att att gtc ttc att ctg atc ttc ttc tgattctttt gtttcaataa 711
 Phe Ile Ile Val Phe Ile Leu Ile Phe Phe
 160 165
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 aa 773

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 Met Pro Arg Ser Ser Arg Ser
 1 5

cct ggg gac cca ggc gcc cta ctc gaa gat gtg gcc cac aat ccc aga	162
Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Val Ala His Asn Pro Arg	
10 15 20	
ccc cgg agg att gcc cag cga ggc cgg aac acc agc agg atg gca gag	210
Pro Arg Arg Ile Ala Gln Arg Gly Arg Asn Thr Ser Arg Met Ala Glu	
25 30 35	
gac acc tcc cca aac atg aat gac aac atc ctg ttg cct gtc cgc aac	258
Asp Thr Ser Pro Asn Met Asn Asp Asn Ile Leu Leu Pro Val Arg Asn	
40 45 50 55	
aat gac caa gcc cta ggc ctg act cag tgc atg ctg gga tgt gtg tcc	306
Asn Asp Gln Ala Leu Gly Leu Thr Gln Cys Met Leu Gly Cys Val Ser	
60 65 70	
tgg ttc acc tgt ttt gcc tgc tcc ctg aga act cag gcc cag cag gtt	354
Trp Phe Thr Cys Phe Ala Cys Ser Leu Arg Thr Gln Ala Gln Gln Val	
75 80 85	
ctg ttt aac acg tgc aga gac aga gtt tca cca tgt tgc cca ggc tgg	402
Leu Phe Asn Thr Cys Arg Asp Arg Val Ser Pro Cys Cys Pro Gly Trp	
90 95 100	
tct caa act cca gtg atc ctc cca cct cag cct tcc gaa gtg ctg gga	450
Ser Gln Thr Pro Val Ile Leu Pro Pro Gln Pro Ser Glu Val Leu Gly	
105 110 115	
tta cag atg caa gct gct gtg cca gaa gct cat gga gaa gac agg cat	498
Leu Gln Met Gln Ala Ala Val Pro Glu Ala His Gly Glu Asp Arg His	
120 125 130 135	
tct gct cct ctg tgc ttt cgg tgt gtc cca ggg ccc tgc cca gtc cca	546
Ser Ala Pro Leu Cys Phe Arg Cys Val Pro Gly Pro Cys Pro Val Pro	
140 145 150	
ggg gga ggt atc cct ggg ccc tgg cac tgattatagg acactgggca	593
Gly Gly Gly Ile Pro Gly Pro Trp His	
155 160	
agacactgca ctgccacgtg actcagtttc cccatctgcc tgatgggtgt tgctgtgaga	653
attatgaaat gaaatgatga ccatgaaaat attgtagaag ccaagaaatg cttcagaagt	713
tataaagctc tccccaacc gtgttaaaaa aaaaaaaaaa	753

<210> 187
 <211> 754
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 181..462

<400> 187	
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ctgtgccaac acagcctgat ggcttcttgt ttcaggaaac atccagaatt acaactggcc	120
attgagttat tacatatcaa ttgaacaagg tagttttaaa atgaaagaaa atcttgcaac	180
atg aat aaa gag ata gac tct ttg aat ctg gca tac agc ttt ccc ttc	228
Met Asn Lys Glu Ile Asp Ser Leu Asn Leu Ala Tyr Ser Phe Pro Phe	
1 5 10 15	
ctt ctt cct gct ttc ctg gac aca ccg tgg aca gac cca ttt ccc tct	276
Leu Leu Pro Ala Phe Leu Asp Thr Pro Trp Thr Asp Pro Phe Pro Ser	
20 25 30	
gga ttc atg gta agg tcc cga gtg ctt ctg ata cag ctg ctg agc aga	324
Gly Phe Met Val Arg Ser Arg Val Leu Leu Ile Gln Leu Leu Ser Arg	
35 40 45	
ccc cgc tca tct cag gag tcc cga gga cac tcg ctt ccc tgc agc ccg	372
Pro Arg Ser Ser Gln Glu Ser Arg Gly His Ser Leu Pro Cys Ser Pro	

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      50              55              60
tcc gcc ctc cat aag cct ggg ggc atc tgc cct gca gca ctg ggg agg 420
Ser Ala Leu His Lys Pro Gly Gly Ile Cys Pro Ala Ala Leu Gly Arg
65              70              75              80
agc cac ctc ctt gtc tgg gaa cag cca agc ctc cgt gac agc 462
Ser His Leu Leu Val Trp Glu Gln Pro Ser Leu Arg Asp Ser

      85              90
tgaggattct tgtggattgt tctttctgta actggacagc acatccggaa ttccttgcca 522
tagctctgtg ccttgctggg gtctgaggtt cacagggtcag atgctgctgt ctggtccttc 582
ccaattgcgg cgtgaattcc ttcattcctca ccagtagctt cttgctctcc ccaagggagg 642
cacgtgctta gtagggagag aggcctacca aggttgccat ctgccatggg ctcaattgtg 702
tccccaaccc ccttgcaaat tatatatattga agtccccaaa aaaaaaaaaa aa 754

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<210> 188
 <211> 998
 <212> DNA
 <213> Homo sapiens

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 <222> 6..290

<220>
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 <222> 871
 <223> n=a, g, c or t

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<400> 188
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      Met Lys Ala Ser Gly Pro Asp Leu Ser Asp Gly Leu His Cys Pro
      1              5              10              15
agt cta att aga cat tta aga acc ttc tct gca gct gct gcc tta gcc 98
Ser Leu Ile Arg His Leu Arg Thr Phe Ser Ala Ala Ala Ala Leu Ala
      20              25              30
cca aga tac cca acc aga ctt ccc agt tca ctg ctt cta tgg cac ctc 146
Pro Arg Tyr Pro Thr Arg Leu Pro Ser Ser Leu Leu Leu Trp His Leu
      35              40              45
tgc cag tgc ctc cat ctc ctc tat gca gtt tct acc tca tgc aac agc 194
Cys Gln Cys Leu His Leu Leu Tyr Ala Val Ser Thr Ser Cys Asn Ser
      50              55              60
cat ggg aag aga tcg gct gcc tgg gca atg acc aga aca gaa gac aca 242
His Gly Lys Arg Ser Ala Ala Trp Ala Met Thr Arg Thr Glu Asp Thr
      65              70              75
gat gcg cta aca gat tcc ttc gat gac agt ttc atc agt tct gca gat 290
Asp Ala Leu Thr Asp Ser Phe Asp Asp Ser Phe Ile Ser Ser Ala Asp
      80              85              90              95
taaagacttt caccagaaaa aaaaattacc tgattttgcc ctgaggcagc caggaggaggc 350
tttgtccttg acaatcccac tgacttattt aacaggtagc tcaaaaccca acaaaaaactg 410
gaggaggctg ctccactgca gggatggttt caattcggtg actggagtat tgtactctcc 470
ttgcaccctg gctcatcccc acaaaagacc tttcaaagaa aacacttaat tacctccttg 530
cacaagccct gtaagcccta aggtgaaaag aaactcagca gacaagggtc acagagaagg 590
agaaggcaca attcagtagg gacctacgct cagcaccagg ataaagaaac tgtccattcc 650
tgccacctcc taggaagcta aaagaattaa ggggaggccg ggcacggtgg ctcacgcctg 710
taatcccagc actttgggag gccgaggcgg gtggatcatg aggtcaggag atcgagacca 770
tcctggctaa catggtgaaa ccccatctct actaaaaata caaaaaatta gccgggcgtg 830
gtggcggggc ccctgtagtc ccagctactc gggagggtga nggcaggaga atggtgtgaa 890
cctgggaggc ggagcttgca gtgagccgag attgcgcctt gctccactcc agcctgagcg 950
acagagcgag actccgtctc aaaaaaaaaa argaaaaaaa aaaaaaaaaa 998

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<210> 189
 <211> 605
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 115..411

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 ggacaggaag aaccacagat accagatacg ggtactgttg taactctgtt ctcc atg 117
 Met
 1
 aaa aaa aag gaa gaa aca aca ctt tca gag atg gag cct gtt gag cca 165
 Lys Lys Lys Glu Glu Thr Thr Leu Ser Glu Met Glu Pro Val Glu Pro
 5 10 15
 cag tac caa cta gtc aat gct gaa tcg act tct ccc ttt cta cat tgc 213
 Gln Tyr Gln Leu Val Asn Ala Glu Ser Thr Ser Pro Phe Leu His Cys
 20 25 30
 ctg aga gaa gtc att ggg gaa tac tct gta cac gaa ttt tca ctg ttg 261
 Leu Arg Glu Val Ile Gly Glu Tyr Ser Val His Glu Phe Ser Leu Leu
 35 40 45
 ggg aaa aca gag agt caa ggg att gga ttg tgg att gca ttg gtg gtt 309
 Gly Lys Thr Glu Ser Gln Gly Ile Gly Leu Trp Ile Ala Leu Val Val
 50 55 60 65
 ttc ctc agt ttc ctc atc ttc tcc aca agt ttc tac ata tcg aat gca 357
 Phe Leu Ser Phe Leu Ile Phe Ser Thr Ser Phe Tyr Ile Ser Asn Ala
 70 75 80
 gag cag ccc ttc ttc aaa gaa cct cct acg gaa gct gct aag gaa ctc 405
 Glu Gln Pro Phe Phe Lys Glu Pro Pro Thr Glu Ala Ala Lys Glu Leu
 85 90 95
 agt ctg tagctctgcg tggagccatg tgtaaact gaactgagac ctgccacctc 461
 Ser Leu
 ctactacctta agggccatt ttcattctgat atcatcccc agaaacaaac tcatgatgac 521
 ttccatgttt ttttttagatt agatacatgg agaattttcc tttcccttag aattaaaatc 581
 ctgcattcta aaaaaaaaaa aaaa 605

<210> 190
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 3..368

<400> 190
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 Ile Arg Ala Thr Met Val Ala Arg Val Trp Ser Leu Met Arg Phe
 1 5 10 15
 ctc atc aag gga agt gtg gct ggg ggc gcc gtc tac ctg gtg tac gac 95
 Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp
 20 25 30
 cag gag ctg ctg ggg ccc agc gac aag agc cag gca gcc cta cag aag 143
 Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys
 35 40 45

gct ggg gag gtg gtc ccc ccc gcc atg tac cag ttc agc cag tac gtg	191
Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr Val	
50 55 60	
tgt cag cag aca ggc ctg cag ata ccc cag ctc cca gcc cct cca aag	239
Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys	
65 70 75	
att tac ttt ccc atc cgt gac tcc tgg aat gca ggc atc atg acg gtg	287
Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr Val	
80 85 90 95	
atg tca gct ctg tgc gtg gcc ccc tcc aag gcc cgc gag tac tcc aag	335
Met Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser Lys	
100 105 110	
gag ggc tgg gag tat gtg aag gcg cgc acc aag tagcgagtca gcaggggccg	388
Glu Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys	
115 120	
cctgccccgg ccagaacggg cagggctgcc actgacctga agactccgga ctgggacccc	448
actccgaggg cagctcccg ccttgccggc ccaataaagg acttcagaag tgaaaaaaaa	508
ataaaaaaaaa aaaaaaaa	526

<210> 191

<211> 910

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 174..527

<400> 191

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tcccttgctt gtgggcatat gtgggtcata tttccctccc atcaccctct gcacgccacc	120
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cccatcaccg ccacagaccc ccagcccttc agttgccttg cacctccttg gtg atg	176
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Met

1

cag ccg tcc ttg tta agg tca tac agg ttg aag gcc caa tta agc ctg	224
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Gln Pro Ser Leu Leu Arg Ser Tyr Arg Leu Lys Ala Gln Leu Ser Leu	
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5

10

15

tca tct aca gtt ccc cga aga atc acg gac aaa cca gcc aca aag tcc	272
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Ser Ser Thr Val Pro Arg Arg Ile Thr Asp Lys Pro Ala Thr Lys Ser	
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20

25

30

tgg gaa gga ggc agg agg gag ctg tgt cct cgg gta ctc ttc acc caa	320
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Trp Glu Gly Gly Arg Arg Glu Leu Cys Pro Arg Val Leu Phe Thr Gln	
---	--

35

40

45

ctc ctt ctc tgg gtt tgg cct gga gat cct ggc cct gaa ctc cag gaa	368
---	-----

Leu Leu Leu Trp Val Trp Pro Gly Asp Pro Gly Pro Glu Leu Gln Glu	
---	--

50

55

60

65

aca ggc ttc cct ggc cca cct cgc cca gct cac ctc aaa act gac cga	416
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Thr Gly Phe Pro Pro Pro Arg Pro Ala His Leu Lys Thr Asp Arg	
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70

75

80

gcc atc atg gtt ggt gtc aaa ggc att gaa gag aaa agt ggc ata ggt	464
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Ala Ile Met Val Gly Val Lys Gly Ile Glu Glu Lys Ser Gly Ile Gly	
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85

90

95

gct gga gtc tgc agg gtg agt gtg gag aag ttg gct tcc aca cag gag	512
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Ala Gly Val Cys Arg Val Ser Val Glu Lys Leu Ala Ser Thr Gln Glu	
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100

105

110

agg act tcc tcc ctc taaggagctc cccatacccc ccatcacctt ggcattccca	567
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Arg Thr Ser Ser Leu	
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115

gctcctccag	aatccctccc	tcctcagcc	tagagaagga	caactgcttc	cccttggggc	627
ttgtcccctc	acctccttga	ggaaagaact	gggagtaa	ctgcttgaag	ttctcctcat	687
tgacaattcc	gctgggacat	tcctggaagg	agagggcacc	aggctgaggg	cagagacaaa	747
atccccttcc	gttcaccgcc	cccaccctcc	atggcccaag	actcccaggg	aggggggataa	807
tcttcaagcc	tccagaggac	tcaccacgtg	gctcatgtga	tgggagggaa	gacttctttc	867
ccagtgcaca	aataaaaaaac	atggaacgaa	aaaaaaaaaaa	aaa		910

<210> 192
 <211> 668
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 57..203

<400> 192																
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						Met										
						1										
gag	ctc	gag	gcc	atg	agc	aga	tat	acc	agc	cca	gtg	aac	cca	cct	gtc	107
Glu	Leu	Glu	Ala	Met	Ser	Arg	Tyr	Thr	Ser	Pro	Val	Asn	Pro	Pro	Val	
			5					10					15			
ttc	ccc	cat	ctg	acc	gtg	gtg	ctt	ttg	gcc	att	ggc	atg	ttc	ttc	acc	155
Phe	Pro	His	Leu	Thr	Val	Val	Leu	Leu	Ala	Ile	Gly	Met	Phe	Phe	Thr	
			20				25				30					
gcc	tgg	ttc	ttc	gtg	tat	cct	ttc	act	gag	cag	cca	gag	gac	cag	cat	203
Ala	Trp	Phe	Phe	Val	Tyr	Pro	Phe	Thr	Glu	Gln	Pro	Glu	Asp	Gln	His	
	35				40					45						
tagtgatgtg	ggaagctcag	ggagaaacca	cgctaggtac	atggaccccg	ccggttttgt											263
acattggatt	ggggctgaga	gaagattgcc	gtgggctggg	ctctctgcac	tccacagtcc											323
accccttcgc	tttgccttaa	ctgctgtgcc	cagttacgag	gtcacctcta	ccaagtacac											383
tcgtgatatc	tataaagagc	tcctcatctc	attagtggcc	tcaactcttca	tgggcttttg											443
agtcctcttc	ctgctgctct	gggttggcat	ctacgtgtga	gcaccaagg	gtaacaacca											503
gatggcttca	ctgaaacctg	cttttgtaaa	ttactttttt	ttactgttgc	tggaagtgtc											563
ccacctgctg	ctcataataa	atgcagatgt	atagcaaaaa	aaaaaaaaaaa	aaaaaaaaaaa											623
aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaat	aaaaaaaaaaa	aaaaaa												668

<210> 193
 <211> 637
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..334

<400> 193																
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cccaggc	atg	ctg	gct	ctc	ttc	cac	ttc	cac	ctt	cca	cca	tgg	gat	gac		109
	Met	Leu	Ala	Leu	Phe	His	Phe	His	Leu	Pro	Pro	Trp	Asp	Asp		
	1				5					10						
gca	gta	aga	agg	cca	tca	gta	gat	gcc	agt	ccc	tca	acc	ttg	aac	ttt	157
Ala	Val	Arg	Arg	Pro	Ser	Val	Asp	Ala	Ser	Pro	Ser	Thr	Leu	Asn	Phe	
	15				20				25				30			
cca	gac	gca	gaa	ctt	tat	gcc	tcc	att	ttc	ctc	tgc	tgc	atg	gcc	cca	205
Pro	Asp	Ala	Glu	Leu	Tyr	Ala	Ser	Ile	Phe	Leu	Cys	Cys	Met	Ala	Pro	
			35				40						45			

gga gag att tta att agc ttt cta acc ttg gtc cag att gca cat gca	253
Gly Glu Ile Leu Ile Ser Phe Leu Thr Leu Val Gln Ile Ala His Ala	
50 55 60	
aat ggt aga gga tgc aac acc ccc gct tgt gga gct gcc gct tgt gtc	301
Asn Gly Arg Gly Cys Asn Thr Pro Ala Cys Gly Ala Ala Cys Val	
65 70 75	
tgg cat gaa aat tca caa gaa gag agg aaa tac tgaggagaaa atggcagatt	354
Trp His Glu Asn Ser Gln Glu Arg Lys Tyr	
80 85	
gtgtttgctg aatttgattg acgaagaagt caccatgaaa atcacagtga accatttgga	414
aagcaaaactg ccaaaaaaat aatagttagt catgctctca ggctgggtgt tttggctgtt	474
gtgggtttct tgcatttcca gatgattgca aagagctgtt tctcaatttc tgcaacaagt	534
gccagctgaa attttggtac cagtttcatt aaatatgtat aacaaaakaa aaaaaaaaaa	594
aaaaaaaaa aaaaaaaaaa aaaaaaagaa aaaaaaaaaa aaa	637

<210> 194
 <211> 706
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 183..443

<400> 194	
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cacagaaacc cagggccgaa gcaaagtccc aatcccagag aggctggggc acacctacaa	120
ctgaaaggag gcttagaaat ccttcagaga ccacctatc gggtctctc cacctggaca	180
gg atg agc cag caa cac aga agg aag agg cct tcc tcc gaa aga aaa	227
Met Ser Gln Gln His Arg Arg Lys Arg Pro Ser Ser Glu Arg Lys	
1 5 10 15	
agc aca aga aag atg gac aca tgg cag agt ctt aaa gtc aaa gaa gta	275
Ser Thr Arg Lys Met Asp Thr Trp Gln Ser Leu Lys Val Lys Glu Val	
20 25 30	
ttc tgt aag cat aat tct tcc tat gaa tgc ctt ctc tat aaa gag gtt	323
Phe Cys Lys His Asn Ser Ser Tyr Glu Cys Leu Leu Tyr Lys Glu Val	
35 40 45	
gaa gca aga cag gtt tct aag aca gcc acc gat ggg tcc tac ctc ctc	371
Glu Ala Arg Gln Val Ser Lys Thr Ala Thr Asp Gly Ser Tyr Leu Leu	
50 55 60	
gta ttc aca tcc tat gta atc tcc tcc cca gtg tgg act gga cct ggt	419
Val Phe Thr Ser Tyr Val Ile Ser Ser Pro Val Trp Thr Gly Pro Gly	
65 70 75	
gac ttg ctt cca gtg aat aga ata tagcaaaagt gattgatgtc acctccaaga	473
Asp Leu Leu Pro Val Asn Arg Ile	
80 85	
ttcagctata gaagactatg actatgactt tcctcttggc tagcattctc gctaaccctt	533
cctgcttgct tgtactgagc tgccctatga agaggcccat gtaggggtggc ctgggtgggg	593
gtgatctgtg gccaacagcc agcaaggaac taaatcctgt ttacaaccac atgagcttgg	653
aaggagatcc ttccccagta aagccaggag atgaatacaa aaaaaaaaaa aaa	706

<210> 195
 <211> 670
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 94..228

<400> 195

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actttttcagg ggacattcag aggcattcagc cccttcctcc tcaccagctc ccagagttcc 60
catctccatc cccaatccta aagaaggaaa tcg atg cca cgg tcc tca agg agc 114
                               Met Pro Arg Ser Ser Arg Ser
                               1           5
cct ggg gac cca ggc gcc cta ctc gaa gat ggc cca caa tcc cag acc 162
Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Gly Pro Gln Ser Gln Thr
      10           15           20
ccg gag gat tgc cca gcg agg ccg gaa cac cag cag gat ggc aga gga 210
Pro Glu Asp Cys Pro Ala Arg Pro Glu His Gln Gln Asp Gly Arg Gly
      25           30           35
cac ctc ccc aaa cat gaa tgacaacatc ctgttgctg tccgcaacaa 258
His Leu Pro Lys His Glu
40           45
tgaccaagcc ctaggcctga ctcagtgcac gctgggatgt gtgtcctggg tcacctgttt 318
tgctgtctcc ctgagaactc aggccacgca gggtctgttt aacacgtgca gatgcaagct 378
gctgtgccag aagctcatgg agaagacagg cattctgctc ctctgtgctt tcggtgtgctc 438
ccagggccct gccagtcacc aggtggaagg tatccctggg ccctggcact gattatagga 498
cactgggcaa gacactgcac cgccacgtga ctcagtttcc ccctctgcct gatgggtgtt 558
gctgtgagaa ttatgaaatg aaatgatgac catgaaaata ttgtagaagc caagaaatgc 618
ttcagaagtt ataaagctct ccccaaaccg tgttatgaaa aaaaaaaaaa aa 670
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<210> 196

<211> 510

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 133..327

<400> 196

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ctccaataacc caaaccaggg gtagttgcct aatccatcct catgtggata gctctttact 120
taggaaacct tg atg gct tat ttg gat gac aaa ggt tcc ctt ttg gcg ata 171
                               Met Ala Tyr Leu Asp Asp Lys Gly Ser Leu Leu Ala Ile
                               1           5           10
cat agc cat gcg aga caa cat agc cat gaa aca aac caa gtc cac cag 219
His Ser His Ala Arg Gln His Ser His Glu Thr Asn Gln Val His Gln
      15           20           25
tgg ctt cct agg aac aca ttt gct ttc ctg ata aaa gag gac aga tgc 267
Trp Leu Pro Arg Asn Thr Phe Ala Phe Leu Ile Lys Glu Asp Arg Cys
      30           35           40           45
agt tgc aga agt acc tgt gcc tct ttt tct ttt tct tct tct ttt tct 315
Ser Cys Arg Ser Thr Cys Ala Ser Phe Ser Phe Ser Ser Ser Phe Ser
      50           55           60
ttt tta atc tct taaatgcaga tataagaact ggtactgaag cagccatctt 367
Phe Leu Ile Ser
      65
gtgaccataa ggaagaagcc aagaacatca gaaccagtgg cctagccatt gcacagtcac 427
ctaaacacac ctctggactt gttattatgt aaaaaaaaaa aaacacctgc tcttggttatt 487
tgcaatccaa aaaaaaaaaa aaa 510
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<210> 197

<211> 500

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 22..357

<400> 197

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                        1      5      10
aaa aaa aca aat aca tac gaa gaa agt aat gca gga aat gaa gga caa      99
Lys Lys Thr Asn Thr Tyr Glu Glu Ser Asn Ala Gly Asn Glu Gly Gln
                        15      20      25
aaa gaa gct ata agc att tgt att tgc aga aga gat ggt tta ctt cct      147
Lys Glu Ala Ile Ser Ile Cys Ile Cys Arg Arg Asp Gly Leu Leu Pro
                        30      35      40
ctg tgg gta acc agg tta tca gat ttg gtg ttt tcc aaa gaa aag gca      195
Leu Trp Val Thr Arg Leu Ser Asp Leu Val Phe Ser Lys Glu Lys Ala
                        45      50      55
cat ggc atg att cca ctt ctt ggc tcc cat agg gaa aag aag aca agt      243
His Gly Met Ile Pro Leu Leu Gly Ser His Arg Glu Lys Lys Thr Ser
                        60      65      70
aaa gag atg aag act tct tcc agg aac ctg agg tac ttc att gtc tgc      291
Lys Glu Met Lys Thr Ser Ser Arg Asn Leu Arg Tyr Phe Ile Val Cys
                        75      80      85      90
aga gat gcc tca tcc tac acc cct cag tca ctc ata tct gga tac att      339
Arg Asp Ala Ser Ser Tyr Thr Pro Gln Ser Leu Ile Ser Gly Tyr Ile
                        95      100      105
gga cct tgt caa cat caa taatggacat acctctgata tttgaactct      387
Gly Pro Cys Gln His Gln
                        110
gaatctcact ctgtgaccac aactttgtat ctttctaagt ctttaatctt caacctcaca      447
gaactcttca taccctaaaa tatagtattt tcacctggaa aaaaaaaaaa aaa      500
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<211> 667

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 4..333

<400> 198

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      Met Val Phe Gly Ala Met Val Leu Leu Val Gly Leu Glu Glu Leu
      1      5      10      15
acc aat atc cgc aac gtg gag aga ctg aag aag gac ttg agg gcc agt      96
Thr Asn Ile Arg Asn Val Glu Arg Leu Lys Lys Asp Leu Arg Ala Ser
      20      25      30
tat tgc ctc atc gac agc ttc ctg ggg gac tcg gag ctc atc ggg gac      144
Tyr Cys Leu Ile Asp Ser Phe Leu Gly Asp Ser Glu Leu Ile Gly Asp
      35      40      45
ctg acc cag tgt gtg gac tgc gtg att cct cca gag ggg tcc ctc ttg      192
Leu Thr Gln Cys Val Asp Cys Val Ile Pro Pro Glu Gly Ser Leu Leu
      50      55      60
cag atc tct agc tac ctc tac tta aat act gct ctt gtg gac ttg cct      240
Gln Ile Ser Ser Tyr Leu Tyr Leu Asn Thr Ala Leu Val Asp Leu Pro
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65	70	75	
ggt gtg gcg gcc tcc cag gca tgt gac tct cag cag gtg act tgg ctt			288
Gly Val Ala Ala Ser Gln Ala Cys Asp Ser Gln Gln Val Thr Trp Leu			
80	85	90	95
ctc tac gtt gct aat ggt gcc tac tcg gca tgt aac agg cct gga			333
Leu Tyr Val Ala Asn Gly Ala Tyr Ser Ala Cys Asn Arg Pro Gly			
100	105	110	
tgaacggtag ctgctgcggt tacattatta gcttcagttt gcccgccag gctagatgtt			393
taatcagatt tcacagactt cacagtgtga gttggggatg tgacttcgta tgaaagtga			453
ggaactcagg ctgagagagg gtgagacgta ggagcatggc cactgcgcga gctcggggct			513
ggctgtgggt ttctcccat tccctgccc tctgggaagt cgctgccacc ccctacgctt			573
gtctgtgac tcccagtcct cctaaccctc cagaatgtaa acagcagcag atgaacaaaa			633
ataaaaatac aaaaggccga aaaaaaaaaa aaaa			667

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..363

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1	5
ctt ggt ctg cgg cct gtc aaa cag gtt cgg gtt cag ttc tgt ccc ttc	96
Leu Gly Leu Arg Pro Val Lys Gln Val Arg Val Gln Phe Cys Pro Phe	
20	25
gag aaa aac gtg gaa tcg acg agg acc ttc ctg cag acg gtg agc agt	144
Glu Lys Asn Val Glu Ser Thr Arg Thr Phe Leu Gln Thr Val Ser Ser	
35	40
gag aag gtc cgc tcc act aat ctc aac tgc tca gtg att gcg gac gtg	192
Glu Lys Val Arg Ser Thr Asn Leu Asn Cys Ser Val Ile Ala Asp Val	
50	55
agg cat gac ggc tcc gag ccc tgc gtg gac gtg ctg ttc gga gac ggg	240
Arg His Asp Gly Ser Glu Pro Cys Val Asp Val Leu Phe Gly Asp Gly	
65	70
cat cgc ctg att atg cgc ggc gct cat ctc acc gct ctg gaa atg ctc	288
His Arg Leu Ile Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu	
85	90
acc gcc ttc gcc tcc cac atc cgg gcc agg gac gcg gcg ggc agc ggg	336
Thr Ala Phe Ala Ser His Ile Arg Ala Arg Asp Ala Ala Gly Ser Gly	
100	105
gac aag ccg ggc gct gat act ggt cgc tgacagcgcc aaagagacca	383
Asp Lys Pro Gly Ala Asp Thr Gly Arg	
115	120
acaagatgat ttgcgtggac taggacactt aacctaagaa gagtttcact taatcattca	443
aatcactatc tgaagggtca cggagcgcaa aataaagttt aaaaccctgc taccaaaaaa	503
aaaaaaaaa a	514

<210> 200
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 <212> DNA
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<220>

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<222> 41..337
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<400> 200

[illegible]

<210> 201

<211> 551

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 1..549

<400> 201

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Arg	Glu	Gly	Ala	Arg	Ala	Arg	Pro	Ser	Pro	Thr	Met	Ser	Asp	Glu	Ala		
1				5					10					15			
tcg	gcc	atc	act	tcc	tac	gag	aag	ttt	cta	acc	ccc	gag	gag	ccc	ttc		96
Ser	Ala	Ile	Thr	Ser	Tyr	Glu	Lys	Phe	Leu	Thr	Pro	Glu	Glu	Pro	Phe		
			20					25					30				
cca	ctc	ctg	gga	cct	cct	cgc	ggg	gtg	ggc	acc	tgc	ccg	agc	gag	gag		144
Pro	Leu	Leu	Gly	Pro	Pro	Arg	Gly	Val	Gly	Thr	Cys	Pro	Ser	Glu	Glu		
		35				40					45						
ccg	ggc	tgc	ctg	gac	atc	agc	gac	ttc	ggc	tgc	cag	ctg	tcc	tcc	tgc		192
Pro	Gly	Cys	Leu	Asp	Ile	Ser	Asp	Phe	Gly	Cys	Gln	Leu	Ser	Ser	Cys		
	50					55					60						
cat	cgc	acc	gac	ccg	ctc	cac	cgc	ttc	cac	acc	aac	agg	tgg	aac	cta		240
His	Arg	Thr	Asp	Pro	Leu	His	Arg	Phe	His	Thr	Asn	Arg	Trp	Asn	Leu		
65				70					75					80			
act	tct	tgt	gga	aca	agt	gtt	gcc	agc	tca	gaa	ggc	agt	gag	gag	ctg		288
Thr	Ser	Cys	Gly	Thr	Ser	Val	Ala	Ser	Ser	Glu	Gly	Ser	Glu	Glu	Leu		
			85					90					95				
ttt	tca	tct	qtq	tct	qtt	qqa	qat	caa	qat	qat	tqc	tat	tcc	ctq	tta		336

Phe	Ser	Ser	Val	Ser	Val	Gly	Asp	Gln	Asp	Asp	Cys	Tyr	Ser	Leu	Leu		
			100					105				110					
gat	gat	cag	gac	ttc	act	tct	ttt	gat	tta	ttt	cct	gag	ggg	agt	gtc	384	
Asp	Asp	Gln	Asp	Phe	Thr	Ser	Phe	Asp	Leu	Phe	Pro	Glu	Gly	Ser	Val		
		115					120				125						
tgc	agt	gat	gtc	tct	tct	tct	att	agc	act	tac	tgg	gat	tgg	tca	gat	432	
Cys	Ser	Asp	Val	Ser	Ser	Ser	Ile	Ser	Thr	Tyr	Trp	Asp	Trp	Ser	Asp		
	130					135					140						
agc	gag	ttt	gaa	tgg	cag	tta	cca	ggc	agt	gac	att	gcc	agt	ggg	agt	480	
Ser	Glu	Phe	Glu	Trp	Gln	Leu	Pro	Gly	Ser	Asp	Ile	Ala	Ser	Gly	Ser		
145					150					155				160			
gat	gta	ctt	tct	gat	gtc	ata	ccc	agt	att	cca	agt	tca	cct	tgc	ctg	528	
Asp	Val	Leu	Ser	Asp	Val	Ile	Pro	Ser	Ile	Pro	Ser	Ser	Pro	Cys	Leu		
			165					170						175			
ctt	cct	aaa	aaa	aaa	aaa	aaa	aa									551	
Leu	Pro	Lys	Lys	Lys	Lys	Lys											
			180														

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 <212> DNA
 <213> Homo sapiens

<220>
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					Met	Ser	Asp	Glu	Ala	Ser	Ala					
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atc	act	tcc	tac	gag	aag	ttt	cta	acc	ccc	gag	gag	ccc	ttc	cca	ctc	102
Ile	Thr	Ser	Tyr	Glu	Lys	Phe	Leu	Thr	Pro	Glu	Glu	Pro	Phe	Pro	Leu	
		10				15					20					
ctg	gga	cct	cct	cgc	ggg	gtg	ggc	acc	tgc	ccg	agc	gag	gag	ccg	ggc	150
Leu	Gly	Pro	Pro	Arg	Gly	Val	Gly	Thr	Cys	Pro	Ser	Glu	Glu	Pro	Gly	
	25				30				35							
tgc	ctg	gac	atc	agc	gac	ttc	ggc	tgc	cag	ctg	tcc	tcc	tgc	cat	cgc	198
Cys	Leu	Asp	Ile	Ser	Asp	Phe	Gly	Cys	Gln	Leu	Ser	Ser	Cys	His	Arg	
40				45				50					55			
acc	gac	ccg	ctc	cac	cgc	ttc	cac	acc	aac	agg	tgg	aac	cta	act	tct	246
Thr	Asp	Pro	Leu	His	Arg	Phe	His	Thr	Asn	Arg	Trp	Asn	Leu	Thr	Ser	
			60			65					70					
tgt	gga	aca	agt	gtt	gcc	agc	tca	gaa	ggc	agt	gag	gag	ctg	ttt	tca	294
Cys	Gly	Thr	Ser	Val	Ala	Ser	Ser	Glu	Gly	Ser	Glu	Glu	Leu	Phe	Ser	
		75				80					85					
tct	gtc	tgt	tgg	aga	tca	aga	tgattgctat	tccttgtag	atgatcagga							345
Ser	Val	Cys	Trp	Arg	Ser	Arg										
			90													
cttcacttct	tttgatttat	ttcctgaggg	gagtgtctgc	agtgatgtct	cttcttctat											405
tagcacttac	tgggattggt	cagatagcga	gtttgaatgg	cagttaccag	gcagtgcacat											465
tgccagtggg	agtgatgnta	ctttctgatg	tcataccag	tattccaagt	tcaccttgc											525
tgcttcctaa	aaaaaaaaaa	aaaaa														550

<210> 203
 <211> 408
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 1..315

<400> 203
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 Ile Gly Pro Arg Ala Pro Ser Pro Ser Phe Ser Val Arg Asp Val Glu
 1 5 10 15
 ctg agc gac cca gcc cgc gag cga ggt gag atg ccg gtg gcc gtg ggt 96
 Leu Ser Asp Pro Ala Arg Glu Arg Gly Glu Met Pro Val Ala Val Gly
 20 25 30
 ccc tac gga cag tcc cag cca agc tgc ttc gac cgt gtc aaa atg ggc 144
 Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly
 35 40 45
 ttc gtg atg ggt tgc gcc gtg ggc atg gcg gcc ggg gcg ctc ttc ggc 192
 Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly
 50 55 60
 acc ttt tcc tgt ctc agg atc gga atg cgg ggt cga gag ctg atg ggc 240
 Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly
 65 70 75 80
 ggc att ggg aaa acc atg atg cag agt ggc ggc acc ttt ggc aca ttc 288
 Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe
 85 90 95
 atg gcc att ggg atg ggc atc cga tgc taaccatggt tgccaactac 335
 Met Ala Ile Gly Met Gly Ile Arg Cys
 100 105
 atctgtccct tcccatcaat ccagagccat gtactaataa aagaaagtct ttgagcaaaa 395
 aaaaaaaaaa aaa 408

<210> 204
 <211> 665
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 94..582

<400> 204
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 Met Pro Arg Ser Ser Arg Ser
 1 5
 cct ggg gac cca ggc gcc cta ctc gaa gat gtg gcc cac aat ccc aga 162
 Pro Gly Asp Pro Gly Ala Leu Glu Asp Val Ala His Asn Pro Arg
 10 15 20
 ccc cgg agg att gcc cag cga ggc cgg aac acc agc agg atg gca gag 210
 Pro Arg Arg Ile Ala Gln Arg Gly Arg Asn Thr Ser Arg Met Ala Glu
 25 30 35
 gac acc tcc cca aac atg aat gac aac atc ctg ttg cct gtc cgc aac 258
 Asp Thr Ser Pro Asn Met Asn Asp Asn Ile Leu Leu Pro Val Arg Asn
 40 45 50 55

aat gac caa gcc cta ggc ctg act cag tgc atg ctg gga tgt gtg tcc	306
Asn Asp Gln Ala Leu Gly Leu Thr Gln Cys Met Leu Gly Cys Val Ser	
60 65 70	
tgg ttc acc tgt ttt gcc tgc tcc ctg aga act cag gcc cag cag gtt	354
Trp Phe Thr Cys Phe Ala Cys Ser Leu Arg Thr Gln Ala Gln Gln Val	
75 80 85	
ctg ttt aac acg tgc aga tgc aag ctg ctg tgc cag aag ctc atg gag	402
Leu Phe Asn Thr Cys Arg Cys Lys Leu Leu Cys Gln Lys Leu Met Glu	
90 95 100	
aag aca ggc att ctg ctc ctc tgt gct ttc ggt gtg tcc cag ggc cct	450
Lys Thr Gly Ile Leu Leu Leu Cys Ala Phe Gly Val Ser Gln Gly Pro	
105 110 115	
gcc cag tcc cag gtg gag gta tcc ctg ggc cct ggc act gat tat agg	498
Ala Gln Ser Gln Val Glu Val Ser Leu Gly Pro Gly Thr Asp Tyr Arg	
120 125 130 135	
aca ctg ggc aag aca ctg cac tgc cac gtg act cag ttt ccc cat ctg	546
Thr Leu Gly Lys Thr Leu His Cys His Val Thr Gln Phe Pro His Leu	
140 145 150	
cct gat ggg tgt tgc tgt gag aat tat gaa atg aaa tgatgacat	592
Pro Asp Gly Cys Cys Cys Glu Asn Tyr Glu Met Lys	
155 160	
gaaaatattg tagaagccaa gaaatgcttc agaagttata aagctctccc caaacgcgaa	652
aaaaaaaaaa aaa	665

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 540..923

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ccaaggcagc atttcagaag gtgatccacg gcaaagccgt cccttcaaata ccgtctttgt	180
gcccaactgcc atagtcaacc ccgtgagaag cacagccggc cctgggactt taggacaagg	240
gtctcttcgga aaagggcgga gcagcatgag aaagagtaag tgggtggcaga gagatggatc	300
cctgcagaga cccctccagt ccgggatccc cactctcgtg gtaggctccc tcagacgcag	360
cccaccatg gtccttcggc ctacagcagtt ccaattctac cagccacagg ggatcacctc	420
ctccccctca gccgtggtgg tggagatggg gtccaagcct gccctcacgg gggagcccgc	480
cctcacgtgc atcagcaggg gcagtgaggc ggatccactc cgcggccagc tccctcatt	539
atg gaa gac aaa gaa atc ccc atc aag agt gag cct ctg cca aaa ccg	587
Met Glu Asp Lys Lys Glu Ile Pro Ile Lys Ser Glu Pro Leu Pro Lys Pro	
1 5 10 15	
ccc gca tct gcc cca cca tcc atc ctg gtg aaa cca gaa aac tca aga	635
Pro Ala Ser Ala Pro Pro Ser Ile Leu Val Lys Pro Glu Asn Ser Arg	
20 25 30	
aat gga atc gaa aag caa gtc aaa acc gtg aga ttt cag aat tac agc	683
Asn Gly Ile Glu Lys Gln Val Lys Thr Val Arg Phe Gln Asn Tyr Ser	
35 40 45	
cct cct ccc acc aaa cat tac acc tcc cat ccc acc tcc gga aag cct	731
Pro Pro Pro Thr Lys His Tyr Thr Ser His Pro Thr Ser Gly Lys Pro	
50 55 60	
gaa cag cca gcc acc ctc aag gcg tcc cag cct gaa gca gcg tcc ttg	779
Glu Gln Pro Ala Thr Leu Lys Ala Ser Gln Pro Glu Ala Ala Ser Leu	
65 70 75 80	

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ggc cca gag atg acc gtc cta ttt gcc cac cga agt ggc tgc cac tcc      827
Gly Pro Glu Met Thr Val Leu Phe Ala His Arg Ser Gly Cys His Ser
      85      90      95
gga cag cag aca gac ctc cgg aga aag tca gct ctt gcc aag gcc aca      875
Gly Gln Gln Thr Asp Leu Arg Arg Lys Ser Ala Leu Ala Lys Ala Thr
      100      105      110
acc ctg gtg tcc act gcc tca ggc acg cag acc gtg ttt ccc agc aaa      923
Thr Leu Val Ser Thr Ala Ser Gly Thr Gln Thr Val Phe Pro Ser Lys
      115      120      125
tgaacctacg ggtggctttt cctagacccc aaagaggtga attgcattta aatacagtct      983
gcctycactg aaaaaaaaaa aaaaaa      1008

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<210> 206
 <211> 455
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 77..364

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<400> 206
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      Met Leu Thr Arg Val Glu Glu Gln Lys Lys Met Val
      1      5      10
aag gcc tgc agg tat agg tgt tca gca tgt cat ctg aaa tat tcc cca      160
Lys Ala Cys Arg Tyr Arg Cys Ser Ala Cys His Leu Lys Tyr Ser Pro
      15      20      25
cag agg caa aaa gaa agg aaa tta tct ctg aaa agg ggg agg aca agt      208
Gln Arg Gln Lys Glu Arg Lys Leu Ser Leu Lys Arg Gly Arg Thr Ser
      30      35      40
cag cag aat atg tca atg ttt tgg ttg aag aag ctg ctt gaa tct ggg      256
Gln Gln Asn Met Ser Met Phe Trp Leu Lys Lys Leu Leu Glu Ser Gly
      45      50      55      60
ctt ttc tgt gcc atg tgt tct ccc agg gcc agc aca aag aag ggc ttt      304
Leu Phe Cys Ala Met Cys Ser Pro Arg Ala Ser Thr Lys Lys Gly Phe
      65      70      75
tgg tgc agg ccc aag acc acc ata atc atc att gat tat tcc tct cca      352
Trp Cys Arg Pro Lys Thr Thr Ile Ile Ile Ile Asp Tyr Ser Ser Pro
      80      85      90
cgc cag tgt ctc taaataaaact ttctcttctt tctctgaaaa aaaaaaaaaa      404
Arg Gln Cys Leu
      95
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaagaaaa aaaaaaaaaa a      455

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<210> 207
 <211> 749
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 65..544

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<400> 207
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tacc atg ggg aaa atc gcg ctg caa ctc aaa gcc acg ctg gag aac atc      109

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	Met	Gly	Lys	Ile	Ala	Leu	Gln	Leu	Lys	Ala	Thr	Leu	Glu	Asn	Ile	
	1				5					10					15	
acc aac ctc cgg ccc gtg ggc gag gac ttc cgg tgg tac ctg aag atg																157
Thr Asn Leu Arg Pro Val Gly Glu Asp Phe Arg Trp Tyr Leu Lys Met																
					20					25					30	
aaa tgt ggc aac tgt ggt gag att tcg gac aag tgg cag tac atc cgg																205
Lys Cys Gly Asn Cys Gly Glu Ile Ser Asp Lys Trp Gln Tyr Ile Arg																
					35					40					45	
ctg atg gac agt gtg gca ctg aag ggg ggc cgt ggc agt gct tcc atg																253
Leu Met Asp Ser Val Ala Leu Lys Gly Gly Arg Gly Ser Ala Ser Met																
					50					55					60	
gtc cag aag tgc aag ctg tgt gca aga gaa aat tcc atc gag att tta																301
Val Gln Lys Cys Lys Leu Cys Ala Arg Glu Asn Ser Ile Glu Ile Leu																
					65					70					75	
agc agc acc atc aag cct tac aat gct gaa gac aat gag aac ttc aag																349
Ser Ser Thr Ile Lys Pro Tyr Asn Ala Glu Asp Asn Glu Asn Phe Lys																
					80					85					90	
aca ata gtg gag ttt gag tgc cgg ggc ctt gaa cca gtt gat ttc cag																397
Thr ile Val Glu Phe Glu Cys Arg Gly Leu Glu Pro Val Asp Phe Gln																
					100					105					110	
ccg cas gwg rtw ttg ctg ctg aag gtg tgg agt cag gga cag cct tca																445
Pro Xaa Xaa Xaa Leu Leu Leu Lys Val Trp Ser Gln Gly Gln Pro Ser																
					115					120					125	
gtg aca tta atc tgc agg aga agg act ggg act gac tat gat gaa aag																493
Val Thr Leu Ile Cys Arg Arg Arg Thr Gly Thr Asp Tyr Asp Glu Lys																
					130					135					140	
gcc cag gag tct gtg gga atc tat gag gtc acc cac cag ttt gtg aag																541
Ala Gln Glu Ser Val Gly Ile Tyr Glu Val Thr His Gln Phe Val Lys																
					145					150					155	
tgc tgatccctct tccttcccag ttgcccttaa gaactgagaa aggacaaagt																594
Cys																
					160											
actctaagca gcagagccca cagaggctcg ttcctttgac ccttgctctcc tgggtggctat																654
acgaaacctt cacaatctgc atgctggact ttattacagc ttcccaagcc ccatcaataa																714
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<210> 208
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 117..467

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	Met
	1
gac tcc ctg gct gct gga gag ttg aat gcc agc cac cag cca tgg gtg	167
Asp Ser Leu Ala Ala Gly Glu Leu Asn Ala Ser His Gln Pro Trp Val	
	5
	10
cca gag ttt gta gcc tat tgg agg aaa aca cac caa gat cac ctc tgc	215
Pro Glu Phe Val Ala Tyr Trp Arg Lys Thr His Gln Asp His Leu Cys	
	20
	25
agc ctg cac agc cgg gcc ttt gga ctc ctg gat gct aga gtg acc tgg	263
Ser Leu His Ser Arg Ala Phe Gly Leu Leu Asp Ala Arg Val Thr Trp	

35	40	45	
gcg ctg agg agg gcc ccc gag cca gta cca gga aag gat aga ctc ctg			311
Ala Leu Arg Arg Ala Pro Glu Pro Val Pro Gly Lys Asp Arg Leu Leu			
50	55	60	65
ctt gca gca ttc cca gca gag gca tcg cct gtg gac acc gcg tct gtg			359
Leu Ala Ala Phe Pro Ala Glu Ala Ser Pro Val Asp Thr Ala Ser Val			
70	75	80	
tct gta tat ggc aga gct ccc aga tat atg cac aag gga gtg aaa aaa			407
Ser Val Tyr Gly Arg Ala Pro Arg Tyr Met His Lys Gly Val Lys Lys			
85	90	95	
tgt gtt tgc acc cca gtc tct aaa aat tca aca gcc tgg tta ctt ctg			455
Cys Val Cys Thr Pro Val Ser Lys Asn Ser Thr Ala Trp Leu Leu Leu			
100	105	110	
ggg ggt ata tcg taggtggctt taatacgtgt tatttgctca tctgtatttc			507
Gly Gly Ile Ser			
115			
ttactctttg cacaattaaa ccatgttctt tttacttatg tacattttta ataaaagaaa			567
gttggttaacg aaaaaaaaaa aaaaaaa			591

<210> 209
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 893..1897

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gcccttgagt ggcgggggtgg acagcgcagc caccgcctgc ctcactact cc atg tgc	898		
	Met Cys		
	1		
tgc cag gtc tgc gag gcc gtg agg agt gga aat gag gaa gtg ctg gct	946		
Cys Gln Val Cys Glu Ala Val Arg Ser Gly Asn Glu Glu Val Leu Ala			
5	10	15	
gat gtc cgc acc atc gtg aac cag atc agc tac acc ccc cag gat ccc	994		
Asp Val Arg Thr Ile Val Asn Gln Ile Ser Tyr Thr Pro Gln Asp Pro			
20	25	30	
cga gac ctc tgt gga cgc ata ctg acc acc tgc tac atg gcc agc aag	1042		
Arg Asp Leu Cys Gly Arg Ile Leu Thr Thr Cys Tyr Met Ala Ser Lys			
35	40	45	50
aac tcc tcc cag gag acg tgc acc cgg gcc aga gag ttg gcc cag cag	1090		
Asn Ser Ser Gln Glu Thr Cys Thr Arg Ala Arg Glu Leu Ala Gln Gln			
55	60	65	

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Ile Gly Ser His His Ile Ser Leu Asn Ile Asp Pro Ala Val Lys Ala	
70 75 80	
gtc atg ggc atc ttc agc ctg gtg acg ggg aag agc cct ctg ttt gca	1186
Val Met Gly Ile Phe Ser Leu Val Thr Gly Lys Ser Pro Leu Phe Ala	
85 90 95	
gct cat gga gga agc agc agg gaa aac ctg gcg ctg caa aat gtg cag	1234
Ala His Gly Gly Ser Ser Arg Glu Asn Leu Ala Leu Gln Asn Val Gln	
100 105 110	
gct cga ata cgg atg gtc ctc gcc tat ctg ttt gct cag ttg agc ctc	1282
Ala Arg Ile Arg Met Val Leu Ala Tyr Leu Phe Ala Gln Leu Ser Leu	
115 120 125 130	
tgg tct cgg ggt gtc cac ggt ggg ctc ctc gtg ctg gga tcc gcc aac	1330
Trp Ser Arg Gly Val His Gly Gly Leu Leu Val Leu Gly Ser Ala Asn	
135 140 145	
gtg gat gag agt ctc ctg ggc tac ctg acc aag tac gac tgc tcc agt	1378
Val Asp Glu Ser Leu Leu Gly Tyr Leu Thr Lys Tyr Asp Cys Ser Ser	
150 155 160	
gcg gac atc aac ccc ata ggc ggg atc agc aag acg gac ctc agg gcc	1426
Ala Asp Ile Asn Pro Ile Gly Gly Ile Ser Lys Thr Asp Leu Arg Ala	
165 170 175	
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Phe Val Gln Phe Cys Ile Gln Arg Phe Gln Leu Pro Ala Leu Gln Ser	
180 185 190	
atc ctg ttg gcg ccg gcc acc gca gag ctg gag ccc ttg gct gat gga	1522
Ile Leu Leu Ala Pro Ala Thr Ala Glu Leu Glu Pro Leu Ala Asp Gly	
195 200 205 210	
cag gtg tcc cag acc gac gag gaa gat atg ggg atg aca tat gcg gag	1570
Gln Val Ser Gln Thr Asp Glu Glu Asp Met Gly Met Thr Tyr Ala Glu	
215 220 225	
ctc tcg gtc tat ggg aaa ctc agg aag gtg gcc aag atg ggg ccc tac	1618
Leu Ser Val Tyr Gly Lys Leu Arg Lys Val Ala Lys Met Gly Pro Tyr	
230 235 240	
agc atg ttc tgc aaa ctc ctc ggc atg tgg aga cac atc tgc acc ccg	1666
Ser Met Phe Cys Lys Leu Leu Gly Met Trp Arg His Ile Cys Thr Pro	
245 250 255	
aga cag gtc gct gac aaa gtg aag cgg ttt ttc tcc aag tac tcc atg	1714
Arg Gln Val Ala Asp Lys Val Lys Arg Phe Phe Ser Lys Tyr Ser Met	
260 265 270	
aac aga cac aag atg acc acg ctc aca ccc gcg tac cac gcc gag aac	1762
Asn Arg His Lys Met Thr Thr Leu Thr Pro Ala Tyr His Ala Glu Asn	
275 280 285 290	
tac agc cct gag gac aac agg ttt gat ctg cga cca ttt ctg tac aac	1810
Tyr Ser Pro Glu Asp Asn Arg Phe Asp Leu Arg Pro Phe Leu Tyr Asn	
295 300 305	
aca agc tgg cct tgg cag ttt cgg tgc ata gaa aat cag gtg cta cag	1858
Thr Ser Trp Pro Trp Gln Phe Arg Cys Ile Glu Asn Gln Val Leu Gln	
310 315 320	
ctc gag agg gca gag cca cag tcc ctg gac ggc gtg gac tgaggccggt	1907
Leu Glu Arg Ala Glu Pro Gln Ser Leu Asp Gly Val Asp	
325 330 335	
tccttccttg aggctcctg tcctcgggga cccagcacc tcatcatcag cattgctgga	1967
gccaagggtta ggagccctac actaggagcc caggatggga cggcgcatca gccgagaggg	2027
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aaaaaaaaa a	2098

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<211> 428

<212> DNA
<213> Homo sapiens

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<222> 85..342

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ctacaattta cagttcctct atcc atg tgc tgg gtt ata aat cat gcc atc 111
Met Cys Trp Val Ile Asn His Ala Ile
1 5
ctc cct aga atg aga atg cac agc aag cgg cag aca atc acc cgg cat 159
Leu Pro Arg Met Arg Met His Ser Lys Arg Gln Thr Ile Thr Arg His
10 15 20 25
tcg gca tct ctt tct ttt cac gcg ctc cct cgc tcc gcc ttt ctc cag 207
Ser Ala Ser Leu Ser Phe His Ala Leu Pro Arg Ser Ala Phe Leu Gln
30 35 40
ctc tgc ctt ctc agg cag ata cat cag ata cct tgt tta tcc atc ttc 255
Leu Cys Leu Leu Arg Gln Ile His Gln Ile Pro Cys Leu Ser Ile Phe
45 50 55
agc tcc act ctg agg gcg cag acg cac gat tcc ggg atc ggg tgc acc 303
Ser Ser Thr Leu Arg Ala Gln Thr His Asp Ser Gly Ile Gly Cys Thr
60 65 70
acg gcg aas cca ggc ggg aga cgg cag gag cag ctc agg taaccagggg 352
Thr Ala Xaa Pro Gly Gly Arg Arg Gln Glu Gln Leu Arg
75 80 85
aagcttgctg gcccacggag atgcagccgt ggagctgtga ggaaagacgg tctggcttca 412
aaaaaaaaa aaaaaa 428

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<212> DNA
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<222> 155..433

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gaatggtgga tgctgtgggg caccacctcc ttgaggacca aggcactcca gctgccagga 120
atttggtctg taacctcaca cagctgagcc ttcc atg aaa att gct ctc tgc caa 175
Met Lys Ile Ala Leu Cys Gln
1 5
aga gaa ctt cct agt cca agg tca tgt cta ctc tcc aga gat gtg act 223
Arg Glu Leu Pro Ser Pro Arg Ser Cys Leu Leu Ser Arg Asp Val Thr
10 15 20
gga gtg att tgc acc cgg atg cct aga ctc gcc atc tgc tca aag act 271
Gly Val Ile Cys Thr Arg Met Pro Arg Leu Ala Ile Cys Ser Lys Thr
25 30 35
gct cag aaa gcc ctc cca tgc att ccc ctg ctg cat acc agc cca ctc 319
Ala Gln Lys Ala Leu Pro Cys Ile Pro Leu Leu His Thr Ser Pro Leu
40 45 50 55
tgc ctg cag ctg ctg tct gca gga ctt cat atc tat gcc aca ctg tgt 367
Cys Leu Gln Leu Leu Ser Ala Gly Leu His Ile Tyr Ala Thr Leu Cys
60 65 70
aaa agc tgt gct tca aga aat cac aaa aac att ttc ctg cac cta cta 415

Lys Ser Cys Ala Ser Arg Asn His Lys Asn Ile Phe Leu His Leu Leu
75 80 85
cac agc ctg agt gcg gca taagttgacc ttgcttgcta agaaatgggg 463
His Ser Leu Ser Ala Ala
90
caagaaatgc ttttttgtat gtgtcatgtc tgtttgtttt tcaattaaga gaggaaagca 523
ttaggcagat ggaatgtaca tgtgaggatg aggagacaga aaacaagtag ccctttccat 583
caagatagag ggttttctgg ggttgctggc tattgaatgt cactcctgat ttctctttcc 643
aaggcactgt accaccagcc tactgagatt gtgtgggagc tttcatgggg gttgtatttc 703
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aaaaaa 769

<210> 212
<211> 914
<212> DNA
<213> Homo sapiens

<220>
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<222> 63..386

<400> 212
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tc atg gcg gtc cga gct tcg ttc gag aac aac tgt gag atc ggc tgc 107
Met Ala Val Arg Ala Ser Phe Glu Asn Asn Cys Glu Ile Gly Cys
1 5 10 15
ttt gcc aag ctc acc aac acc tac tgt ctg gta gcg atc gga ggc tca 155
Phe Ala Lys Leu Thr Asn Thr Tyr Cys Leu Val Ala Ile Gly Gly Ser
20 25 30
gag aac ttc tac agt gtg ttc gag ggc gag ctc tcc gat acc atc ccc 203
Glu Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro
35 40 45
gtg gtg cac gcg tct atc gcc ggc tgc cgc atc atc ggg cgc atg tgt 251
Val Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys
50 55 60
gtg gga gac aga aga aat tct ggc aga tgt gct caa ggt gga agt ctt 299
Val Gly Asp Arg Arg Asn Ser Gly Arg Cys Ala Gln Gly Gly Ser Leu
65 70 75
cag aca gac agt ggc cga cca ggt gct agt agg aag cta ctg tgt ctt 347
Gln Thr Asp Ser Gly Arg Pro Gly Ala Ser Arg Lys Leu Leu Cys Leu
80 85 90 95
cag caa tca ggg agg gct ggt gca tcc caa gac ttc aat tgaagaccag 396
Gln Gln Ser Gly Arg Ala Gly Ala Ser Gln Asp Phe Asn
100 105
gatgagctgt cctctcttct tcaagtcccc cttgtggcgg ggactgtgaa ccgaggcagt 456
gaggtgattg ctgctgggat ggtggtgaat gactggtgtg ccttctgtgg cctggacaca 516
accagcacag agctgtcagt ggtggagagt gtcttcaagc tgaatgaagc ccagcctagc 576
accattgcca ccagcatgcg ggattccctc attgacagcc tcacctgagt caccttccaa 636
gttgttccat gggctcctgg ctctggactg tggccaacct tctccacatt ccgccaatc 696
tgtacctgat gctggcaggg aggtggcaga gagctcactg ggactgaggg gctgggcacc 756
caaccctttt ccacctgtgc ttatcgcttg gatctatcat tactgcaaaa acctgctctg 816
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cattaaagtg cagttccctc caaaaaaaaa aaaaaaaa 914

<210> 213
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<212> DNA
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<220>
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 <222> 460..1290

<400> 213

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ggcttggatt	tggatattct	caacagaaag	ggttaaaggc	tgatgggtacc	taaagcctgg	180
tacttgaatt	ttgatcaaga	taagctgcct	taagttctct	tcattacaca	aatgatccta	240
gataattgat	agatcctgtg	gttcaactgg	atttctagat	agaagctgga	ttcatgtgat	300
gccagaggag	taaaatttca	agagactgaa	accagatctg	agtttcgctg	ttccagtcctg	360
gacctctttg	gtgctgtaaa	tcttgatat	actgtagatg	agtactgcgt	ttttctttta	420
tggactctct	tcagcttctg	gagacctcac	tatcctatt	atg tct ttg tgt gaa		474
				Met Ser Leu Cys Glu		
				1	5	
gac atg ctg ctt tgt aat tat cga aag tgt cgc atc aaa ctc tct ggc						522
Asp Met Leu Leu Cys Asn Tyr Arg Lys Cys Arg Ile Lys Leu Ser Gly						
	10		15		20	
tat gca tgg gtc act gcc tgc tct cac atc ttc tgt gat cag cat ggc						570
Tyr Ala Trp Val Thr Ala Cys Ser His Ile Phe Cys Asp Gln His Gly						
	25		30		35	
agt ggt gag ttt agt cgc tca cca gct atc tgt cct gcc tgc aac agt						618
Ser Gly Glu Phe Ser Arg Ser Pro Ala Ile Cys Pro Ala Cys Asn Ser						
	40		45		50	
acc ctt tct gga aag cta gat att gtc cgc aca gaa ctc agt cca tca						666
Thr Leu Ser Gly Lys Leu Asp Ile Val Arg Thr Glu Leu Ser Pro Ser						
	55		60		65	
gag gaa tat aaa gct atg gta ttg gca gga ctg cga cca gag atc gtg						714
Glu Glu Tyr Lys Ala Met Val Leu Ala Gly Leu Arg Pro Glu Ile Val						
	70		75		80	85
ttg gac att agc tcc cga gcg ctg gcc ttc tgg aca tat cag gta cat						762
Leu Asp Ile Ser Ser Arg Ala Leu Ala Phe Trp Thr Tyr Gln Val His						
	90		95		100	
cag gaa cgt ctc tat caa gaa tac aat ttc agc aag gct gag ggc cat						810
Gln Glu Arg Leu Tyr Gln Glu Tyr Asn Phe Ser Lys Ala Glu Gly His						
	105		110		115	
ctg aaa cag atg gag aag ata tat act cag caa ata caa agc aag gat						858
Leu Lys Gln Met Glu Lys Ile Tyr Thr Gln Gln Ile Gln Ser Lys Asp						
	120		125		130	
gta gaa ttg acc tct atg aaa ggg gag gtt acc tcc atg aag aaa gta						906
Val Glu Leu Thr Ser Met Lys Gly Glu Val Thr Ser Met Lys Lys Val						
	135		140		145	
cta gaa gaa tac aag aaa aag ttc agt gac atc tct gag aaa ctt atg						954
Leu Glu Glu Tyr Lys Lys Lys Phe Ser Asp Ile Ser Glu Lys Leu Met						
	150		155		160	165
gag cgc aat cgt cag tat caa aag ctc caa ggc ctc tat gat agc ctt						1002
Glu Arg Asn Arg Gln Tyr Gln Lys Leu Gln Gly Leu Tyr Asp Ser Leu						
	170		175		180	
agg cta cga aac atc act att gct aac cat gaa ggc acc ctt gaa cca						1050
Arg Leu Arg Asn Ile Thr Ile Ala Asn His Glu Gly Thr Leu Glu Pro						
	185		190		195	
tcc atg att gca cag tct ggt gtt ctt ggc ttc cca tta ggt aac aac						1098
Ser Met Ile Ala Gln Ser Gly Val Leu Gly Phe Pro Leu Gly Asn Asn						
	200		205		210	
tcc aag ttt cct ttg gat aat aca cct gtt cga aat cgg ggc gat gga						1146
Ser Lys Phe Pro Leu Asp Asn Thr Pro Val Arg Asn Arg Gly Asp Gly						
	215		220		225	

gat gga gat ttt cag ttc aga cca ttt ttt gcg ggt tct ccc aca gca	1194
Asp Gly Asp Phe Gln Phe Arg Pro Phe Phe Ala Gly Ser Pro Thr Ala	
230 235 240 245	
cct gaa ccc agc aac agc ttt ttt agt ttt gtc tct cca agt cgt gaa	1242
Pro Glu Pro Ser Asn Ser Phe Phe Ser Phe Val Ser Pro Ser Arg Glu	
250 255 260	
tta gag cag cag caa gtt tct agc agg gcc ttc aaa gta aaa aga att	1290
Leu Glu Gln Gln Gln Val Ser Ser Arg Ala Phe Lys Val Lys Arg Ile	
265 270 275	
tgagccacgc atagtgtcac gcacctgtga tcccagctac ttaggagggtt gaggctggga	1350
ggatcacttg agcccaggag tctgaggctt tagtgatcta agatcatgcc actgcactcc	1410
agcctgggca acagagtga accctgtttc taaaaaaaaa taaagataat ttagctaact	1470
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<210> 214

<211> 776

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 21..539

<400> 214

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1 5 10	
ggt tac cta acc ttc tat gga gaa gtt gaa gat gaa tta ctt cat gcc	101
Gly Tyr Leu Thr Phe Tyr Gly Glu Val Glu Asp Glu Leu Leu His Ala	
15 20 25	
tac agc aaa gtg tat aca tta gac atc cct ctt ctc atg gtt cgc ctg	149
Tyr Ser Lys Val Tyr Thr Leu Asp Ile Pro Leu Leu Met Val Arg Leu	
30 35 40	
gca gtc ctt gtg gca gta aca cta act gtg ccc att gtc ctc ttc cca	197
Ala Val Leu Val Ala Val Thr Leu Thr Val Pro Ile Val Leu Phe Pro	
45 50 55	
att cgt aca tca gtg atc aca ctg tta ttt ccc aaa cga ccc ttc agc	245
Ile Arg Thr Ser Val Ile Thr Leu Leu Phe Pro Lys Arg Pro Phe Ser	
60 65 70 75	
tgg ata cga cat ttc ctg att gca gct gtg ctt att gca ctt aat aat	293
Trp Ile Arg His Phe Leu Ile Ala Ala Val Leu Ile Ala Leu Asn Asn	
80 85 90	
gtt ctg gtc atc ctt gtg cca act ata aaa tac atc ttc gga ttc ata	341
Val Leu Val Ile Leu Val Pro Thr Ile Lys Tyr Ile Phe Gly Phe Ile	
95 100 105	
ggg gct tct tct gcc act atg ctg att ttt att ctt cca gca gtt ttt	389
Gly Ala Ser Ser Ala Thr Met Leu Ile Phe Ile Leu Pro Ala Val Phe	
110 115 120	
tat ctt aaa ctt gtc aag aaa gaa act ttt agg tca ccc caa aag gtc	437
Tyr Leu Lys Leu Val Lys Lys Glu Thr Phe Arg Ser Pro Gln Lys Val	
125 130 135	
ggg gct tta att ttc ctt gtg gtt gga ata ttc ttc atg att gga agc	485
Gly Ala Leu Ile Phe Leu Val Val Gly Ile Phe Phe Met Ile Gly Ser	
140 145 150 155	
atg gca ctc att ata att gac tgg att tat gat cct cca aat tcc aag	533
Met Ala Leu Ile Ile Ile Asp Trp Ile Tyr Asp Pro Pro Asn Ser Lys	
160 165 170	
cat cac taacacaagg aaaaatactt tctttttcta ttggaaatgg ttacaagtta	589

His His
tactccaaaa gatatttgaa ttatcttgat tggaatgtta ttcataggaa ataacaggaa 649
gattccaaag acgtttacca gtmatatcac caggcacctg cagaagagga aaatcactgt 709
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aaaaaaa 776

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<212> DNA
<213> Homo sapiens

<220>
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<222> 34..1143

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Met Ser Ala Ser Ala Ala Thr
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ggg gtc ttc gtg ctg tcc ctc tcg gcc atc ccg gtc acc tat gtc ttc 102
Gly Val Phe Val Leu Ser Leu Ser Ala Ile Pro Val Thr Tyr Val Phe
10 15 20
aac cac ctg gcg gcc cag cat gat tcc tgg act att gta ggg gtt gct 150
Asn His Leu Ala Ala Gln His Asp Ser Trp Thr Ile Val Gly Val Ala
25 30 35
gcc ctc atc ctg ttc ctg gta gca ctg ctg gct cgt gtc ctc gtc aaa 198
Ala Leu Ile Leu Phe Leu Val Ala Leu Leu Ala Arg Val Leu Val Lys
40 45 50 55
aga aaa cca ccc cgg gac cca ctg ttc tat gtg tat gca gtt ttt gga 246
Arg Lys Pro Pro Arg Asp Pro Leu Phe Tyr Val Tyr Ala Val Phe Gly
60 65 70
ttt acc agc gtg gtg aac ctc atc ata gga ctg gag caa gat gga atc 294
Phe Thr Ser Val Val Asn Leu Ile Ile Gly Leu Glu Gln Asp Gly Ile
75 80 85
att gac ggg ttc atg aca cac tac ttg aga gag ggt gaa ccg tat ctg 342
Ile Asp Gly Phe Met Thr His Tyr Leu Arg Glu Gly Glu Pro Tyr Leu
90 95 100
aac acc gca tat ggg cac atg atc tgc tac tgg gat ggc tct gct cat 390
Asn Thr Ala Tyr Gly His Met Ile Cys Tyr Trp Asp Gly Ser Ala His
105 110 115
tat ctg atg tac ctg gtg atg gtg gca gcc ata gca tgg gag gaa act 438
Tyr Leu Met Tyr Leu Val Met Val Ala Ala Ile Ala Trp Glu Glu Thr
120 125 130 135
tat aga acc att ggc cta tat tgg gtt gga tct att att atg agt gtt 486
Tyr Arg Thr Ile Gly Leu Tyr Trp Val Gly Ser Ile Ile Met Ser Val
140 145 150
gtt gtt ttt gtg cca gga aac att gta ggg aag tat gga aca cga att 534
Val Val Phe Val Pro Gly Asn Ile Val Gly Lys Tyr Gly Thr Arg Ile
155 160 165
tgc cct gct ttt ttc tta agc ata cca tat act tgt ctt cct gtc tgg 582
Cys Pro Ala Phe Phe Leu Ser Ile Pro Tyr Thr Cys Leu Pro Val Trp
170 175 180
gct ggt ttc aga atc tat aat cag cca tca gaa aat tat aat tac ccc 630
Ala Gly Phe Arg Ile Tyr Asn Gln Pro Ser Glu Asn Tyr Asn Tyr Pro
185 190 195
tca aag gtt att caa gaa gcc caa gcg aaa gac ctg ctg aga aga cca 678
Ser Lys Val Ile Gln Glu Ala Gln Ala Lys Asp Leu Leu Arg Arg Pro
200 205 210 215

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Phe Asp Leu Met Leu Val Val Cys Leu Leu Leu Ala Thr Gly Phe Cys	
220 225 230	
ctg ttc aga ggt ttg att gct ttg gat tgc cca tct gag ctc tgc cga	774
Leu Phe Arg Gly Leu Ile Ala Leu Asp Cys Pro Ser Glu Leu Cys Arg	
235 240 245	
tta tat acg caa ttt caa gag ccc tat cta aag gat cct gct gct tat	822
Leu Tyr Thr Gln Phe Gln Glu Pro Tyr Leu Lys Asp Pro Ala Ala Tyr	
250 255 260	
cct aaa att cag atg ctg gca tat atg ttc tat tct gtt cct tac ttt	870
Pro Lys Ile Gln Met Leu Ala Tyr Met Phe Tyr Ser Val Pro Tyr Phe	
265 270 275	
gtg act gca ctg tat ggc tta gtg gtt cct gga tgt tcc tgg atg cct	918
Val Thr Ala Leu Tyr Gly Leu Val Val Pro Gly Cys Ser Trp Met Pro	
280 285 290 295	
gac atc aca ttg ata cat gct gga ggt ctg gct cag gct cag ttt tct	966
Asp Ile Thr Leu Ile His Ala Gly Gly Leu Ala Gln Ala Gln Phe Ser	
300 305 310	
cac att ggt gca tct ctt cat gct aga act gct tat gtc tac aga gtc	1014
His Ile Gly Ala Ser Leu His Ala Arg Thr Ala Tyr Val Tyr Arg Val	
315 320 325	
cct gaa gaa gca aaa atc ctt ttt tta gca tta aac ata gca tat gga	1062
Pro Glu Glu Ala Lys Ile Leu Phe Leu Ala Leu Asn Ile Ala Tyr Gly	
330 335 340	
gtt ctt cct cag ctc ttg gcc tat cgt tgt atc tac aaa cca gag ttc	1110
Val Leu Pro Gln Leu Leu Ala Tyr Arg Cys Ile Tyr Lys Pro Glu Phe	
345 350 355	
ttc ata aaa aca aag gca gaa gaa aaa gtg gaa taaaaatatt acttcatggt	1163
Phe Ile Lys Thr Lys Ala Glu Glu Lys Val Glu	
360 365 370	
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<222> 6..1184

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Glu Pro Arg Pro Gly Phe His Gly Val Leu Gly Ile Asn Ser Ile Thr	
20 25 30	
ggg aag gag gag cct ctg tac ccc agc tac aag aga cag ttg cgc att	146
Gly Lys Glu Glu Pro Leu Tyr Pro Ser Tyr Lys Arg Gln Leu Arg Ile	
35 40 45	
tac ctg gtc tcc ctg cca ttc gtg tgc ctc tgc ctc tat ttc tca ctg	194
Tyr Leu Val Ser Leu Pro Phe Val Cys Leu Cys Leu Tyr Phe Ser Leu	
50 55 60	

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Tyr Val Met Met Ile Tyr Phe Asp Met Glu Val Trp Ala Leu Gly Leu	
65 70 75	
cat gag aac agc ggg tct gag tgg acc agt gtc ctg ttg tat gtg ccc	290
His Glu Asn Ser Gly Ser Glu Trp Thr Ser Val Leu Leu Tyr Val Pro	
80 85 90 95	
agc atc atc tat gcc att gtg att gag atc atg aat cgt ctc tat cga	338
Ser Ile Ile Tyr Ala Ile Val Ile Glu Ile Met Asn Arg Leu Tyr Arg	
100 105 110	
tat gct gcc gag ttt tta act tca tgg gag aat cac aga ttg gaa tct	386
Tyr Ala Ala Glu Phe Leu Thr Ser Trp Glu Asn His Arg Leu Glu Ser	
115 120 125	
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Ala Tyr Gln Asn His Leu Ile Leu Lys Val Leu Val Phe Asn Phe Leu	
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Asn Cys Phe Ala Ser Leu Phe Tyr Ile Ala Phe Val Leu Lys Asp Met	
145 150 155	
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Lys Leu Leu Arg Gln Ser Leu Ala Thr Leu Leu Ile Thr Ser Gln Ile	
160 165 170 175	
ctc aac caa att atg gaa tct ttt ctt cct tat tgg ctc caa agg aag	578
Leu Asn Gln Ile Met Glu Ser Phe Leu Pro Tyr Trp Leu Gln Arg Lys	
180 185 190	
cat ggt gtg cgg gtg aag agg aag gtg cag gct tta aag gca gac att	626
His Gly Val Arg Val Lys Arg Lys Val Gln Ala Leu Lys Ala Asp Ile	
195 200 205	
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Asp Ala Thr Leu Tyr Glu Gln Val Ile Leu Glu Lys Glu Met Gly Thr	
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Tyr Leu Gly Thr Phe Asp Asp Tyr Leu Glu Leu Phe Leu Gln Phe Gly	
225 230 235	
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Tyr Val Ser Leu Phe Ser Cys Val Tyr Pro Leu Ala Ala Ala Phe Ala	
240 245 250 255	
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Val Leu Asn Asn Phe Thr Glu Val Asn Ser Asp Ala Leu Lys Met Cys	
260 265 270	
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Arg Val Phe Lys Arg Pro Phe Ser Glu Pro Ser Ala Asn Ile Gly Val	
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tgg cag ttg gct ttt gaa acg atg agt gtt ata tct gtg gtc act aac	914
Trp Gln Leu Ala Phe Glu Thr Met Ser Val Ile Ser Val Val Thr Asn	
290 295 300	
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Cys Ala Leu Ile Gly Met Ser Pro Gln Val Asn Ala Val Phe Pro Glu	
305 310 315	
tca aaa gca gac ctc att ttg att gta gta gca gtg gag cac gca ctc	1010
Ser Lys Ala Asp Leu Ile Leu Ile Val Val Ala Val Glu His Ala Leu	
320 325 330 335	
ctg gct tta aag ttt ata ctt gca ttt gcc ata cct gat aag cca cgg	1058
Leu Ala Leu Lys Phe Ile Leu Ala Phe Ala Ile Pro Asp Lys Pro Arg	
340 345 350	
cat atc cag atg aaa cta gcc aga ctg gaa ttt gag tct ttg gag gca	1106
His Ile Gln Met Lys Leu Ala Arg Leu Glu Phe Glu Ser Leu Glu Ala	
355 360 365	
ctc aag cag cag caa atg aag ctc gtg acc gag aac ctg aag gag gaa	1154

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Pro	Met	Glu	Ser	Gly	Lys	Glu	Lys	Ala	Thr								
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ctg	ccct	ggt	ggc	agag	gcc	tgt	gtct	gtg	ccac	acct	gca	cac	ggt	ggga	gggg	gggt	1264
ccg	gggc	cagc	atcg	tggt	ctc	ctga	accc	cag	accca	atgct	tag	ccaa	acg	aagt	gggt	ctcc	1324
cat	gtgg	caa	gcacc	cttct	cag	tttc	gca	gtgg	cttggc	tcgg	gatc	cct	tgga	gttcc			1384
ccc	agcccc	ccct	gtct	gtc	tcct	ttcc	cag	ttc	cttccc	ggcccc	acac	gct	gtc	ccag			1444
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gtg	gacag	gt	gggat	ggg	gtgt	gtg	ccc	actgt	gctca	tcac	aggagc	ctc	agtt	gag			1624
agt	gagc	ggg	gtac	agta	ag	gcagt	gttc	ccac	actgga	cctc	tttct	ct	ggtt	ctct	ttt		1684
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aaaaaaaa	taaaaaaaaa	aaaaaaaa															1773

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 <222> 29..376

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gca	gtg	gag	gag	ctg	gtt	tcg	ggg	gtg	cgg	cag	gcg	gcc	gac	ttc	gcg		100
Ala	Val	Glu	Glu	Leu	Val	Ser	Gly	Val	Arg	Gln	Ala	Ala	Asp	Phe	Ala		
	10					15				20							
gag	cag	ttc	cgc	tcc	tac	tca	gag	agc	gag	aag	caa	tg	aag	gcc	cgc		148
Glu	Gln	Phe	Arg	Ser	Tyr	Ser	Glu	Ser	Glu	Lys	Gln	Trp	Lys	Ala	Arg		
	25				30					35				40			
atg	gaa	ttc	atc	ctg	cgc	cac	ctg	ccc	gac	tac	cgc	gac	ccg	ccc	gac		196
Met	Glu	Phe	Ile	Leu	Arg	His	Leu	Pro	Asp	Tyr	Arg	Asp	Pro	Pro	Asp		
				45				50						55			
ggc	agt	ggc	cgc	ctg	gac	cag	ctg	ctc	tcc	ctc	tcc	atg	gtc	tg	gcc		244
Gly	Ser	Gly	Arg	Leu	Asp	Gln	Leu	Leu	Ser	Leu	Ser	Met	Val	Trp	Ala		
			60			65							70				
aac	cat	ctc	ttc	cta	ggc	tgc	agt	tac	aat	aaa	gac	ctt	tta	gac	aag		292
Asn	His	Leu	Phe	Leu	Gly	Cys	Ser	Tyr	Asn	Lys	Asp	Leu	Leu	Asp	Lys		
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gtg	atg	gaa	atg	gcc	gat	ggg	att	gaa	gtg	gaa	gac	ctg	cca	caa	ttt		340
Val	Met	Glu	Met	Ala	Asp	Gly	Ile	Glu	Val	Glu	Asp	Leu	Pro	Gln	Phe		
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act	acc	aga	agt	gaa	tta	atg	aaa	aag	cat	caa	agc	taag	ccagaa				386
Thr	Thr	Arg	Ser	Glu	Leu	Met	Lys	Lys	His	Gln	Ser						
	105				110					115							
gatt	tat	cat	ca	at	ttt	cat	ca	gc	ag	ct	ac	ag	gatt	agaa	gag	gct	ggga
atag	acc	aca	gc	ag	ct	ct	ct	ta	ag	act	cc	tg	att	acc	ac	ata	aa
tgag	aagg	ac	tct	gt	ct	aga	tt	gg	ct	tt	tt	tt	tt	tt	tt	tt	tt
tgta	aaa	ag	ta	tg	cat	gg	ata	tt	at	gt	att	gc	act	cta	ag	at	gag
caac	att	g	ta	aa	ag	cc	ct	ct	tt	tt	tt	tt	tt	tt	tt	tt	tt
tcac	t	gt	gc	gg	cc	ag	gc	ag	gc	ag	gc	ag	gc	ag	gc	ag	gc
tcct	gg	g	ct	gc	tc	at	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt
tgct	ct	gt	tt	g	ag	gc	ag	gc	ag	gc	ag	gc	ag	gc	ag	gc	ag

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gaatttttgt ttaaaatgcc tttttgggct gggccacagt ggccttatgc ccataataat 926
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tgggaggtgg aggttgagcag gagccaagat cgcaccattg cactccatcc tgggcgacaa 1166
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tgatgtgaaa aaaaaaaaaa aaaaaa 1251

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<212> DNA
<213> Homo sapiens

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<222> 78..566

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Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu
1 5 10
ctc cca gcg cct tcc cca atg ccc cag cta cct cct gat acc ctt gag 158
Leu Pro Ala Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu
15 20 25
atg cgg gtc cga gat ggc agc aaa att cgc aac ctg ctg ggg ttg gct 206
Met Arg Val Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala
30 35 40
ctg ggt cgg ttg gag ggc ggc agt gct cgg cat gta gtg ttc tca ggt 254
Leu Gly Arg Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly
45 50 55
tct ggc agg gct gca gga aag gct gtc agc tgc gct gag att gtc aag 302
Ser Gly Arg Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys
60 65 70 75
cgg cgg gtc cca ggc ctg cac cag ctc acc aag cta cgt ttc ctt cag 350
Arg Arg Val Pro Gly Leu His Gln Leu Thr Lys Leu Arg Phe Leu Gln
80 85 90
act gag gac agc tgg gtc cca gcc tca cct gac aca ggg cta gac ccc 398
Thr Glu Asp Ser Trp Val Pro Ala Ser Pro Asp Thr Gly Leu Asp Pro
95 100 105
ctc aca gtg cgc cgc cat gtg cct gca gtg tgg gtg ctg ctc agc cgg 446
Leu Thr Val Arg Arg His Val Pro Ala Val Trp Val Leu Leu Ser Arg
110 115 120
gac ccc ctg gac ccc aat gag tgt ggt tac caa ccc cca gga gca ccc 494
Asp Pro Leu Asp Pro Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro
125 130 135
cct ggc ctg ggt tcc atg ccc agc tcc agc tgt ggc cct cgt tcc cga 542
Pro Gly Leu Gly Ser Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Arg
140 145 150 155
aga agg gct cga gac acc cga tcg tgaagacctg ctgagccagc ctgttctccg 596
Arg Arg Ala Arg Asp Thr Arg Ser
160
ggcctgaatg tctggggtgc ttgtgccttt tctgagaagc gttgtgactg ctcaacatcc 656
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 <222> 16..705

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 agg gat tca ggt gtg gtg ccg gtg gga act gag gaa gcg ccc aag gtt 99
 Arg Asp Ser Gly Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Val
 15 20 25
 ttc aag atg gca gca tct atg cat ggt cag ccc agt cct tct cta gaa 147
 Phe Lys Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu
 30 35 40
 gat gca aaa ctc aga aga cca atg gtc ata gaa atc ata gaa aaa aat 195
 Asp Ala Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn
 45 50 55 60
 ttt gac tat ctt aga aaa gaa atg aca caa aat ata tat caa atg gcg 243
 Phe Asp Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala
 65 70 75
 aca ttt gga aca aca gct ggt ttc tct gga ata ttc tca aac ttc ctg 291
 Thr Phe Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu
 80 85 90
 ttc aga cgc tgc ttc aag gtt aaa cat gat gct ttg aag aca tat gca 339
 Phe Arg Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala
 95 100 105
 tca ttg gct aca ctt cca ttt ttg tct act gtt gtt act gac aag ctt 387
 Ser Leu Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu
 110 115 120
 ttt gta att gat gct ttg tat tca gat aat ata agc aag gaa aac tgt 435
 Phe Val Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys
 125 130 135 140
 gtt ttc aga agc tca ctg att ggc ata gtt tgt ggt gtt ttc tat ccc 483
 Val Phe Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro
 145 150 155
 agt tct ttg gct ttt act aaa aat gga cgc ctg gca acc aag tat cat 531
 Ser Ser Leu Ala Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His
 160 165 170
 acc gtt cca ctg cca cca aaa gga agg gtt tta atc cat tgg atg acg 579
 Thr Val Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr
 175 180 185
 ctt tgt caa aca caa atg aaa tta atg gcg att cct cta gtc ttt cag 627
 Leu Cys Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln
 190 195 200
 att atg ttt gga ata tta aat ggt cta tac cat tat gca gta ttt gaa 675
 Ile Met Phe Gly Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu
 205 210 215 220
 gag aca ctt gag aaa act ata cat gaa gag taaccaaaaa aatgaatggt 725
 Glu Thr Leu Glu Lys Thr Ile His Glu Glu
 225 230
 tgctaactta gcaaaatgaa gtttctataa agaggactca ggcattgctg aaagagttaa 785
 aagtaactgt gaacaaataa tttgttctgt gccttttgcc tggatatatag caaataactca 845
 aaaaatattc aataattcaa tcaataaata taagtttcat cttacaccaa aaaaaaaaaa 905

aaaaaa 910

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<213> Homo sapiens

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<222> 103..405

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Met Glu Arg Pro
1
gat aag gcg gcg ctg aac gca ctg cag cct cct gag ttc aga aat gaa 162
Asp Lys Ala Ala Leu Asn Ala Leu Gln Pro Pro Glu Phe Arg Asn Glu
5 10 15 20
agc tca tta gca tct aca ctg aag acg ctc ctg ttc ttc aca gct tta 210
Ser Ser Leu Ala Ser Thr Leu Lys Thr Leu Leu Phe Phe Thr Ala Leu
25 30 35
atg atc act gtt cct att ggg tta tat ttc aca act aaa tct tac ata 258
Met Ile Thr Val Pro Ile Gly Leu Tyr Phe Thr Thr Lys Ser Tyr Ile
40 45 50
ttt gaa ggc gcc ctt ggg atg tcc aat agg gac agc tat ttt tac gct 306
Phe Glu Gly Ala Leu Gly Met Ser Asn Arg Asp Ser Tyr Phe Tyr Ala
55 60 65
gct att gtt gca gtg gtc gcc gtc cat gtg gtg ctg gcc ctc ttt gtg 354
Ala Ile Val Ala Val Val Ala Val His Val Val Leu Ala Leu Phe Val
70 75 80
tat gtg gcc tgg aat gaa ggc tca cga cag tgc cgt gaa ggc aaa cag 402
Tyr Val Ala Trp Asn Glu Gly Ser Arg Gln Xaa Arg Glu Gly Lys Gln
85 90 95 100
gat taaagtgaac atcacctttt tatagcatta aattcatttt ttaaaatgat 455
Asp
aatgctggag ggggccatct gatttgaata aagttgaaag aacatgtaaa aaaaaaaaaa 515
aaaa 519

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<212> DNA
<213> Homo sapiens

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<222> 72..350

<400> 221
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tgcaggccggc c atg gat tcc ttg cgg aaa atg ctg atc tca gtc gca atg 110
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met
1 5 10
ctg ggc gca ggg gct ggc gtg ggc tac gcg ctc ctc gtt atc gtg acc 158
Leu Gly Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr
15 20 25
ccg gga gag cgg cgg aag cag gaa atg cta aag gag atg cca ctg cag 206
Pro Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln

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gac cca agg agc aga gag gag gcg gcc agg acc cag cag cta ttg ctg      254
Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu
          50          55          60
gcc act ctg cag gag gca gcg acc acg cag gag aac gtg gcc tgg agg      302
Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg
          65          70          75
aag aac tgg atg gtt ggc ggc gaa ggc ggc gcc ggc ggg agg tca ccg      350
Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Gly Gly Arg Ser Pro
          80          85          90
tgagaccgga cttgcctccg tgggcgcggg accttggtt gggcgcagga atccgaggca      410
gcctttctcc ttcgtgggcc cagcggagag tccggaccga gataccatgc caggactctc      470
cggggtcctg tgagctgccg tcgggtgagc acgtttcccc caaacctgg actgactgct      530
ttaaggtccg caaggcgggc cagggccgag acgcgagtcg gatgtggtga actgaaagaa      590
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<222> 38..436

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atc gtt ctt gcg gac ttg aac ttc ccg gcc tcc tcc atc tgc cag tgt      103
Ile Val Leu Ala Asp Leu Asn Phe Pro Ala Ser Ser Ile Cys Gln Cys
          10          15          20
ggg ccc atg gag atc cgt gca gac ggc ctg ggc atc ccg cag ctc ctg      151
Gly Pro Met Glu Ile Arg Ala Asp Gly Leu Gly Ile Pro Gln Leu Leu
          25          30          35
gag gcc gtg ctg aag ctg ctg ccc ctg gac acc tat gtg gag agt ccg      199
Glu Ala Val Leu Lys Leu Leu Pro Leu Asp Thr Tyr Val Glu Ser Pro
          40          45          50
gct gca gtc atg gag ctg gtg ccc agc gac aag gag agg ggc ctg cag      247
Ala Ala Val Met Glu Leu Val Pro Ser Asp Lys Glu Arg Gly Leu Gln
          55          60          65          70
acc cca gtg tgg acg gag tac gag tcc atc cta cgc agg gcc ggc tgt      295
Thr Pro Val Trp Thr Glu Tyr Glu Ser Ile Leu Arg Arg Ala Gly Cys
          75          80          85
gtg aga gcc ctg gca aag ata gag agg ttt gag ttt tat gaa cgg gct      343
Val Arg Ala Leu Ala Lys Ile Glu Arg Phe Glu Phe Tyr Glu Arg Ala
          90          95          100
aag aag gct ttt gct gtt gtg gca acg ggg gag acg gcc ctc tac gga      391
Lys Lys Ala Phe Ala Val Val Ala Thr Gly Glu Thr Ala Leu Tyr Gly
          105          110          115
aac ctc atc ctc agg aag ggg gtg ctt gcc ctc aac ccc ctg ctg      436
Asn Leu Ile Leu Arg Lys Gly Val Leu Ala Leu Asn Pro Leu Leu
          120          125          130
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ccaccactca caacaggcct cccagtggca gctcccagac ctgggccctg gccagggtc      556
taggggccgg cagtcttggg gtgggccctg ccaattggga cgagtatccc tgatttgtga      616
aatgatgga aaaacgttca aaaaaaaaaa aaaaaa                        652

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Ser Ser Tyr Cys Lys Arg Gly Asn Gly Tyr Arg Ser Arg Val Pro Lys
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Glu Cys Glu Cys Asn Trp Leu His Leu Glu Ser Asp Thr Leu Lys Lys
  45          50          55
tta ccc ata att tct ccc tct tgg aca tgc aga att atc ctg ttc ttg      423
Leu Pro Ile Ile Ser Pro Ser Trp Thr Cys Arg Ile Ile Leu Phe Leu
  60          65          70
tat ttt tct ggc cag ctt ctc caa ctt tcc ctt tct tgt ttg caa cta      471
Tyr Phe Ser Gly Gln Leu Leu Gln Leu Ser Leu Ser Cys Leu Gln Leu
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Ile Lys Leu

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<212> DNA
<213> Homo sapiens

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<222> 171..1670

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tgagctctga ttcaagtgcc tgcctctgcc ccttggtggg ctgaagcttc atg gag      176
Met Glu
1
gta tcc acc aac ccc tcc tcc aac atc gat cca ggc aac tat gtt gaa      224
Val Ser Thr Asn Pro Ser Ser Asn Ile Asp Pro Gly Asn Tyr Val Glu
  5          10          15
atg aat gat tca atc acc cac cta ccc tct aaa gtg gtg ata caa gat      272
Met Asn Asp Ser Ile Thr His Leu Pro Ser Lys Val Val Ile Gln Asp
  20          25          30
att act atg gag cta cac tgc cct ctg tgc aat gat tgg ttc cga gac      320
Ile Thr Met Glu Leu His Cys Pro Leu Cys Asn Asp Trp Phe Arg Asp
  35          40          45          50
cca ctg atg cta agc tgt ggc cac aac ttc tgt gaa gcc tgt atc caa      368
Pro Leu Met Leu Ser Cys Gly His Asn Phe Cys Glu Ala Cys Ile Gln
  55          60          65
gac ttt tgg agg ctg caa gca aag gaa aca ttc tgt cct gag tgt aag      416
Asp Phe Trp Arg Leu Gln Ala Lys Glu Thr Phe Cys Pro Glu Cys Lys
  70          75          80
atg cta tgt cag tat aac aac tgt aca ttc aac cct gta ctg gac aag      464
Met Leu Cys Gln Tyr Asn Asn Cys Thr Phe Asn Pro Val Leu Asp Lys
  85          90          95
ttg gta gag aag att aag aag tta ccc tta ctc aag ggc cat cca cag      512
Leu Val Glu Lys Ile Lys Lys Leu Pro Leu Leu Lys Gly His Pro Gln
  100          105          110
tgc cca gag cat gga gag aac ctg aaa ctg ttc agt aaa cca gat ggg      560
Cys Pro Glu His Gly Glu Asn Leu Lys Leu Phe Ser Lys Pro Asp Gly
  115          120          125          130
aaa ctg atc tgc ttt caa tgc aag gat gct cgg ttg tct gtg ggg cag      608
Lys Leu Ile Cys Phe Gln Cys Lys Asp Ala Arg Leu Ser Val Gly Gln
  135          140          145
tct aag gag ttc ctg caa atc tct gat gct gtc cat ttc ttc atg gag      656
Ser Lys Glu Phe Leu Gln Ile Ser Asp Ala Val His Phe Phe Met Glu

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				150				155				160					
gag	ctt	gcc	atc	caa	cag	ggt	caa	ctg	gag	aca	act	ctg	aag	gag	ctt		704
Glu	Leu	Ala	Ile	Gln	Gln	Gly	Gln	Leu	Glu	Thr	Thr	Leu	Lys	Glu	Leu		
		165					170					175					
cag	acc	ctg	agg	aac	atg	cag	aag	gaa	gct	att	gct	gct	cac	aag	gaa		752
Gln	Thr	Leu	Arg	Asn	Met	Gln	Lys	Glu	Ala	Ile	Ala	Ala	His	Lys	Glu		
		180					185					190					
aac	aag	cta	cat	ctg	cag	caa	cat	gtg	tcc	atg	gag	ttt	cta	aag	ctg		800
Asn	Lys	Leu	His	Leu	Gln	Gln	His	Val	Ser	Met	Glu	Phe	Leu	Lys	Leu		
		195				200					205				210		
cat	cag	ttc	ctg	cac	agc	aaa	gaa	aag	gac	att	tta	act	gag	ctc	cgg		848
His	Gln	Phe	Leu	His	Ser	Lys	Glu	Lys	Asp	Ile	Leu	Thr	Glu	Leu	Arg		
				215					220					225			
gaa	gag	ggg	aaa	gcc	ttg	aat	gag	gag	atg	gag	ttg	aat	ctg	agc	cag		896
Glu	Glu	Gly	Lys	Ala	Leu	Asn	Glu	Glu	Met	Glu	Leu	Asn	Leu	Ser	Gln		
			230					235					240				
ctt	cag	gag	caa	tgt	ctc	tta	gcc	aag	gat	atg	ttg	gtg	agc	att	cag		944
Leu	Gln	Glu	Gln	Cys	Leu	Leu	Ala	Lys	Asp	Met	Leu	Val	Ser	Ile	Gln		
		245					250					255					
gca	aag	acg	gaa	caa	cag	aac	tcc	ttc	gac	ttt	ctc	aaa	gac	atc	aca		992
Ala	Lys	Thr	Glu	Gln	Gln	Asn	Ser	Phe	Asp	Phe	Leu	Lys	Asp	Ile	Thr		
		260				265					270						
act	ctc	tta	cat	agc	ttg	gag	caa	gga	atg	aag	gtg	ctg	gca	acc	aga		1040
Thr	Leu	Leu	His	Ser	Leu	Glu	Gln	Gly	Met	Lys	Val	Leu	Ala	Thr	Arg		
				280					285						290		
gag	ctt	att	tcc	aga	aag	ctg	aac	ctg	ggc	cag	tac	aaa	ggg	cct	atc		1088
Glu	Leu	Ile	Ser	Arg	Lys	Leu	Asn	Leu	Gly	Gln	Tyr	Lys	Gly	Pro	Ile		
				295				300						305			
cag	tac	atg	gta	tgg	agg	gaa	atg	cag	gac	act	ctc	tgc	cca	ggc	ctg		1136
Gln	Tyr	Met	Val	Trp	Arg	Glu	Met	Gln	Asp	Thr	Leu	Cys	Pro	Gly	Leu		
			310				315						320				
tct	cca	cta	act	ctg	gac	cct	aaa	aca	gct	cac	cca	aat	ctg	gtg	ctc		1184
Ser	Pro	Leu	Thr	Leu	Asp	Pro	Lys	Thr	Ala	His	Pro	Asn	Leu	Val	Leu		
			325			330					335						
tcc	aaa	agc	caa	acc	agc	gtc	tgg	cat	ggg	gac	att	aag	aag	ata	atg		1232
Ser	Lys	Ser	Gln	Thr	Ser	Val	Trp	His	Gly	Asp	Ile	Lys	Lys	Ile	Met		
		340				345					350						
cct	gat	gat	cct	gag	agg	ttt	gac	tca	agt	gtg	gct	gta	ctg	ggc	tca		1280
Pro	Asp	Asp	Pro	Glu	Arg	Phe	Asp	Ser	Ser	Val	Ala	Val	Leu	Gly	Ser		
				360			365							370			
aga	ggc	ttc	acc	tct	gga	aag	tgg	tac	tgg	gaa	gta	gaa	gta	gca	aag		1328
Arg	Gly	Phe	Thr	Ser	Gly	Lys	Trp	Tyr	Trp	Glu	Val	Glu	Val	Ala	Lys		
				375			380							385			
aag	aca	aaa	tgg	aca	gtt	gga	gtt	gtc	aga	gaa	tcc	atc	att	cgg	aag		1376
Lys	Thr	Lys	Trp	Thr	Val	Gly	Val	Val	Arg	Glu	Ser	Ile	Ile	Arg	Lys		
			390				395						400				
ggc	agc	tgt	cct	cta	act	cct	gag	caa	gga	ttc	tgg	ctt	tta	aga	cta		1424
Gly	Ser	Cys	Pro	Leu	Thr	Pro	Glu	Gln	Gly	Phe	Trp	Leu	Leu	Arg	Leu		
		405				410						415					
agg	aac	caa	act	gat	cta	aag	gct	ctg	gat	ttg	cct	tct	ttc	agt	ctg		1472
Arg	Asn	Gln	Thr	Asp	Leu	Lys	Ala	Leu	Asp	Leu	Pro	Ser	Phe	Ser	Leu		
		420				425					430						
aca	ctg	act	aac	aac	ctc	gac	aag	gtg	ggc	ata	tac	ctg	gat	tat	gaa		1520
Thr	Leu	Thr	Asn	Asn	Leu	Asp	Lys	Val	Gly	Ile	Tyr	Leu	Asp	Tyr	Glu		
		435			440				445						450		
gga	gga	cag	ttg	tcc	ttc	tac	aat	gct	aaa	acc	atg	act	cac	att	tac		1568
Gly	Gly	Gln	Leu	Ser	Phe	Tyr	Asn	Ala	Lys	Thr	Met	Thr	His	Ile	Tyr		
				455				460						465			

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acc ttc agt aac act ttc atg gag aaa ctt tat ccc tac ttc tgc ccc 1616
Thr Phe Ser Asn Thr Phe Met Glu Lys Leu Tyr Pro Tyr Phe Cys Pro
      470                      475                      480
tgc ctt aat gat ggt aga gag aat aaa gaa cca ttg cac atc tta cat 1664
Cys Leu Asn Asp Gly Arg Glu Asn Lys Glu Pro Leu His Ile Leu His
      485                      490                      495
cca cag taatgagtca taatattata caaattcaga gtgttattaa agagggttttg 1720
Pro Gln
      500
aaataaaaaaa aaaaaaaaaa 1739

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<210> 226
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<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 199..618

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ctacctaatag ctttctcaga taaataagca tgaagaaaag tcaaagtcca ttctagctct 120
aaaataagga atgaaatgtt ttcttgatat gattttttgt ttccatctga taataatttt 180
atatatcaca gaaacagc atg gtt ctt act aaa cct ctt caa aga aat ggc 231
                Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly
                1                5                10
agc atg atg agc ttt gaa aat gtg aaa gaa aag agc aga gaa gga ggg 279
Ser Met Met Ser Phe Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly
      15                20                25
ccc cat gca cac aca ccc gaa gaa gaa ttg tgt ttc gtg gta aca cac 327
Pro His Ala His Thr Pro Glu Glu Glu Leu Cys Phe Val Val Thr His
      30                35                40
tac cct cag gtt cag acc aca ctc aac ctg ttt ttc cat ata ttc aag 375
Tyr Pro Gln Val Gln Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys
      45                50                55
gtt ctt act caa cca ctt tcc ctt ctg tgg ggt tgt gat cag aag cct 423
Val Leu Thr Gln Pro Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro
      60                65                70                75
cgt act gtt cct acc ctt gga aac ggc gca tgg gat acc tgc caa caa 471
Arg Thr Val Pro Thr Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln Gln
      80                85                90
cac ata cgc act tca tca tgg aca gca aac aca ctc gtc att caa aac 519
His Ile Arg Thr Ser Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn
      95                100                105
cag cat tca cgg gaa agc act gtt tct gtt tgc ctt ttt atg tta atc 567
Gln His Ser Arg Glu Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile
      110                115                120
cgc atg caa cat att ttg aaa aca gat aca ctt caa cag ttc aga ata 615
Arg Met Gln His Ile Leu Lys Thr Asp Thr Leu Gln Phe Arg Ile
      125                130                135
tgc tagtactaat aaaaccaaca tggtaaaaaa aaaaaaaaaa 657
Cys
140

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<210> 227
<211> 888
<212> DNA

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<213> Homo sapiens

<220>

<221> CDS

<222> 182..481

<400> 227

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atTTTgcctc tCagTgttca agcttgagcc cAcgcAtcca actcctgaga tcttactggg      60
aagctgctga tcatcagttt caggaagtca gcatggatca gccttacgtt catggcctcc      120
aggccctatt ctccTgcctc acagggaccg gccaggatct ctatccttac agcacgttgg      180
a atg tat atg ctc ctc tcc cca cat cgc ctt agg gag cag gca ggt gtc      229
Met Tyr Met Leu Leu Ser Pro His Arg Leu Arg Glu Gln Ala Gly Val
  1           5           10          15
agg ggc agc ata agg acg gcc aac agg aca gaa gac ggg ttg aag atc      277
Arg Gly Ser Ile Arg Thr Ala Asn Arg Thr Glu Asp Gly Leu Lys Ile
          20          25          30
cga gag gct gag tca ctt cca caa agt aac aca gct gat ttt aaa tgc      325
Arg Glu Ala Glu Ser Leu Pro Gln Ser Asn Thr Ala Asp Phe Lys Cys
          35          40          45
ctg cat tca gca tcc ctg cag cag gct cca ggt gga att cta atg gga      373
Leu His Ser Ala Ser Leu Gln Ala Pro Gly Gly Ile Leu Met Gly
          50          55          60
cca gcc tcc agt ccc tgg acc tta gcc gtg gaa gga gag aag agg aca      421
Pro Ala Ser Ser Pro Trp Thr Leu Ala Val Glu Gly Glu Lys Arg Thr
          65          70          75          80
tct gca cct cct ctc aga gaa agc ctg atg cct act aaa gga ctt ggg      469
Ser Ala Pro Pro Leu Arg Glu Ser Leu Met Pro Thr Lys Gly Leu Gly
          85          90          95
tgg tgg acg cag tgaccctcag tctggagctt gttcactgaa cattggagac      521
Trp Trp Thr Gln
          100
tatcatttgc gcagatggtc ttgggcctct atgagcagca ggctgcaccc cacagtgacc      581
tcctcattct actctgaggc atcttcatga aagcagatgt ccattgaaaa gcacccaagt      641
gcagtctcag ctgatgaact tcagaggcga ttgagacaaa ggctctcggt cccctctgcc      701
cttggatggg gcctctggta tgcacttggc ctctgtgtct ttatttagac tggtcacttc      761
acaacccatc atgtcacccc acccctaacc gtgccactc tgggtcctcc cctcaactgc      821
ctgacttccc actttgagct cagcaaaggc aatagatgtt ttgtctgctt cgaaaaaaaa      881
aaaaaaaaa      888
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<210> 228

<211> 716

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 161..517

<400> 228

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caggggtgtg tgaccccggt ggTtactgtg ctgcgtaga gcacctaggg cctgctgaag      120
ccctccctcg cccgcgcctc tccttagtcc ttgagatgag atg gca agt tac agc      175
Met Ala Ser Tyr Ser
          1           5
ggc ttc tcc ggc ctg ctg gag att cgc tac ggg cca gga cac cgc agc      223
Gly Phe Ser Gly Leu Leu Glu Ile Arg Tyr Gly Pro Gly His Arg Ser
          10          15          20
tgc ctt ccc caa ttc gct ttc ttt ccg cag ccg ccg ctg ccc cga ccc      271
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Cys	Leu	Pro	Gln	Phe	Ala	Phe	Phe	Pro	Gln	Pro	Pro	Leu	Pro	Arg	Pro		
			25					30					35				
cgg	atc	tgc	atg	tgg	gtg	ctg	gct	gag	ctg	ctg	gag	cta	ggg	tgt	cct		319
Arg	Ile	Cys	Met	Trp	Val	Leu	Ala	Glu	Leu	Leu	Glu	Leu	Gly	Cys	Pro		
		40					45					50					
gag	cag	agc	ctg	agg	gac	gcc	atc	acc	ctg	gac	ctc	ttc	tgc	cac	gcg		367
Glu	Gln	Ser	Leu	Arg	Asp	Ala	Ile	Thr	Leu	Asp	Leu	Phe	Cys	His	Ala		
		55				60					65						
ctc	att	ttc	tgc	cgc	cag	cag	ggc	ttc	tca	ctg	gag	cag	acg	tca	gcg		415
Leu	Ile	Phe	Cys	Arg	Gln	Gln	Gly	Phe	Ser	Leu	Glu	Gln	Thr	Ser	Ala		
		70			75			80						85			
gct	tgt	gcc	ctg	ctc	cag	gat	ctt	cac	aag	gct	tgt	att	ggg	gag	agg		463
Ala	Cys	Ala	Leu	Leu	Gln	Asp	Leu	His	Lys	Ala	Cys	Ile	Gly	Glu	Arg		
			90					95					100				
ggg	cag	cta	cca	ggg	ttg	agc	ccc	agg	gag	aag	agg	aac	cgg	gcc	tgg		511
Gly	Gln	Leu	Pro	Gly	Leu	Ser	Pro	Arg	Glu	Lys	Arg	Asn	Arg	Ala	Trp		
		105					110					115					
cac	aag	tgaccatggg	aagcagaagc	aggggatttc	tgccctggaat	atgtcattat											567
His	Lys																
tagtagcatc	atcatacaca	agccatcagc	tttccaatcc	actgcttcct	tatctagaaa												627
ttaaggatac	agcacacatt	ttacaggact	gttctgagaa	ataatatatg	caaatatatg												687
catagtgcac	aataaaaaaaaa	aaaaaaaaaa															716
<210>	229																
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<213>	Homo sapiens																
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<222>	86..505																
<400>	229																
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ccggtgaatc	ctgccgctgg	cgtgg	atg	aga	agt	gaa	tgc	gtg	ctc	gga	gct						112
			Met	Arg	Ser	Glu	Cys	Val	Leu	Gly	Ala						
			1				5										
gcg	agt	gac	agc	ggg	cag	gag	gcg	ccc	agg	gac	act	tgg	ttt	ctc	cag		160
Ala	Ser	Asp	Ser	Gly	Gln	Glu	Ala	Pro	Arg	Asp	Thr	Trp	Phe	Leu	Gln		
					15				20					25			
ggc	tgg	aag	gct	tct	aga	agg	ttc	ctc	atc	aag	gga	agt	gtg	gct	ggg		208
Gly	Trp	Lys	Ala	Ser	Arg	Arg	Phe	Leu	Ile	Lys	Gly	Ser	Val	Ala	Gly		
			30				35						40				
ggc	gcc	gtc	tac	ctg	gtg	tac	gac	cag	gag	ctg	ctg	ggg	ccc	agc	gac		256
Gly	Ala	Val	Tyr	Leu	Val	Tyr	Asp	Gln	Glu	Leu	Leu	Gly	Pro	Ser	Asp		
			45				50					55					
aag	agc	cag	gca	gcc	cta	cag	aag	gct	ggg	gag	gtg	gtc	ccc	ccc	gcc		304
Lys	Ser	Gln	Ala	Ala	Leu	Gln	Lys	Ala	Gly	Glu	Val	Val	Pro	Pro	Ala		
		60				65					70						
atg	tac	cag	ttc	agc	cag	tac	gtg	tgt	cag	cag	aca	ggc	ctg	cag	ata		352
Met	Tyr	Gln	Phe	Ser	Gln	Tyr	Val	Cys	Gln	Gln	Thr	Gly	Leu	Gln	Ile		
		75				80					85						
ccc	cag	ctc	cca	gcc	cct	cca	aag	att	tac	ttt	ccc	atc	cgt	gac	tcc		400
Pro	Gln	Leu	Pro	Ala	Pro	Pro	Lys	Ile	Tyr	Phe	Pro	Ile	Arg	Asp	Ser		
				95					100					105			
tgg	aat	gca	ggc	atc	atg	acg	gtg	atg	tca	gct	ctg	tcg	gtg	gcc	ccc		448
Trp	Asn	Ala	Gly	Ile	Met	Thr	Val	Met	Ser	Ala	Leu	Ser	Val	Ala	Pro		
			110						115					120			

tcc aag gcc cgc gag tac tcc aag gag ggc tgg gag tat gtg aag gcg	496
Ser Lys Ala Arg Glu Tyr Ser Lys Glu Gly Trp Glu Tyr Val Lys Ala	
125 130 135	
cgc acc aag tagcgagtca gcaggggccc cctgccccgg ccagaacggg	545
Arg Thr Lys	
140	
cagggctgcc actgacctga agactccgga ctgggacccc actccgaggg cagctccccg	605
ccttgccggc ccaataaagg acttcagaag tcaaaaaaaaa aaaaaaaaa	654

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 <213> Homo sapiens

<220>
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 <222> 56..382

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	Met
	1
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Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala Ser	
5 10 15	
cag act gtt aag aca ttt tca caa aac aga cca gca gca gct agg aca	154
Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg Thr	
20 25 30	
ttt caa cag att cgg tgc tat tct gca cct gtt gct gct gag ccc ttt	202
Phe Gln Gln Ile Arg Cys Tyr Ser Ala Pro Val Ala Ala Glu Pro Phe	
35 40 45	
ctc agt ggg act agt tgc aac tat gtg gag gag atg tac tgt gct tgg	250
Leu Ser Gly Thr Ser Ser Asn Tyr Val Glu Glu Met Tyr Cys Ala Trp	
50 55 60 65	
ctg gaa aac ccc aaa agt gta cat aag aca ggg tcc cac tgt tgt cca	298
Leu Glu Asn Pro Lys Ser Val His Lys Thr Gly Ser His Cys Cys Pro	
70 75 80	
ggc tgg agt gca gtg gcg gga tct cgg ctt gct gca acc tcc gac tcc	346
Gly Trp Ser Ala Val Ala Gly Ser Arg Leu Ala Ala Thr Ser Asp Ser	
85 90 95	
tgg gtt caa gtg att ctt atg cct cag cct ccc gag taactgggac	392
Trp Val Gln Val Ile Leu Met Pro Gln Pro Pro Glu	
100 105	
tacaggtgca cgtcaccacg cctgactagt ttttgtatatt ttagtagaga tgggatttta	452
ctttgtttggc caggettggtc ttgaaccctt ggcctcaagt gatccaccca ccttggcctc	512
ccaaagtgtc gggattacag gtatgatcaa ccacgcctgg ccatgtcatg ccttgtgaca	572
gaattccttt attctgtttt gagccaataa atatttatag gtttcgaaaa aaaaaaaaaa	632
aaa	635

<210> 231
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<220>
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 <222> 56..355

<400> 231

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                                     Met
                                     1
ttt cat tta agg act tgt gct gct aag ttg agg cca ttg acg gct tcc      106
Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala Ser
                                     5      10      15
cag act gtt aag aca ttt tca caa aac aga cca gca gca gct agg aca      154
Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg Thr
                                     20      25      30
ttt caa cag att cgt gct att ctg cac ctg ttg ctg ctg agc cct ttc      202
Phe Gln Gln Ile Arg Ala Ile Leu His Leu Leu Leu Leu Ser Pro Phe
                                     35      40      45
tca gtg gga cta gtt cga act atg tgg agg aga tgt act gtg ctt ggc      250
Ser Val Gly Leu Val Arg Thr Met Trp Arg Arg Cys Thr Val Leu Gly
50      55      60      65
tgg aaa acc cca aaa gtg tac ata aga cag ggt ccc act gtt gtc cag      298
Trp Lys Thr Pro Lys Val Tyr Ile Arg Gln Gly Pro Thr Val Val Gln
                                     70      75      80
gct gga gtg cag tgg cgg gat ctc ggc ttg ctg caa cct ccg act cct      346
Ala Gly Val Gln Trp Arg Asp Leu Gly Leu Leu Gln Pro Pro Thr Pro
                                     85      90      95
ggg ttc aag tgattcttat gcctcagcct cccgagtaac tgggactaca      395
Gly Phe Lys
                                     100
ggtgcacgtc accacgcctg actagttttt gtatttttag tagagatggg attttacttt      455
gttggccagg ctggtcttga acccctggcc tcaagtgatc caccacactt ggcctcccaa      515
agtgctggga ttacaggat gatcaaccac gcctggccat gtcatgcctt gtgacagaat      575
tcctttattc tgttttgagc caataaatat ttatagggtt cgaaaaaaaa aaaaaaaaaa      634

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<210> 232

<211> 583

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 76..498

<400> 232

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tcgagattgc gggct atg gcg ccg aag gtt ttt cgt cag tac tgg gat atc      111
                                     Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile
                                     1      5      10
ccc gat ggc acc gat tgc cac cgc aaa gcc tac agc acc acc agt att      159
Pro Asp Gly Thr Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile
                                     15      20      25
gcc agc gtc gct ggc ctg acc gcc gct gcc tac aga gtc aca ctc aat      207
Ala Ser Val Ala Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn
30      35      40
cct ccg ggc acc ttc ctt gaa gga gtg gct aag gtt gga caa tac acg      255
Pro Pro Gly Thr Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr
45      50      55      60
ttc act gca gct gct gtc ggg gcc gtg ttt ggc ctc acc acc tgc atc      303
Phe Thr Ala Ala Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile
                                     65      70      75
agc gcc cat gtc cgc gag aag ccc gac gac ccc ctg aac tac ttc ctc      351
Ser Ala His Val Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu

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ggg ggc tgc gcc gga ggc ctg act ctg gga gca cgc acg cac aac tac      399
Gly Gly Cys Ala Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr
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ggg att ggc gcc gcc gcc tgc gtg tac ttt ggc ata gcg gcc tcc ctg      447
Gly Ile Gly Ala Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu
      110      115      120
gtc aag atg ggc cgg ctg gag ggc tgg gag gtg ttt gca aaa ccc aag      495
Val Lys Met Gly Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys
      125      130      135      140
gtg tgagccctgt gcctgccggg acctccagcc tgcagaatgc gtccagaaat      548
Val
aaattctgtg tctgtgtgaa aaaaaaaaaa aaaaa      583

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gacgtgggag cgagaacgtc acactggagg cagctggtgg cacgatgggg gacagagtga      180
aagagccttc gtgtcacc atg gcc aca cac ccc gat ggc ttc cgg ctt gag      231
                Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu
                1                5                10
gga ccc ctg gct gca gcc cac agc cct ggg cct tgc act gtg ctc tac      279
Gly Pro Leu Ala Ala Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr
                15                20                25
gaa ggc cct gtc cgt ggg ctc tgc ccy ttt gcc ccg cga aat tcc aac      327
Glu Gly Pro Val Arg Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn
                30                35                40
acc atg gcg gcg gct gcc ctg gct gcc ccc agc ctg ggc ttc gat ggg      375
Thr Met Ala Ala Ala Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly
                45                50                55
gtg att ggg gtg ctc gtg gct gat acc agc ctc acg gac atg cac gtg      423
Val Ile Gly Val Leu Val Ala Asp Thr Ser Leu Thr Asp Met His Val
                60                65                70                75
gtg gat gta gag ctg agc gga ccc cgg ggc ccc act ggc cga agc ttt      471
Val Asp Val Glu Leu Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe
                80                85                90
gct gtg cac acc cgc aga gag aac cct gcc gag cca ggc gcg gtc acc      519
Ala Val His Thr Arg Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr
                95                100                105
ggc tcc gcc acc gtc acg gcc ttc tgg cgg agc ctc ctg gcc tgc tgc      567
Gly Ser Ala Thr Val Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys
                110                115                120
cag ctc ccc tcc agg ccg ggg atc cat ctc tgc tgagaagcct cctccctccc      620
Gln Leu Pro Ser Arg Pro Gly Ile His Leu Cys
                125                130
gagacaagat catctgcctg gcctctcacc accaccatcc caccctgcc ctgccccact      680
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 aggtagcaag tcaagagcct tcgtgtcacc atg gcc aca cac ccc gat ggc ttc 234
 Met Ala Thr His Pro Asp Gly Phe
 1 5
 cgg ctt gag gga ccc ctg gct gca gcg cac agc cct ggg cct tgc act 282
 Arg Leu Glu Gly Pro Leu Ala Ala Ala His Ser Pro Gly Pro Cys Thr
 10 15 20
 gtg ctc tac gaa ggc cct gtc cgt ggg ctc tgc ccc ttt gcc ccg cga 330
 Val Leu Tyr Glu Gly Pro Val Arg Gly Leu Cys Pro Phe Ala Pro Arg
 25 30 35 40
 aat tcc aac acc atg tcg gcg gct gcc ctg gct gcc ccc agc ctg ggc 378
 Asn Ser Asn Thr Met Ser Ala Ala Ala Leu Ala Ala Pro Ser Leu Gly
 45 50 55
 ttc gat ggg gtg att ggg gtg ctc gtg gct gat acc agc ctc acg gac 426
 Phe Asp Gly Val Ile Gly Val Leu Val Ala Asp Thr Ser Leu Thr Asp
 60 65 70
 atg cac gtg gtg gat gta gag ctg agc gga ccc cgg ggc ccc acg tgc 474
 Met His Val Val Asp Val Glu Leu Ser Gly Pro Arg Gly Pro Thr Cys
 75 80 85
 cga agc ttt gct gtg cac acc cgc aga gag aac cct gcc gag cca ggc 522
 Arg Ser Phe Ala Val His Thr Arg Arg Glu Asn Pro Ala Glu Pro Gly
 90 95 100
 gcg gtc acc ggc tcc gcc acc gtc acg gcc ttc tgg cgg agc ctc ctg 570
 Ala Val Thr Gly Ser Ala Thr Val Thr Ala Phe Trp Arg Ser Leu Leu
 105 110 115 120
 gcc tgc tgc cag ctc ccc tcc agg ccg ggg atc cat ctc tgc 612
 Ala Cys Cys Gln Leu Pro Ser Arg Pro Gly Ile His Leu Cys
 125 130
 tgagaagcct cctccctccc gagacaagat catctgcctg gcctctcacc accaccatcc 672
 caccctgcc ctgccccact tccccagggt ctcccttctg actcagtaaa gatcaccgct 732
 gcctcccccc gccaaaaaaaa aaaaaaaaaa 762

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 Met Leu Lys Val Glu Ala Thr Gly Ser Pro Glu Glu Gly Trp Ala
 1 5 10 15
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Gly	Gly	Glu	Pro	Arg	Thr	Gly	Ala	Pro	Ala	Asn	Ser	Pro	Ser	Cys	Pro		
			20						25					30			
cag	gag	atg	cca	ctg	cag	gac	cca	agg	agc	agg	gag	gag	gag	gcc	agg	145	
Gln	Glu	Met	Pro	Leu	Gln	Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg		
			35					40					45				
acc	cag	cag	cta	ttg	ctg	gcc	act	ctg	cag	gag	gca	gag	acc	acc	cag	193	
Thr	Gln	Gln	Leu	Leu	Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln		
			50					55					60				
gag	aac	gtg	gcc	tgg	agg	aag	aac	tgg	atg	gtt	ggc	ggc	gaa	ggc	ggc	241	
Glu	Asn	Val	Ala	Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly		
			65				70					75					
gcc	agc	ggg	agg	tca	ccg	tgagaccgga	cttgccctccg	tgggcgccgg								289	
Ala	Ser	Gly	Arg	Ser	Pro												
80					85												
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			Met	Gly	Arg	Pro	Trp	Met	Val	Met	Ile	Leu					
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gag	tca	aaa	tct	gaa	gaa	aag	atg	tgg	tat	ggg	gta	ttc	ctg	tgg	gca	100	
Glu	Ser	Lys	Ser	Glu	Glu	Lys	Met	Trp	Tyr	Gly	Val	Phe	Leu	Trp	Ala		
				15				20				25					
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Leu	Val	Ser	Ser	Leu	Phe	Phe	His	Val	Pro	Ala	Gly	Leu	Leu	Ala	Leu		
				30				35				40					
ttc	acc	ctc	aga	cat	cac	aaa	tat	ggg	agg	ttc	atg	tct	gta	agc	atc	196	
Phe	Thr	Leu	Arg	His	His	Lys	Tyr	Gly	Arg	Phe	Met	Ser	Val	Ser	Ile		
			45				50				55						
ctg	ttg	atg	ggc	atc	gtg	gga	cca	att	act	gct	gga	atc	ttg	aca	agt	244	
Leu	Leu	Met	Gly	Ile	Val	Gly	Pro	Ile	Thr	Ala	Gly	Ile	Leu	Thr	Ser		
			60			65					70						
gca	gct	att	gct	gga	gtt	tac	cga	gca	gca	ggg	aag	gaa	atg	ata	cca	292	
Ala	Ala	Ile	Ala	Gly	Val	Tyr	Arg	Ala	Ala	Gly	Lys	Glu	Met	Ile	Pro		
				80				85				90					
ttt	gaa	gcc	ctc	aca	ctg	ggc	act	gga	cag	aca	ttt	tgc	gtc	ttg	gtg	340	
Phe	Glu	Ala	Leu	Thr	Leu	Gly	Thr	Gly	Gln	Thr	Phe	Cys	Val	Leu	Val		
				95				100				105					
gtc	tcc	ttt	tta	cgg	att	tta	gct	act	cta	tagcatatcat	ccttatgctg					390	
Val	Ser	Phe	Leu	Arg	Ile	Leu	Ala	Thr	Leu								
			110				115										
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cagccttttc	ttcattttga	agctcctaga	attgaagact	tatgtggact	cctattgttc	570											
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tgtgtacctt	taccaagcc	aagtcacag	tgtctctggg	gtggcatcct	ttgcactgaa	690
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agttttgaaa	acaaatttgg	tgaaataaag	caggaaaaaa	aatttaagta	taactcaagt	930
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aaaa						994

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 <222> 41..352

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				1				5							
ggc aag ata ttt gtc tct gtc atg gtt aaa ttg caa aaa aat aaa ctt	103														
Gly Lys Ile Phe Val Ser Val Met Val Lys Leu Gln Lys Asn Lys Leu															
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acc tcc ttc ccc agg cag cca ttg tta aca ttt ttt gaa tat cta gaa	151														
Thr Ser Phe Pro Arg Gln Pro Leu Thr Phe Phe Glu Tyr Leu Glu															
	25	30	35												
aaa gtc ctt tgt tca gga tta ttt tcc cac tct gcc aag agt cac cat	199														
Lys Val Leu Cys Ser Gly Leu Phe Ser His Ser Ala Lys Ser His His															
	40	45	50												
gac ctg ctc aca cgc cac cct tat gaa act gcc gcg cca ctt ctc agc	247														
Asp Leu Leu Thr Arg His Pro Tyr Glu Thr Ala Ala Pro Leu Leu Ser															
	55	60	65												
tcc cat ttg att ctc aca gaa gct cta cga aat ggg ttg ggc aaa tgt	295														
Ser His Leu Ile Leu Thr Glu Ala Leu Arg Asn Gly Leu Gly Lys Cys															
	70	75	80												
cat gat cct cat ttc aca ggg gaa gaa act gag gcc cag agg ggg aaa	343														
His Asp Pro His Phe Thr Gly Glu Glu Thr Glu Ala Gln Arg Gly Lys															
	90	95	100												
ctg act acc taaaattgcc atgtaggccg gcgcggtggc tcacgcctgt	392														
Leu Thr Thr															
aatcccagca ctgtggggagg ccaaggcgagg tggatcgaga ggtcaggaga tcgagaccat	452														
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Leu	Trp	Gly	Gly	Val	Val	Lys	Ser	Cys	Phe	Glu	Gly	Lys	Gly	Pro	Gln	
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aga	gaa	gcc	caa	cca	gcc	agc	ccc	cag	gcc	gcc	ccg	cca	gga	ccc	acc	143
Arg	Glu	Ala	Gln	Pro	Ala	Ser	Pro	Gln	Ala	Ala	Pro	Pro	Gly	Pro	Thr	
				35				40					45			
aat	gag	gca	cag	atg	gca	gcc	gct	gcc	gcc	cta	gcc	cgg	ctg	gag	cag	191
Asn	Glu	Ala	Gln	Met	Ala	Ala	Ala	Ala	Ala	Leu	Ala	Arg	Leu	Glu	Gln	
				50			55					60				
aag	cag	tcc	cgg	gcc	tgg	ggc	ccc	aca	tgc	cag	gac	acc	atc	cga	aac	239
Lys	Gln	Ser	Arg	Ala	Trp	Gly	Pro	Thr	Ser	Gln	Asp	Thr	Ile	Arg	Asn	
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cag	gtg	aga	aag	gaa	ctt	caa	gcc	gaa	gcc	acc	gtc	agc	ggg	agc	ccc	287
Gln	Val	Arg	Lys	Glu	Leu	Gln	Ala	Glu	Ala	Thr	Val	Ser	Gly	Ser	Pro	
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gag	gcc	cca	ggg	acc	gtg	gta	tct	gag	ccc	aga	gag	gaa	ggc	tct		335
Glu	Ala	Pro	Gly	Thr	Asn	Val	Val	Ser	Glu	Pro	Arg	Glu	Glu	Gly	Ser	
				100					105					110		
gcc	cac	ctg	gct	gtg	cct	ggc	gtg	tac	ttc	acc	tgt	ccg	ctc	act	ggg	383
Ala	His	Leu	Ala	Val	Pro	Gly	Val	Tyr	Phe	Thr	Cys	Pro	Leu	Thr	Gly	
				115				120					125			
gcc	acc	ctg	agg	aag	gac	cag	cgg	gac	gcc	tgc	atc	aag	gag	gcc	att	431
Ala	Thr	Leu	Arg	Lys	Asp	Gln	Arg	Asp	Ala	Cys	Ile	Lys	Glu	Ala	Ile	
				130			135					140				
ctc	ttg	cac	ttc	tcc	acc	gac	cca	gtg	gcc	gcc	tcc	atc	atg	aag	atc	479
Leu	Leu	His	Phe	Ser	Thr	Asp	Pro	Val	Ala	Ala	Ser	Ile	Met	Lys	Ile	
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Tyr	Thr	Phe	Asn	Lys	Asp	Gln	Asp	Arg	Val	Lys	Leu	Gly	Val	Asp	Thr	
160				165				170					175			
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Ile	Ala	Lys	Tyr	Leu	Asp	Asn	Ile	His	Leu	His	Pro	Glu	Glu	Glu	Lys	
				180			185						190			
tac	cgg	aag	atc	aag	ctg	cag	aac	aag	gtg	ttt	cag	gag	cgc	att	aac	623
Tyr	Arg	Lys	Ile	Lys	Leu	Gln	Asn	Lys	Val	Phe	Gln	Glu	Arg	Ile	Asn	
				195			200						205			
tgc	ctg	gaa	ggg	acc	cac	gag	ttt	ttt	gag	gcc	att	ggg	ttc	cag	aag	671
Cys	Leu	Glu	Gly	Thr	His	Glu	Phe	Phe	Glu	Ala	Ile	Gly	Phe	Gln	Lys	
				210		215						220				
gtg	ttg	ctt	ccc	gcc	cag	gat	cag	gag	gac	ccc	gag	gag	ttc	tac	gtg	719
Val	Leu	Leu	Pro	Ala	Gln	Asp	Gln	Glu	Asp	Pro	Glu	Glu	Phe	Tyr	Val	
				225		230					235					
ctg	agc	gag	acc	acc	ttg	gcc	cag	ccc	cag	agc	ctg	gag	agg	cac	aag	767
Leu	Ser	Glu	Thr	Thr	Leu	Ala	Gln	Pro	Gln	Ser	Leu	Glu	Arg	His	Lys	
				240		245				250				255		
gaa	cag	ctg	ctg	gct	gcg	gag	ccc	gtg	cgc	gcc	aag	ctg	gac	agg	cag	815
Glu	Gln	Leu	Leu	Ala	Ala	Glu	Pro	Val	Arg	Ala	Lys	Leu	Asp	Arg	Gln	
				260				265					270			
cgc	cgc	gtc	ttc	cag	ccc	tgc	ccc	ctg	gcc	tgc	cag	ttc	gaa	ctg	cct	863
Arg	Arg	Val	Phe	Gln	Pro	Ser	Pro	Leu	Ala	Ser	Gln	Phe	Glu	Leu	Pro	
				275			280						285			
ggg	gac	ttc	ttc	aac	ctc	aca	gca	gag	gag	atc	aag	cgg	gag	cag	agg	911
Gly	Asp	Phe	Phe	Asn	Leu	Thr	Ala	Glu	Glu	Ile	Lys	Arg	Glu	Gln	Arg	
				290		295					300					
ctc	agg	tcc	gag	gcg	gtg	gag	cgg	ctg	agc	gtg	ctg	cgg	acc	aag	gcc	959
Leu	Arg	Ser	Glu	Ala	Val	Glu	Arg	Leu	Ser	Val	Leu	Arg	Thr	Lys	Ala	

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Met Arg Glu Lys Glu Glu Gln Arg Gly Leu Arg Lys Tyr Asn Tyr Thr			
320	325	330	335
ctg ctg cgc gtg cgc ctc ccc gat ggc tgc ctc ctg cag ggc act ttc			1055
Leu Leu Arg Val Arg Leu Pro Asp Gly Cys Leu Leu Gln Gly Thr Phe			
340	345	350	
tac gct cgg gag cgg ctg ggg gcg gtg tac ggg ttc gtc cgg gag gcc			1103
Tyr Ala Arg Glu Arg Leu Gly Ala Val Tyr Gly Phe Val Arg Glu Ala			
355	360	365	
ctg cag agc gac tgg ctg cct ttt gag ctg ctg gcc tcg gga ggg cag			1151
Leu Gln Ser Asp Trp Leu Pro Phe Glu Leu Leu Ala Ser Gly Gly Gln			
370	375	380	
aag ctg tcc gag gac gag aac ctg gcc ttg aac gag tgc ggg ctg gtg			1199
Lys Leu Ser Glu Asp Glu Asn Leu Ala Leu Asn Glu Cys Gly Leu Val			
385	390	395	
ccc tct gcc ctc ctg acc ttc tcg tgg gac atg gct gtg ctg gag gac			1247
Pro Ser Ala Leu Leu Thr Phe Ser Trp Asp Met Ala Val Leu Glu Asp			
400	405	410	415
atc aag gcc gcg ggg gcc gag ccg gac tcc atc ctg aaa ccc gag ctc			1295
Ile Lys Ala Ala Gly Ala Glu Pro Asp Ser Ile Leu Lys Pro Glu Leu			
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Leu Ser Ala Ile Glu Lys Leu Leu			
435			
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tctgtggatg tgggtgacaa cggcaggagg ggacgtggc cttcctgcac atagacctgc			1769
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<211> 1083

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 421..768

<400> 239

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taaaatgcca cggaagaacc tagggatgca ccaggaacca cgcgcctgaa tgccacaggt	180
ttgatttgat tcatgacctc catctggaca caagctctaa aatacttgag ccttggcaga	240
aatggctgat agagtccaca gaacacgctg tcctcatctc agagaggaga actctgaacc	300
cagaggggaa ggatttacct gcagttgtat ggcaagccag aggtaggcgc tgcactggaa	360
cgcagcctaa ccagcctaaa gaaaccatgg gaggagaggc tcttaccctc tcctttgcag	420
atg tgg gcc cgg ctg cct cac act cca gag cag atg ggc cac agg ctt	468
Met Trp Ala Arg Leu Pro His Thr Pro Glu Gln Met Gly His Arg Leu	
1 5 10 15	
ata ggt ccc aag gaa gct tca ctt cat gtg gta ccc agc tgg cca gcc	516
Ile Gly Pro Lys Glu Ala Ser Leu His Val Val Pro Ser Trp Pro Ala	
20 25 30	
agg aag atg gag ggg ctt ctg gct ggc ctc tct tcc tct cct aga aag	564

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Arg Lys Met Glu Gly Leu Leu Ala Gly Leu Ser Ser Ser Pro Arg Lys
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Ser Cys Trp Pro Phe Trp Val His Gly Pro Lys Val His Glu Gly Gly
    50          55          60
tct gcc tgt gag aca tca agc tcc tgg gtt gaa gga ctt gga tta aga      660
Ser Ala Cys Glu Thr Ser Ser Ser Trp Val Glu Gly Leu Gly Leu Arg
    65          70          75          80
aga gtg aca tca gtg cac agt tta tgc caa ggg ctt ggg gcc tca gtc      708
Arg Val Thr Ser Val His Ser Leu Cys Gln Gly Leu Gly Ala Ser Val
    85          90          95
cag ctt ctt cct gga cca cca cca aca acc agt gat aaa aat aat      756
Gln Leu Leu Pro Gly Pro Pro Pro Thr Thr Thr Ser Asp Lys Asn Asn
    100          105          110
tat act agt ggc tgacatttat ggattcttcc tacacactag gctataccac      808
Tyr Thr Ser Gly
    115
agcgagtgcc tcgaaaggaa atatagtata gcactgtgcc gtccaacatg gggggcacta      868
gccacatgca ctactgagca cttgaaatgt ggctagccca cattgagatg tgctgtaaat      928
aaagaataga caccagattt ccaagactta gtaccaaaaa aagaatgtaa aatttctcat      988
taacaatttt ttttcttaca tttattacat gttaacatga cgctatttgg agtttaaata     1048
aatgcattat taaaattcaa aaaaaaaaaa aaaaaa
                                1083

<210> 240
<211> 1831
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 78..590

<400> 240
aaggacttaa gcgccccgga gccgggaggc gaacttgga cccgctggcc tcgctcggtg      60
cgcgcctccc tccccgc atg cag ccc gcc gag cgc tcg cgg gtc ccc agg      110
                Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg
                1          5          10
atc gac ccg tac gga ttc gag cgg cct gag gac ttc gac gac gcc gcc      158
Ile Asp Pro Tyr Gly Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala
                15          20          25
tac gag aag ttt ttc tcc agc tac ctg gtc acg ctc acc cgc agg gcg      206
Tyr Glu Lys Phe Phe Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala
                30          35          40
atc aaa tgg tcc cgg ctg ctg cag ggc ggg ggc gtc ccc agg agc cgg      254
Ile Lys Trp Ser Arg Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg
                45          50          55
aca gtg aag cgc tat gtc cgg aaa ggg gtc ccg ctg gag cac cgt gcc      302
Thr Val Lys Arg Tyr Val Arg Lys Gly Val Pro Leu Glu His Arg Ala
                60          65          70          75
cgc gtc tgg atg gtg ctg agt ggg gcc cag gcg cag atg gac cag aat      350
Arg Val Trp Met Val Leu Ser Gly Ala Gln Ala Gln Met Asp Gln Asn
                80          85          90
ccc ggc tac tac cac cag ctt ctc cag gga gag aga aac ccc agg ctg      398
Pro Gly Tyr Tyr His Gln Leu Leu Gln Gly Glu Arg Asn Pro Arg Leu
                95          100          105
gag gac gcc atc agg aca gac ctg aac cgg acc ttc ccc gac aac gtg      446
Glu Asp Ala Ile Arg Thr Asp Leu Asn Arg Thr Phe Pro Asp Asn Val
                110          115          120

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aag ttc cgg aag acc acg gac ccc tgc tta cag agg acc ctg tac aat 494
 Lys Phe Arg Lys Thr Thr Asp Pro Cys Leu Gln Arg Thr Leu Tyr Asn
 125 130 135
 gtg ctg ctg gca tat ggg cac cat aac cag gga gtg ggc tac tgc cag 542
 Val Leu Leu Ala Tyr Gly His His Asn Gln Gly Val Gly Tyr Cys Gln
 140 145 150 155
 gga atg aat ttt ata gca gga tat ctg att ctt ata aca aat aat gaa 590
 Gly Met Asn Phe Ile Ala Gly Tyr Leu Ile Leu Ile Thr Asn Asn Glu
 160 165 170
 taagaatctt tttggctgtt agatgctctt gttggaagaa tactaccaga ttactacagc 650
 ccggccatgc tgggcctgaa gaccgaccag gaggtcctcg gggagctggt gcgggcgaag 710
 ctgccggctg tgggggccct gatggagcgt ctcggtgtgc tgtggacgct gctggtgtcc 770
 cgctgggttca tctgcctgtt tgtggacatc ttgcccgtgg agacagtgtc tcggatcttg 830
 gactgtttgt ttaacgaagg ctgcaagatt atcttccggt tggccctgac cttaattaag 890
 cagcaccagg agttgatttt ggaagccacc agcgttccag acatttgca taagttaaag 950
 cagataacca aaggaggttt cgtgatggag tgtcacacgt ttatgcagg gtgtggggct 1010
 gcacgtggct cagtccccct ccagggggcc ccgcctcacc tgcagcccgg gggctgctct 1070
 gaccacccgg aggatgcaca ggatgggacac cagtgggcat agggcacagg atgagcctcc 1130
 agctctgtcc tgcactgtcc ccctgcgcct ggccctccag ggctttcctg tctatggcgg 1190
 ccctgtcttc ttggccctgg cactgcggac gctgctcctg gtccctaatg ctgtactcat 1250
 ctgctgtgtg tggcgccaga agtgtggctt cccgaggccc ggccctccca ctgggtcctg 1310
 gacctggcgc agggccgtata gactcaggct ctgatgaggg cgttgtggga gctgtacctg 1370
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 cctaagaggg agtggaggct cggggccact ctgggtgcag catggcaaac gtgggcggta 1490
 tttcagcagc tgggccttca tcaaagagaa gaccatgttg gccgggcgcg gtggctcacg 1550
 cctgcagtc cagcactttg ggaggccaag gcgtgtggat cacctgagg caggagtcca 1610
 agaccagcct ggccaacacg gtgaaacccc gtctctacta aaaaatacaa aaattagcca 1670
 ggtgtggtgg ctcacgctta ttagtcccca gttactcggg aggctgaggc acgagaatca 1730
 cttgaacctg ggaggcggag gttgcagtga gccgagatcg cggcactgca ctccagcctg 1790
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<210> 241
 <211> 1830
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 78..608

<400> 241
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 cgcgcctccc tccccgc atg cag ccc gcc gag cgc tcg cgg gtc ccc agg 110
 Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg
 1 5 10
 atc gac ccg tac gga ttc gag cgg cct gag gac ttc gac gac gcc gcc 158
 Ile Asp Pro Tyr Gly Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala
 15 20 25
 tac gag aag ttt ttc tcc agc tac ctg gtc acg ctc acc cgc agg gcg 206
 Tyr Glu Lys Phe Phe Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala
 30 35 40
 atc aaa tgg tcc cgg ctg ctg cag ggc ggc ggc gtc ccc agg agc cgg 254
 Ile Lys Trp Ser Arg Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg
 45 50 55
 aca gtg aag cgc tat gtc cgg aaa ggc gtc ccg ctg gag cac cgt gcc 302
 Thr Val Lys Arg Tyr Val Arg Lys Gly Val Pro Leu Glu His Arg Ala
 60 65 70 75
 cgc gtc tgg atg gtg ctg agt ggg gcc cag gcg cag atg gac cag aat 350

Arg	Val	Trp	Met	Val	Leu	Ser	Gly	Ala	Gln	Ala	Gln	Met	Asp	Gln	Asn	
				80					85					90		
ccc	ggc	tac	tac	cac	cag	ctt	ctc	cag	gga	gag	aga	aac	ccc	agg	ctg	398
Pro	Gly	Tyr	Tyr	His	Gln	Leu	Leu	Gln	Gly	Glu	Arg	Asn	Pro	Arg	Leu	
			95					100				105				
gag	gac	gcc	atc	agg	aca	gac	ctg	aac	cgg	acc	ttc	ccc	gac	aac	gtg	446
Glu	Asp	Ala	Ile	Arg	Thr	Asp	Leu	Asn	Arg	Thr	Phe	Pro	Asp	Asn	Val	
		110					115				120					
aag	ttc	cgg	aag	acc	acg	gac	ccc	tgc	tta	cag	agg	acc	ctg	tac	aat	494
Lys	Phe	Arg	Lys	Thr	Thr	Asp	Pro	Cys	Leu	Gln	Arg	Thr	Leu	Tyr	Asn	
	125					130					135					
gtg	ctg	ctg	gca	tat	ggg	cac	cat	aac	cag	gga	gtg	ggc	tac	tgc	cag	542
Val	Leu	Leu	Ala	Tyr	Gly	His	His	Asn	Gln	Gly	Val	Gly	Tyr	Cys	Gln	
	140				145				150						155	
gga	atg	aat	ttt	ata	gca	gga	tat	ctg	att	ctt	ata	aca	aat	aat	gat	590
Gly	Met	Asn	Phe	Ile	Ala	Gly	Tyr	Leu	Ile	Leu	Ile	Thr	Asn	Asn	Asp	
				160				165						170		
aag	aat	ctt	ttt	ggc	tgt	tagatgctct	tgttggaaga	atactaccag								638
Lys	Asn	Leu	Phe	Gly	Cys											
			175													
attactacag	cccgccatg	ctgggcctga	agaccgacca	ggaggtcctc	ggggagctgg											698
tgcgggcgaa	gctgccggct	gtggggggccc	tgatggagcg	tctcggtgtg	ctgtggacgc											758
tgctggtgtc	ccgctgggttc	atctgcctgt	ttgtggacat	cttgcccgtg	gagacagtgc											818
ttcggatctg	ggactgtttg	tttaacgaag	gctcgaagat	tatcttccgg	ttggccctga											878
ccttaattaa	gcagcaccag	gagttgattt	tggaagccac	cagcgttcca	gacatttgcg											938
ataagtttaa	gcagataacc	aaagggagtt	tcgtgatgga	gtgtcacacg	tttatgcagg											998
tgtgtggggc	tgcacgtggc	tcagtcacct	cccagggggc	cccgcctcac	ctgcagcccg											1058
ggggctgctc	tgaccacccg	gaggatgcac	aggatgggca	ccagtgggca	tagggcacag											1118
gatgagcctc	cagctctgtc	ctgcactctg	cccctgcgcc	tggcctccga	gggctttcct											1178
gtctatggcg	gccctgtctt	cttgcccctg	gcactgcgga	cgctgctcct	ggtcctaattg											1238
gctgtactca	tctgctgtgt	gtggtgccag	aagtgtggct	ttccgaggcc	cggcctcccc											1298
actgggtcct	ggacctggcg	caggccgtat	agactcaggt	cctgatgagg	gcgttgtggg											1358
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gtcagtagtt	tcctaagagg	gagtggaggc	tcggggccac	tctgggtgca	gcatggcaaa											1478
cgtgggcggg	atttcagcag	ctgggccttc	atcaaagaga	agaccatgtt	ggccgggcgc											1538
ggtggctcac	gcctgcagtc	ccagcacttt	gggaggccaa	ggcgtgtgga	tcacctgagg											1598
tcaggagttc	aagaccagcc	tggccaacac	ggtgaaaccc	cgtctctact	aaaaaataca											1658
aaaattagcc	aggtgtggcg	gtcacgctt	atgtagtccc	agttactcgg	gaggctgagg											1718
cacgagaatc	acttgaacct	gggaggcgga	ggttgcaagt	agccgagatc	gcgccactgc											1778
actccagcct	gggcaacaga	gtgagactct	gtctcaaaaa	aaaaaaaaaa	aa											1830

<210> 242

<211> 508

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27..-1

<400> 242

Met	Asp	Pro	Lys	Leu	Gly	Arg	Met	Ala	Ala	Ser	Leu	Leu	Ala	Val	Leu	
	-25						-20					-15				
Leu	Leu	Leu	Leu	Glu	Arg	Gly	Met	Phe	Ser	Ser	Pro	Ser	Pro	Pro		
	-10				-5				1					5		
Pro	Ala	Leu	Leu	Glu	Lys	Val	Phe	Gln	Tyr	Ile	Asp	Leu	His	Gln	Asp	
				10				15						20		
Glu	Phe	Val	Gln	Thr	Leu	Lys	Glu	Trp	Val	Ala	Ile	Glu	Ser	Asp	Ser	

<210> 243
 <211> 331
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<400> 243
 Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe
 -30 -25 -20
 Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys
 -15 -10 -5 1
 Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu
 5 10 15
 Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg
 20 25 30
 Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn
 35 40 45
 Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val
 50 55 60 65
 Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His
 70 75 80
 Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp
 85 90 95
 Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg
 100 105 110
 Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Met Glu Ala
 115 120 125
 Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys
 130 135 140 145
 Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu
 150 155 160
 Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu
 165 170 175
 Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu
 180 185 190
 Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg
 195 200 205
 Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu
 210 215 220 225
 Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser
 230 235 240
 Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys
 245 250 255
 Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe
 260 265 270
 Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr
 275 280 285
 Asp Ser Met Val Glu Asp Cys Glu Pro His Phe
 290 295 300

<210> 244
 <211> 274
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 244
 Met Asp Arg Pro Gly Phe Val Ala Ala Leu Val Ala Gly Gly Val Ala
 -15 -10 -5
 Gly Val Ser Val Asp Leu Ile Leu Phe Pro Leu Asp Thr Ile Lys Thr
 1 5 10 15
 Arg Leu Gln Ser Pro Gln Gly Phe Ser Lys Ala Gly Gly Phe His Gly
 20 25 30
 Ile Tyr Ala Gly Val Pro Ser Ala Ala Ile Gly Ser Phe Pro Asn Ala
 35 40 45
 Ala Ala Phe Phe Ile Thr Tyr Glu Tyr Val Lys Trp Phe Leu His Ala
 50 55 60
 Asp Ser Ser Ser Tyr Leu Thr Pro Met Lys His Met Leu Ala Ala Ser
 65 70 75
 Ala Gly Glu Val Val Ala Cys Leu Ile Arg Val Pro Ser Glu Val Val
 80 85 90 95
 Lys Gln Arg Ala Gln Val Ser Ala Ser Thr Arg Thr Phe Gln Ile Phe
 100 105 110
 Ser Asn Ile Leu Tyr Glu Glu Gly Ile Gln Gly Leu Tyr Arg Gly Tyr
 115 120 125
 Lys Ser Thr Val Leu Arg Glu Ile Pro Phe Ser Leu Val Gln Phe Pro
 130 135 140
 Leu Trp Glu Ser Leu Lys Ala Leu Trp Ser Trp Arg Gln Asp His Val
 145 150 155
 Val Asp Ser Trp Gln Ser Ala Val Cys Gly Ala Phe Ala Gly Gly Phe
 160 165 170 175
 Ala Ala Ala Val Thr Thr Pro Leu Asp Val Ala Lys Thr Arg Ile Met
 180 185 190
 Leu Ala Lys Ala Gly Ser Ser Thr Ala Asp Gly Asn Val Leu Ser Val
 195 200 205
 Leu His Gly Val Trp Arg Ser Gln Gly Leu Ala Gly Leu Phe Ala Gly
 210 215 220
 Val Phe Pro Arg Met Ala Ala Ile Ser Leu Gly Gly Phe Ile Phe Leu
 225 230 235
 Gly Ala Tyr Asp Arg Thr His Ser Leu Leu Leu Glu Val Gly Arg Lys
 240 245 250 255
 Ser Pro

<210> 245
 <211> 406
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35..-1

<400> 245
 Met Arg Gly Ser Val Glu Cys Thr Trp Gly Trp Gly His Cys Ala Pro
 -35 -30 -25 -20
 Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly
 -15 -10 -5
 Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn
 1 5 10
 Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr

Pro Ser Ala Ser Val Ile Arg Thr
1 5

<210> 247
<211> 348
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29...-1

<400> 247
Met Ala Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro Leu Gly Met
-25 -20 -15
Leu Leu Gly Pro Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser His
-10 -5 1
Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr
5 10 15
Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Leu Asp Ala
20 25 30 35
Glu Val Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln
40 45 50
Pro Gly Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln
55 60 65
Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn
70 75 80
Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser
85 90 95
Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met
100 105 110 115
Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg Leu
120 125 130
Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn Val
135 140 145
Val Ile Glu Thr Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys Phe
150 155 160
Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe Asp
165 170 175
Leu Glu Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu Ser
180 185 190 195
Phe Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu Pro
200 205 210
Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser Ser
215 220 225
Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala Leu Gln Lys
230 235 240
Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala Lys Lys Lys
245 250 255
Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe Pro Tyr Ala Gln
260 265 270 275
Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val Leu Arg Thr Leu Val
280 285 290
Gln Glu Lys Gly Thr Glu Val Leu Ala Val Arg Val Val Thr Leu Leu
295 300 305
Tyr Asp Leu Val Thr Glu Lys Met Phe Ala Glu Glu
310 315

<210> 248
 <211> 397
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36..-1

<400> 248
 Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Gln Leu Arg Leu Cys Phe
 -35 -30 -25
 Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp Ala
 -20 -15 -10 -5
 Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro Val
 1 5 10
 Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro Gly
 15 20 25
 Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu Gly
 30 35 40
 Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser Gly
 45 50 55 60
 Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile Ile
 65 70 75
 Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly His
 80 85 90
 Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr Gly
 95 100 105
 Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu Glu
 110 115 120
 Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser Leu
 125 130 135 140
 Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser Gln
 145 150 155
 Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser Ala
 160 165 170
 Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr Val
 175 180 185
 Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Ser Pro
 190 195 200
 Leu Gln Gly Leu Thr Asn Gln Asp Leu Gln Glu Gly Glu Asp Trp Glu
 205 210 215 220
 Gln Glu Asp Glu Asp Met Asp Pro Arg Leu Glu His Ser Ser Ser Val
 225 230 235
 Gln Glu Asp Ser Glu Ser Pro Ser Pro Glu Asp Ile Pro Asp Tyr Leu
 240 245 250
 Leu Gln Tyr Arg Ala Ile His Ser Ala Glu Gln Gln His Ala Tyr Glu
 255 260 265
 Gln Asp Phe Glu Thr Asp Tyr Ala Glu Tyr Arg Ile Leu His Ala Arg
 270 275 280
 Val Gly Thr Ala Ser Gln Arg Phe Ile Glu Leu Gly Ala Glu Ile Lys
 285 290 295 300
 Arg Val Arg Arg Gly Thr Pro Glu Tyr Lys Val Leu Glu Asp Lys Ile
 305 310 315
 Ile Gln Glu Tyr Lys Lys Phe Arg Lys Gln Tyr Pro Ser Tyr Arg Glu
 320 325 330
 Glu Lys Arg Arg Cys Glu Tyr Leu His Gln Lys Leu Ser His Ile Lys
 335 340 345

Gly Leu Ile Leu Glu Phe Glu Glu Lys Asn Arg Gly Ser
 350 355 360

<210> 249
 <211> 403
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 249

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Gly	Gln	Val	Leu	Ala	Gly	Arg	Ala	Arg	Arg	Leu	Leu	Leu	Gln	Phe	Gly
-5					1			5						10	
Val	Leu	Phe	Cys	Thr	Ile	Leu	Leu	Leu	Leu	Trp	Val	Scr	Val	Phe	Leu
			15					20					25		
Tyr	Gly	Ser	Phe	Tyr	Tyr	Ser	Tyr	Met	Pro	Thr	Val	Ser	His	Leu	Ser
		30					35					40			
Pro	Val	His	Phe	Tyr	Tyr	Arg	Thr	Asp	Cys	Asp	Ser	Ser	Thr	Thr	Ser
		45				50					55				
Leu	Cys	Ser	Phe	Pro	Val	Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly	Gly	Arg
60					65			70							75
Asp	Arg	Val	Leu	Met	Tyr	Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu	Glu	Leu
				80				85						90	
Glu	Leu	Pro	Glu	Ser	Pro	Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	Leu	Val
			95					100					105		
Thr	Ile	Ser	Cys	Tyr	Thr	Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr	Ser	Ser
		110					115					120			
Arg	Ser	Val	Met	Leu	His	Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	Leu	Asp
		125				130						135			
Thr	Leu	Val	Phe	Ser	Ser	Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	Gln	Lys
140					145					150					155
Gln	Leu	Leu	Glu	Val	Glu	Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	Ser	Val
				160					165						170
Ser	Glu	Tyr	Val	Pro	Thr	Thr	Gly	Ala	Ile	Ile	Glu	Ile	His	Ser	Lys
			175				180						185		
Arg	Ile	Gln	Leu	Tyr	Gly	Ala	Tyr	Leu	Arg	Ile	His	Ala	His	Phe	Thr
		190					195					200			
Gly	Leu	Arg	Tyr	Leu	Leu	Tyr	Asn	Phe	Pro	Met	Thr	Cys	Ala	Phe	Ile
		205				210					215				
Gly	Val	Ala	Ser	Asn	Phe	Thr	Phe	Leu	Ser	Val	Ile	Val	Leu	Phe	Ser
220					225					230					235
Tyr	Met	Gln	Trp	Val	Trp	Gly	Gly	Ile	Trp	Pro	Arg	His	Arg	Phe	Ser
				240				245						250	
Leu	Gln	Val	Asn	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Arg	Lys	Glu	Val	Gln
			255				260						265		
Arg	Arg	Ile	Ser	Ala	His	Gln	Pro	Gly	Ala	Gly	Pro	Glu	Gly	Gln	Glu
		270					275					280			
Glu	Ser	Thr	Pro	Gln	Ser	Asp	Val	Thr	Glu	Asp	Gly	Glu	Ser	Pro	Glu
		285				290					295				
Asp	Pro	Ser	Gly	Thr	Glu	Gly	Gln	Leu	Ser	Glu	Glu	Glu	Lys	Pro	Asp
300					305					310					315
Gln	Gln	Pro	Leu	Ser	Gly	Glu	Glu	Glu	Leu	Glu	Pro	Glu	Ala	Ser	Asp
				320				325					330		
Gly	Ser	Gly	Ser	Trp	Glu	Asp	Ala	Ala	Leu	Leu	Thr	Glu	Ala	Asn	Leu

335 340 345
 Pro Ala Pro Ala Pro Ala Ser Ala Ser Ala Pro Val Leu Glu Thr Leu
 350 355 360
 Gly Ser Ser Glu Pro Ala Gly Gly Ala Leu Arg Gln Arg Pro Thr Cys
 365 370 375
 Ser Ser Ser
 380

<210> 250
 <211> 111
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 250
 Met Pro His Leu Met Glu Arg Met Val Gly Ser Gly Leu Leu Trp Leu
 -25 -20 -15
 Ala Leu Val Ser Cys Ile Leu Thr Gln Ala Ser Ala Val Gln Arg Gly
 -10 -5 1 5
 Tyr Gly Asn Pro Ile Glu Ala Ser Ser Tyr Gly Leu Asp Leu Asp Cys
 10 15 20
 Gly Ala Pro Gly Thr Pro Glu Ala His Val Cys Phe Asp Pro Cys Gln
 25 30 35
 Asn Tyr Thr Leu Leu Asp Leu Gly Pro Ile Thr Arg Arg Gly Ala Gln
 40 45 50
 Ser Pro Gly Val Met Asn Gly Thr Pro Ser Thr Ala Gly Phe Leu Val
 55 60 65 70
 Ala Trp Pro Met Val Leu Leu Thr Val Leu Leu Ala Trp Leu Phe
 75 80 85

<210> 251
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 251
 Met Asp Arg Pro Gly Phe Val Ala Ala Leu Val Ala Gly Gly Val Ala
 -15 -10 -5
 Gly Val Ser Val Asp Leu Ile Leu Phe Pro Leu Asp Thr Ile Lys Thr
 1 5 10 15
 Arg Leu Gln Ser Pro Gln Gly Phe Asn Lys Ala Gly Gly Phe His Gly
 20 25 30
 Ile Tyr Ala Gly Val Pro Ser Ala Ala Ile Gly Ser Phe Pro Asn Gly
 35 40 45
 Cys Leu Pro Asp Ser Ser Ser Ile
 50 55

<210> 252
 <211> 138
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 252
 Met Lys Phe Thr Thr Leu Leu Phe Leu Ala Ala Val Ala Gly Ala Leu
 -15 -10 -5 1
 Val Tyr Ala Glu Asp Ala Ser Ser Asp Ser Thr Gly Ala Asp Pro Ala
 5 10 15
 Gln Glu Ala Gly Thr Ser Lys Pro Asn Glu Glu Ile Ser Gly Pro Ala
 20 25 30
 Glu Pro Ala Ser Pro Pro Glu Thr Thr Thr Thr Ala Gln Glu Thr Ser
 35 40 45
 Ala Ala Ala Val Gln Gly Thr Ala Lys Val Thr Ser Ser Arg Gln Glu
 50 55 60 65
 Leu Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu
 70 75 80
 Gln Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly
 85 90 95
 Gly Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu
 100 105 110
 Lys Lys Phe Ser Leu Leu Lys Pro Trp Ala
 115 120

<210> 253
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<220>
 <221> UNSURE
 <222> 45
 <223> Xaa = Glu,Gln
 E E

<220>
 <221> UNSURE
 <222> 44
 <223> Xaa = Lys,Asn
 K N

<400> 253
 Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe
 -30 -25 -20
 Leu Leu Leu Val Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys
 -15 -10 -5 1
 Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu
 5 10 15
 Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg
 20 25 30
 Ile Ser Ala Ile Ala His Arg Gly Gly Ser Xaa Xaa Ala Pro Glu Asn
 35 40 45
 Thr Leu Ala Ala Ile Arg Gln Leu Arg Met Glu Gln Gln Ala Trp Ser
 50 55 60 65
 Trp Thr Leu Ser Leu Leu Leu Thr Gly Phe Leu Ser

<210> 254
 <211> 147
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 254
 Met Val Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu
 -20 -15 -10
 Gly Leu Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His
 -5 1 5
 Phe Leu Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg
 10 15 20
 Tyr Cys Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys
 25 30 35 40
 Asp Ile Asn Thr Phe Ile His Gly Asn Lys Arg Thr Ile Lys Ala Ile
 45 50 55
 Cys Glu Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser
 60 65 70
 Lys Ser Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro
 75 80 85
 Trp Pro Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val
 90 95 100
 Val Ala Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe
 105 110 115 120
 Arg Arg Pro

<210> 255
 <211> 381
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 255
 Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser
 -30 -25 -20
 Val Gly Ala Asn Phe Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln
 -15 -10 -5
 Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser
 1 5 10 15
 Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu
 20 25 30
 Lys Pro Val His Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val
 35 40 45
 Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu
 50 55 60
 Leu Ala Leu Val Asp Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met
 65 70 75
 Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro Asn Ile Val Cys
 80 85 90 95

Ser	Lys	Asp	Tyr	Phe	Val	Thr	Ala	Asn	Ser	Asn	Leu	Val	Ile	Ile	Thr
				100					105					110	
Ala	Gly	Ala	Arg	Gln	Glu	Lys	Gly	Glu	Thr	Arg	Leu	Asn	Leu	Val	Gln
			115					120					125		
Arg	Asn	Val	Ala	Ile	Phe	Lys	Leu	Met	Ile	Ser	Ser	Ile	Val	Gln	Tyr
		130					135					140			
Ser	Pro	His	Cys	Lys	Leu	Ile	Ile	Val	Ser	Asn	Pro	Val	Asp	Ile	Leu
	145					150					155				
Thr	Tyr	Val	Ala	Trp	Lys	Leu	Ser	Ala	Phe	Pro	Lys	Asn	Arg	Ile	Ile
160					165				170					175	
Gly	Ser	Gly	Cys	Asn	Leu	Asp	Thr	Ala	Arg	Phe	Arg	Phe	Leu	Ile	Gly
			180						185					190	
Gln	Lys	Leu	Gly	Ile	His	Ser	Glu	Ser	Cys	His	Gly	Trp	Ile	Leu	Gly
			195				200						205		
Glu	His	Gly	Asp	Ser	Ser	Val	Pro	Val	Trp	Ser	Gly	Val	Asn	Ile	Ala
	210					215						220			
Gly	Val	Pro	Leu	Lys	Asp	Leu	Asn	Ser	Asp	Ile	Gly	Thr	Asp	Lys	Asp
	225					230					235				
Pro	Glu	Gln	Trp	Lys	Asn	Val	His	Lys	Glu	Val	Thr	Ala	Thr	Ala	Tyr
240					245					250				255	
Glu	Ile	Ile	Lys	Met	Lys	Gly	Tyr	Thr	Ser	Trp	Ala	Ile	Gly	Leu	Ser
				260					265					270	
Val	Ala	Asp	Leu	Thr	Glu	Ser	Ile	Leu	Lys	Asn	Leu	Arg	Arg	Ile	His
		275						280					285		
Pro	Val	Ser	Thr	Ile	Ile	Lys	Gly	Leu	Tyr	Gly	Ile	Asp	Glu	Glu	Val
	290					295						300			
Phe	Leu	Ser	Ile	Pro	Cys	Ile	Leu	Gly	Glu	Asn	Gly	Ile	Thr	Asn	Leu
	305					310					315				
Ile	Lys	Ile	Lys	Leu	Thr	Pro	Glu	Glu	Glu	Ala	His	Leu	Lys	Lys	Ser
320					325					330					335
Ala	Lys	Thr	Leu	Trp	Glu	Ile	Gln	Asn	Lys	Leu	Lys	Leu			
				340					345						

<210> 256
 <211> 139
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33..-1

<400> 256

Met	Ser	Trp	Thr	Val	Pro	Val	Val	Arg	Ala	Ser	Gln	Arg	Met	Ser	Ser
			-30					-25					-20		
Val	Gly	Ala	Asn	Phe	Leu	Cys	Leu	Gly	Met	Ala	Leu	Cys	Leu	Arg	Gln
		-15					-10					-5			
Ala	Thr	Arg	Ile	Pro	Leu	Asn	Gly	Thr	Trp	Leu	Phe	Thr	Pro	Val	Ser
1				5						10					15
Lys	Met	Ala	Thr	Val	Lys	Ser	Glu	Leu	Ile	Glu	Arg	Phe	Thr	Ser	Glu
				20					25					30	
Lys	Pro	Val	His	His	Ser	Lys	Val	Ser	Ile	Ile	Gly	Thr	Gly	Ser	Val
			35					40					45		
Gly	Met	Ala	Cys	Ala	Ile	Ser	Ile	Leu	Leu	Lys	Gly	Leu	Ser	Asp	Glu
		50					55					60			
Leu	Ala	Leu	Val	Asp	Leu	Asp	Glu	Asp	Lys	Leu	Lys	Gly	Glu	Thr	Met
	65					70					75				
Asp	Leu	Gln	His	Gly	Ser	Pro	Phe	Thr	Lys	Met	Pro	Ile	Leu	Phe	Val

80		85		90		95				
Ala	Lys	Ile	Thr	Leu	Ser	Gln	Gln	Thr	Pro	Thr
				100					105	

<210> 257
 <211> 265
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 257	Met	Asn	Phe	Ile	Leu	Phe	Ile	Phe	Ile	Pro	Gly	Val	Phe	Ser	Leu	Lys
					-10					-5					1	
	Ser	Ser	Thr	Leu	Lys	Pro	Thr	Ile	Glu	Ala	Leu	Pro	Asn	Val	Leu	Pro
			5					10					15			
	Leu	Asn	Glu	Asp	Val	Asn	Lys	Gln	Glu	Glu	Lys	Asn	Glu	Asp	His	Thr
			20				25					30				
	Pro	Asn	Tyr	Ala	Pro	Ala	Asn	Glu	Lys	Asn	Gly	Asn	Tyr	Tyr	Lys	Asp
	35					40				45					50	
	Ile	Lys	Gln	Tyr	Val	Phe	Thr	Thr	Gln	Asn	Pro	Asn	Gly	Thr	Glu	Ser
					55					60					65	
	Glu	Ile	Ser	Val	Arg	Ala	Thr	Thr	Asp	Leu	Asn	Phe	Ala	Leu	Lys	Asn
				70					75					80		
	Gly	Ser	Thr	Pro	Asn	Val	Pro	Ala	Phe	Trp	Thr	Met	Leu	Ala	Lys	Ala
			85					90					95			
	Ile	Asn	Gly	Thr	Ala	Val	Val	Met	Asp	Asp	Lys	Asp	Gln	Leu	Phe	His
			100				105					110				
	Pro	Ile	Pro	Glu	Ser	Asp	Val	Asn	Ala	Thr	Gln	Gly	Glu	Asn	Gln	Pro
	115					120					125					130
	Asp	Leu	Glu	Asp	Leu	Lys	Ile	Lys	Ile	Met	Leu	Gly	Ile	Ser	Leu	Met
					135					140					145	
	Thr	Leu	Leu	Leu	Phe	Val	Val	Leu	Leu	Ala	Phe	Cys	Ser	Ala	Thr	Leu
				150					155					160		
	Tyr	Lys	Leu	Arg	His	Leu	Ser	Tyr	Lys	Ser	Cys	Glu	Ser	Gln	Tyr	Ser
				165				170					175			
	Val	Asn	Pro	Glu	Leu	Ala	Thr	Met	Ser	Tyr	Phe	His	Pro	Ser	Glu	Gly
				180			185					190				
	Val	Ser	Asp	Thr	Ser	Phe	Ser	Lys	Ser	Ala	Glu	Ser	Ser	Thr	Phe	Leu
	195					200					205				210	
	Gly	Thr	Thr	Ser	Ser	Asp	Met	Arg	Arg	Ser	Gly	Thr	Arg	Thr	Ser	Glu
					215					220					225	
	Ser	Lys	Ile	Met	Thr	Asp	Ile	Ile	Ser	Ile	Gly	Ser	Asp	Asn	Glu	Met
				230					235					240		
	His	Glu	Asn	Asp	Glu	Ser	Val	Thr	Arg							
				245				250								

<210> 258
 <211> 200
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

Met	Gln	Asn	Leu	Gly	Pro	Leu	Pro	Asn	Asp	Val	Cys	Leu	Thr	Met	Lys
			125					130					135		
Leu	Phe	Tyr	Tyr	Asp	Glu	Val	Thr	Pro	Pro	Asp	Tyr	Gln	Pro	Pro	Gly
			140					145				150			
Phe	Lys	Asp	Gly	Asp	Cys	Glu	Gly	Val	Ile	Phe	Glu	Gly	Glu	Pro	Met
			155				160				165				
Tyr	Leu	Asn	Val	Gly	Glu	Val	Ser	Thr	Pro	Phe	His	Ile	Phe	Lys	Val
170						175				180					185
Lys	Val	Thr	Thr	Glu	Arg	Glu	Arg	Met	Glu	Asn	Ile	Asp	Ser	Thr	Ile
				190					195					200	
Leu	Ser	Pro	Lys	Gln	Ile	Lys	Thr	Pro	Phe	Gln	Lys	Ile	Leu	Arg	Asp
			205					210					215		
Lys	Asp	Val	Glu	Asp	Glu	Gln	Glu	His	Tyr	Thr	Ser	Asp	Asp	Leu	Asp
			220				225					230			
Ile	Glu	Thr	Lys	Met	Glu	Glu	Gln	Glu	Lys	Asn	Pro	Ala	Ser	Ser	Glu
			235			240					245				
Leu	Glu	Glu	Pro	Ser	Leu	Val	Cys	Glu	Glu	Asp	Glu	Ile	Met	Arg	Ser
250					255					260					265
Lys	Glu	Ser	Pro	Asp	Leu	Ser	Ile	Ser	His	Ser	Gln	Val	Glu	Gln	Leu
				270					275					280	
Val	Asn	Lys	Thr	Ser	Glu	Leu	Asp	Met	Ser	Glu	Ser	Lys	Thr	Arg	Ser
			285					290					295		
Gly	Lys	Val	Phe	Gln	Asn	Lys	Met	Ala	Asn	Gly	Asn	Gln	Pro	Val	Lys
			300				305					310			
Ser	Ser	Lys	Glu	Asn	Arg	Lys	Arg	Ser	Gln	His	Glu	Ser	Gly	Arg	Ile
			315			320					325				
Val	Leu	His	His	Phe	Asp	Ser	Ser	Ser	Gln	Glu	Ser	Val	Pro	Lys	Arg
330					335					340					345
Arg	Lys	Phe	Ser	Glu	Pro	Lys	Glu	His	Ile						
				350					355						

<210> 260

<211> 158

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17..-1

<400> 260

Met	Ala	Leu	Glu	Val	Leu	Met	Leu	Leu	Ala	Val	Leu	Ile	Trp	Thr	Gly
		-15					-10					-5			
Ala	Glu	Asn	Leu	His	Val	Lys	Ile	Ser	Cys	Ser	Leu	Asp	Trp	Leu	Met
					5					10					15
Val	Ser	Val	Ile	Pro	Val	Ala	Glu	Ser	Arg	Asn	Leu	Tyr	Ile	Phe	Ala
				20					25					30	
Asp	Glu	Leu	His	Leu	Gly	Met	Gly	Cys	Pro	Ala	Asn	Arg	Ile	His	Thr
			35				40					45			
Tyr	Val	Tyr	Glu	Phe	Ile	Tyr	Leu	Val	Arg	Asp	Cys	Gly	Ile	Arg	Thr
			50				55					60			
Arg	Val	Val	Ser	Glu	Glu	Thr	Leu	Leu	Phe	Gln	Thr	Glu	Leu	Tyr	Phe
						70					75				
Thr	Pro	Arg	Asn	Ile	Asp	His	Asp	Pro	Gln	Glu	Ile	His	Leu	Glu	Cys
80					85					90					95
Ser	Thr	Ser	Arg	Lys	Ser	Val	Trp	Leu	Thr	Pro	Val	Ser	Thr	Glu	Asn
				100					105					110	
Glu	Ile	Lys	Leu	Asp	Pro	Ser	Pro	Phe	Ile	Ala	Asp	Phe	Gln	Thr	Thr

			115					120				125		
Ala	Glu	Glu	Leu	Gly	Leu	Leu	Ser	Ser	Ser	Pro	Asn	Leu	Leu	
		130					135					140		

<210> 261
 <211> 233
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 261
 Met Ala Thr Pro Pro Phe Arg Leu Ile Arg Lys Met Phe Ser Phe Lys
 -30 -25 -20
 Val Ser Arg Trp Met Gly Leu Ala Cys Phe Arg Ser Leu Ala Ala Ser
 -15 -10 -5
 Ser Pro Ser Ile Arg Gln Lys Lys Leu Met His Lys Leu Gln Glu Glu
 1 5 10 15
 Lys Ala Phe Arg Glu Glu Met Lys Ile Phe Arg Glu Lys Ile Glu Asp
 20 25 30
 Phe Arg Glu Glu Met Trp Thr Phe Arg Gly Lys Ile His Ala Phe Arg
 35 40 45
 Gly Gln Ile Leu Gly Phe Trp Glu Glu Glu Arg Pro Phe Trp Glu Glu
 50 55 60
 Glu Lys Thr Phe Trp Lys Glu Glu Lys Ser Phe Trp Glu Met Glu Lys
 65 70 75 80
 Ser Phe Arg Glu Glu Lys Thr Phe Trp Lys Lys Tyr Arg Thr Phe
 85 90 95
 Trp Lys Glu Asp Lys Ala Phe Trp Lys Glu Asp Asn Ala Leu Trp Glu
 100 105 110
 Arg Asp Arg Asn Leu Leu Gln Glu Asp Lys Ala Leu Trp Glu Glu Glu
 115 120 125
 Lys Ala Leu Trp Val Glu Glu Arg Ala Leu Leu Glu Gly Glu Lys Ala
 130 135 140
 Leu Trp Glu Asp Lys Thr Ser Leu Trp Glu Glu Asn Ala Leu Trp
 145 150 155 160
 Glu Glu Glu Arg Ala Phe Trp Met Glu Asn Asn Gly His Ile Ala Gly
 165 170 175
 Glu Gln Met Leu Glu Asp Gly Pro His Asn Ala Asn Arg Gly Gln Arg
 180 185 190
 Leu Leu Ala Phe Ser Arg Gly Arg Ala
 195 200

<210> 262
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 262
 Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro
 -20 -15 -10 -5
 Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr

1 5 10
 Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
 15 20 25
 Ile Leu Gly Asp Ile His Ser Gly Ala Leu Phe Cys Ser Leu Ile Leu
 30 35 40
 Glu Pro Ser
 45

<210> 263
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<400> 263
 Met Cys Phe Leu Val Ser Phe Asn Leu Pro Ile His Ile Ser Leu Ser
 -25 -20 -15 -10
 His Leu Phe Leu Asp Leu Ser Arg Ser Leu Trp Phe Leu Ala Cys Pro
 -5 1 5
 Gly Leu Asn Leu Val Tyr Leu Ala Leu Asp Ser Phe Ser Asp Leu Arg
 10 15 20
 Pro Ser Leu Asn Leu Leu Phe Tyr Phe Val Pro Gly Phe Gly Val Ser
 25 30 35
 Lys Tyr Leu Thr Ser Ala Gln Pro Val Leu Gly Phe Leu Leu Leu Pro
 40 45 50 55
 Asp Ile Asp Asn Pro Ala Leu Leu Gly Thr Glu Arg Trp Ser
 60 65

<210> 264
 <211> 174
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 264
 Met Phe Leu Thr Val Lys Leu Leu Leu Gly Gln Arg Cys Ser Leu Lys
 -15 -10 -5
 Val Ser Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg
 1 5 10
 Arg Leu Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln
 15 20 25
 Leu Leu Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn
 30 35 40 45
 Ala Ser Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys
 50 55 60
 Glu Ala His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu
 65 70 75
 Val Leu Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln
 80 85 90
 Leu Leu Arg Gln Glu His Glu Glu Arg Leu Gln Lys Ile Ser Leu Glu
 95 100 105
 His Leu Glu Gln Leu Ala Gln Tyr Leu Leu Ala Glu Glu Pro His Val

110 115 120 125
 Glu Pro Ala Gly Glu Arg Glu Leu Glu Ala Lys Ala Arg Pro Gln Ser
 130 135 140
 Ser Cys Asp Met Glu Glu Lys Glu Glu Ala Ala Ala Asp Gln
 145 150 155

<210> 265
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 265
 Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly
 -15 -10 -5
 Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met
 1 5 10 15
 Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala
 20 25 30
 Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr
 35 40 45
 Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr
 50 55 60
 Arg Val Arg Thr Val Ile Val Cys Lys Lys Tyr Cys Met Phe Cys Gln
 65 70 75
 Thr Phe Met Pro Ser Ile Lys Ile Val Phe
 80 85

<210> 266
 <211> 124
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 266
 Met Val Leu Cys Trp Leu Leu Leu Leu Val Met Ala Leu Pro Pro Gly
 -15 -10 -5
 Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met
 1 5 10
 Gln Cys Pro Gly Thr Tyr Met His Cys Gly Asp Asp Glu Asp Cys Phe
 15 20 25 30
 Thr Gly His Gly Val Ala Pro Gly Thr Gly Pro Val Ile Asn Lys Gly
 35 40 45
 Cys Leu Arg Ala Thr Ser Cys Gly Leu Glu Glu Pro Val Ser Tyr Arg
 50 55 60
 Gly Val Thr Tyr Ser Leu Thr Thr Asn Cys Cys Thr Gly Arg Leu Cys
 65 70 75
 Asn Arg Ala Pro Ser Ser Gln Thr Val Gly Ala Thr Thr Ser Leu Ala
 80 85 90
 Leu Gly Leu Gly Met Leu Leu Pro Pro Arg Leu Leu
 95 100 105

<210> 267
 <211> 261
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 267
 Met Glu Asn Phe Ser Leu Leu Ser Ile Ser Gly Pro Pro Ile Ser Ser
 -15 -10 -5
 Ser Ala Leu Ser Ala Phe Pro Asp Ile Met Phe Ser Arg Ala Thr Ser
 1 5 10 15
 Leu Pro Asp Ile Ala Lys Thr Ala Val Pro Thr Glu Ala Ser Ser Pro
 20 25 30
 Ala Gln Ala Leu Pro Pro Gln Tyr Gln Ser Ile Ile Val Arg Gln Gly
 35 40 45
 Ile Gln Asn Thr Val Leu Ser Pro Asp Cys Ser Leu Gly Asp Thr Gln
 50 55 60
 His Gly Glu Lys Leu Arg Arg Asn Cys Thr Ile Tyr Arg Pro Trp Phe
 65 70 75 80
 Ser Pro Tyr Ser Tyr Phe Val Cys Ala Asp Lys Glu Ser Gln Leu Glu
 85 90 95
 Ala Tyr Asp Phe Pro Glu Val Gln Gln Asp Glu Gly Lys Trp Asp Asn
 100 105 110
 Cys Leu Ser Glu Asp Met Ala Glu Asn Ile Cys Ser Ser Ser Ser
 115 120 125
 Pro Glu Asn Thr Cys Pro Arg Glu Ala Thr Lys Lys Ser Arg His Gly
 130 135 140
 Leu Asp Ser Ile Thr Ser Gln Asp Ile Leu Met Ala Ser Arg Trp His
 145 150 155 160
 Pro Ala Gln Gln Asn Gly Tyr Lys Cys Val Ala Cys Cys Arg Met Tyr
 165 170 175
 Pro Thr Leu Asp Phe Leu Lys Ser His Ile Lys Arg Gly Phe Arg Glu
 180 185 190
 Gly Phe Ser Cys Lys Val Tyr Tyr Arg Lys Leu Lys Ala Leu Trp Ser
 195 200 205
 Lys Glu Gln Lys Ala Arg Leu Gly Asp Arg Leu Ser Ser Gly Ser Cys
 210 215 220
 Gln Ala Phe Asn Ser Pro Ala Glu His Leu Arg Gln Ile Gly Gly Glu
 225 230 235 240
 Ala Tyr Leu Cys Leu
 245

<210> 268
 <211> 76
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 268
 Met Cys Met Ser Leu Ser Met Lys Val Pro Cys Cys Leu Cys Ala Leu
 -25 -20 -15 -10
 Leu Ser Asn Phe Cys Pro Ser Thr Thr Val Lys Gly Asp Val Val Thr

Ser Phe Phe Arg Ala Asp Tyr Asp Leu Ala Ser Arg Ser Ala Asp Gln
 10 15 20
 Ser Ser Gln Lys Val Lys Leu Arg Met Phe Thr Gly Arg Leu Pro Ile
 25 30 35
 Gly Pro Phe Ala Ser Val Gly Asn Ala Ala Glu Leu
 40 45 50

<210> 269
 <211> 199
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 269
 Met Glu Thr Phe Pro Leu Leu Leu Leu Ser Leu Gly Leu Val Leu Ala
 -15 -10 -5
 Glu Ala Ser Glu Ser Thr Met Lys Ile Ile Lys Glu Glu Phe Thr Asp
 1 5 10 15
 Glu Glu Met Gln Tyr Asp Met Ala Lys Ser Gly Gln Glu Lys Gln Thr
 20 25 30
 Ile Glu Ile Leu Met Asn Pro Ile Leu Leu Val Lys Asn Thr Ser Leu
 35 40 45
 Ser Met Ser Lys Asp Asp Met Ser Ser Thr Leu Leu Thr Phe Arg Ser
 50 55 60
 Leu His Tyr Asn Asp Pro Lys Gly Asn Ser Ser Gly Asn Asp Lys Glu
 65 70 75 80
 Cys Cys Asn Asp Met Thr Val Trp Arg Lys Val Ser Glu Ala Asn Gly
 85 90 95
 Ser Cys Lys Trp Ser Asn Asn Phe Ile Arg Ser Ser Thr Glu Val Met
 100 105 110
 Arg Arg Val His Arg Ala Pro Ser Cys Lys Phe Val Gln Asn Pro Gly
 115 120 125
 Ile Ser Cys Cys Glu Ser Leu Glu Leu Glu Asn Thr Val Cys Gln Phe
 130 135 140
 Thr Thr Gly Lys Gln Phe Pro Arg Cys Gln Tyr His Ser Val Thr Ser
 145 150 155 160
 Leu Glu Lys Ile Leu Thr Val Leu Thr Gly His Ser Leu Met Ser Trp
 165 170 175
 Leu Val Cys Gly Ser Lys Leu
 180

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<220>
 <221> SIGNAL
 <222> -36...-1

<400> 270
 Met Ala Ser Val Val Pro Val Lys Asp Lys Lys Leu Leu Glu Val Lys
 -35 -30 -25
 Leu Gly Glu Leu Pro Ser Trp Ile Leu Met Arg Asp Phe Ser Pro Ser

-20					-15					-10					-5
Gly	Ile	Phe	Gly	Ala	Phe	Gln	Arg	Gly	Tyr	Tyr	Arg	Tyr	Tyr	Asn	Lys
				1				5					10		
Tyr	Ile	Asn	Val	Lys	Lys	Gly	Ser	Ile	Ser	Gly	Ile	Thr	Met	Val	Leu
		15					20					25			
Ala	Cys	Tyr	Val	Leu	Phe	Ser	Tyr	Ser	Phe	Ser	Tyr	Lys	His	Leu	Lys
	30					35					40				
His	Glu	Arg	Leu	Arg	Lys	Tyr	His								
45					50										

<210> 271
 <211> 481
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<400> 271

Met	Gly	Ala	Leu	Ala	Arg	Ala	Leu	Pro	Ser	Ile	Leu	Leu	Ala	Leu	Leu
-25					-20					-15					-10
Leu	Thr	Ser	Thr	Pro	Glu	Ala	Leu	Gly	Ala	Asn	Pro	Gly	Leu	Val	Ala
				-5					1				5		
Arg	Ile	Thr	Asp	Lys	Gly	Leu	Gln	Tyr	Ala	Ala	Gln	Glu	Gly	Leu	Leu
		10					15					20			
Ala	Leu	Gln	Ser	Glu	Leu	Leu	Arg	Ile	Thr	Leu	Pro	Asp	Phe	Thr	Gly
	25				30						35				
Asp	Leu	Arg	Ile	Pro	His	Val	Gly	Arg	Gly	Arg	Tyr	Glu	Phe	His	Ser
40					45					50					55
Leu	Asn	Ile	His	Ser	Cys	Glu	Leu	Leu	His	Ser	Ala	Leu	Arg	Pro	Val
				60					65					70	
Pro	Gly	Gln	Gly	Leu	Ser	Leu	Ser	Ile	Ser	Asp	Ser	Ser	Ile	Arg	Val
		75					80						85		
Gln	Gly	Arg	Trp	Lys	Val	Arg	Lys	Ser	Phe	Phe	Lys	Leu	Gln	Gly	Ser
	90					95						100			
Phe	Asp	Val	Ser	Val	Lys	Gly	Ile	Ser	Ile	Ser	Val	Asn	Leu	Leu	Leu
	105					110					115				
Gly	Ser	Asp	Ser	Ser	Gly	Arg	Pro	Thr	Val	Thr	Ala	Ser	Ser	Cys	Ser
120					125					130					135
Ser	Asp	Ile	Ala	Asp	Val	Glu	Val	Asp	Met	Ser	Gly	Asp	Leu	Gly	Trp
				140					145					150	
Leu	Leu	Asn	Leu	Phe	His	Asn	Gln	Ile	Glu	Ser	Lys	Phe	Gln	Lys	Val
		155					160						165		
Leu	Glu	Ser	Arg	Ile	Cys	Glu	Met	Ile	Gln	Lys	Ser	Val	Ser	Ser	Asp
	170					175						180			
Leu	Gln	Pro	Tyr	Leu	Gln	Thr	Leu	Thr	Val	Thr	Thr	Glu	Ile	Asp	Ser
	185					190					195				
Phe	Ala	Asp	Ile	Asp	Tyr	Ser	Leu	Val	Glu	Ala	Pro	Arg	Ala	Thr	Ala
200					205					210					215
Gln	Met	Leu	Glu	Val	Met	Phe	Lys	Gly	Glu	Ile	Phe	His	Arg	Asn	His
				220					225					230	
Arg	Ser	Pro	Val	Thr	Leu	Leu	Ala	Ala	Val	Met	Ser	Leu	Pro	Glu	Glu
		235					240						245		
His	Asn	Lys	Met	Val	Tyr	Phe	Ala	Ile	Ser	Asp	Tyr	Val	Phe	Asn	Thr
	250					255						260			
Ala	Ser	Leu	Val	Tyr	His	Glu	Glu	Gly	Tyr	Leu	Asn	Phe	Ser	Ile	Thr
	265					270					275				

Asp	Asp	Met	Ile	Pro	Pro	Asp	Ser	Asn	Ile	Arg	Leu	Thr	Thr	Lys	Ser
280					285					290					295
Phe	Arg	Pro	Phe	Val	Pro	Arg	Leu	Ala	Arg	Leu	Tyr	Pro	Asn	Met	Asn
				300					305						310
Leu	Glu	Leu	Gln	Gly	Ser	Val	Pro	Ser	Ala	Pro	Leu	Leu	Asn	Phe	Ser
			315					320					325		
Pro	Gly	Asn	Leu	Ser	Val	Asp	Pro	Tyr	Met	Glu	Ile	Asp	Ala	Phe	Val
		330					335					340			
Leu	Leu	Pro	Ser	Ser	Ser	Lys	Glu	Pro	Val	Phe	Arg	Leu	Ser	Val	Ala
	345					350					355				
Thr	Asn	Val	Ser	Ala	Thr	Leu	Thr	Phe	Asn	Thr	Ser	Lys	Ile	Thr	Gly
360					365					370					375
Phe	Leu	Lys	Pro	Gly	Lys	Val	Lys	Val	Glu	Leu	Lys	Glu	Ser	Lys	Val
				380					385						390
Gly	Leu	Phe	Asn	Ala	Glu	Leu	Leu	Glu	Ala	Leu	Leu	Asn	Tyr	Tyr	Ile
			395					400					405		
Leu	Asn	Thr	Phe	Tyr	Pro	Lys	Phe	Asn	Asp	Lys	Leu	Ala	Glu	Gly	Phe
		410					415					420			
Pro	Leu	Pro	Leu	Leu	Lys	Arg	Val	Gln	Leu	Tyr	Asp	Leu	Gly	Leu	Gln
	425					430					435				
Ile	His	Lys	Asp	Phe	Leu	Phe	Leu	Gly	Ala	Asn	Val	Gln	Tyr	Met	Arg
440					445					450					455
Val															

<210> 272
 <211> 143
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43...-1

Met	Ala	Lys	Tyr	Gln	Gly	Glu	Val	Gln	Ser	Leu	Lys	Leu	Asp	Asp	Asp
			-40					-35					-30		
Ser	Val	Ile	Glu	Gly	Val	Ser	Asp	Gln	Val	Leu	Val	Ala	Val	Val	Val
		-25					-20					-15			
Ser	Phe	Ala	Leu	Ile	Ala	Thr	Leu	Val	Tyr	Ala	Leu	Phe	Arg	Asn	Val
	-10					-5					1				5
His	Gln	Asn	Ile	His	Pro	Glu	Asn	Gln	Glu	Leu	Val	Arg	Val	Leu	Arg
			10						15					20	
Glu	Gln	Leu	Gln	Thr	Glu	Gln	Asp	Ala	Pro	Ala	Ala	Thr	Arg	Gln	Gln
		25					30					35			
Phe	Tyr	Thr	Asp	Met	Tyr	Cys	Pro	Ile	Cys	Leu	His	Gln	Ala	Ser	Phe
	40					45					50				
Pro	Val	Glu	Thr	Asn	Cys	Gly	His	Leu	Phe	Cys	Gly	Ala	Cys	Ile	Ile
	55					60					65				
Ala	Tyr	Trp	Arg	Tyr	Gly	Ser	Trp	Leu	Gly	Ala	Ile	Ser	Cys	Pro	Ile
70					75					80					85
Cys	Arg	Gln	Thr	Arg	His	Gly	His	Ile	Ala	Leu	Ser	Arg	Thr	Ala	
				90					95					100	

<210> 273
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 273
 Met Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp
 1 5 10 15
 Ser Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val
 20 25 30
 Ser Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val
 35 40 45
 His Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg
 50 55 60
 Glu Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Asp Ser Thr Ala Val
 65 70 75 80
 Leu His

<210> 274

<211> 373

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27...-1

<400> 274
 Met Ala Thr Gln Ala His Ser Leu Ser Tyr Ala Gly Cys Asn Phe Leu
 -25 -20 -15
 Cys Gln Arg Leu Val Leu Ser Thr Leu Ser Gly Arg Pro Val Lys Ile
 -10 -5 1 5
 Arg Lys Ile Arg Ala Arg Asp Asp Asn Pro Gly Leu Arg Asp Phe Glu
 10 15 20
 Ala Ser Phe Ile Arg Leu Leu Asp Lys Ile Thr Asn Gly Ser Arg Ile
 25 30 35
 Glu Ile Asn Gln Thr Gly Thr Thr Leu Tyr Tyr Gln Pro Gly Leu Leu
 40 45 50
 Tyr Gly Gly Ser Val Glu His Asp Cys Ser Val Leu Arg Gly Ile Gly
 55 60 65
 Tyr Tyr Leu Glu Ser Leu Leu Cys Leu Ala Pro Phe Met Lys His Pro
 70 75 80 85
 Leu Lys Ile Val Leu Arg Gly Val Thr Asn Asp Gln Ile Asp Pro Ser
 90 95 100
 Val Asp Val Leu Lys Ala Thr Ala Leu Pro Leu Leu Lys Gln Phe Gly
 105 110 115
 Ile Asp Gly Glu Ser Phe Glu Leu Lys Ile Val Arg Arg Gly Met Pro
 120 125 130
 Pro Gly Gly Gly Glu Val Phe Ser Cys Pro Val Arg Lys Val
 135 140 145
 Leu Lys Pro Ile Gln Leu Thr Asp Pro Gly Lys Ile Lys Arg Ile Arg
 150 155 160 165
 Gly Met Ala Tyr Ser Val Arg Val Ser Pro Gln Met Ala Asn Arg Ile
 170 175 180
 Val Asp Ser Ala Arg Ser Ile Leu Asn Lys Phe Ile Pro Asp Ile Tyr
 185 190 195
 Ile Tyr Thr Asp His Ile Lys Gly Val Asn Ser Gly Lys Ser Pro Gly
 200 205 210
 Phe Gly Leu Ser Leu Val Ala Glu Thr Thr Ser Gly Thr Phe Leu Ser
 215 220 225
 Ala Glu Leu Ala Ser Asn Pro Gln Gly Gln Gly Ala Ala Val Leu Pro
 230 235 240 245
 Glu Asp Leu Gly Arg Asn Cys Ala Arg Leu Leu Leu Glu Glu Ile Tyr

250 255 260
 Arg Gly Gly Cys Val Asp Ser Thr Asn Gln Ser Leu Ala Leu Leu Leu
 265 270 275
 Met Thr Leu Gly Gln Gln Asp Val Ser Lys Val Leu Leu Gly Pro Leu
 280 285 290
 Ser Pro Tyr Thr Ile Glu Phe Leu Arg His Leu Lys Ser Phe Phe Gln
 295 300 305
 Ile Met Phe Lys Ile Glu Thr Lys Pro Cys Gly Glu Glu Leu Lys Gly
 310 315 320 325
 Gly Asp Lys Val Leu Met Thr Cys Val Gly Ile Gly Phe Ser Asn Leu
 330 335 340
 Ser Arg Thr Leu Lys
 345

<210> 275
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 275
 Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser
 -25 -20 -15 -10
 Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
 -5 1 5
 Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
 10 15 20
 Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
 25 30 35
 Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His
 40 45 50 55
 Val Ser Cys Ser Val Ala Ala Pro Leu Phe Pro Phe Leu Gly
 60 65

<210> 276
 <211> 197
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 276
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly
 -20 -15 -10 -5
 Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln
 1 5 10
 Ser Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
 15 20 25
 Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
 30 35 40
 Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala
 45 50 55 60
 Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile

				65					70					75			
Lys	Cys	Leu	Gln	Thr	Thr	Glu	Glu	Pro	Pro	Ser	Arg	Thr	Ala	Gly	Ala		
			80					85					90				
Met	Met	Gln	Phe	Thr	Ala	Pro	Ile	Pro	Gly	Ala	Thr	Gly	Pro	Ile	Lys		
		95					100					105					
Leu	Ser	Gln	Lys	Thr	Ile	Val	Gln	Thr	Leu	Gly	Pro	Ile	Val	Gln	Tyr		
		110					115				120						
Pro	Gly	Ser	Asn	Gly	Arg	Ile	Asn	Ile	Ser	Gln	Leu	Thr	Ser	Glu	Asp		
125					130					135					140		
Leu	Thr	Gly	Ala	Lys	Gly	Arg	Val	Thr	Ser	Gly	Pro	Gln	Phe	Pro	Asn		
				145					150					155			
Ser	His	His	Val	Pro	Glu	Asn	Leu	His	Gly	Tyr	Met	Asn	Ser	Leu	Ser		
			160					165					170				
Leu	Phe	Ser	Pro	Ala													
			175														

<210> 277

<211> 344

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -29..-1

<400> 277

Met	Asp	Phe	Leu	Val	Leu	Phe	Leu	Phe	Tyr	Leu	Ala	Ser	Val	Leu	Met		
				-25					-20					-15			
Gly	Leu	Val	Leu	Ile	Cys	Val	Cys	Ser	Lys	Thr	His	Ser	Leu	Lys	Gly		
			-10					-5					1				
Leu	Ala	Arg	Gly	Gly	Ala	Gln	Ile	Phe	Ser	Cys	Ile	Ile	Pro	Glu	Cys		
	5					10					15						
Leu	Gln	Arg	Ala	Val	His	Gly	Leu	Leu	His	Tyr	Leu	Phe	His	Thr	Arg		
20					25					30					35		
Asn	His	Thr	Phe	Ile	Val	Leu	His	Leu	Val	Leu	Gln	Gly	Met	Val	Tyr		
				40					45					50			
Thr	Glu	Tyr	Thr	Trp	Glu	Val	Phe	Gly	Tyr	Cys	Gln	Glu	Leu	Glu	Leu		
			55					60					65				
Ser	Leu	His	Tyr	Leu	Leu	Leu	Pro	Tyr	Leu	Leu	Leu	Gly	Val	Asn	Leu		
		70					75					80					
Phe	Phe	Phe	Thr	Leu	Thr	Cys	Gly	Thr	Asn	Pro	Gly	Ile	Ile	Thr	Lys		
	85					90					95						
Ala	Asn	Glu	Leu	Leu	Phe	Leu	His	Val	Tyr	Glu	Phe	Asp	Glu	Val	Met		
100					105					110					115		
Phe	Pro	Lys	Asn	Val	Arg	Cys	Ser	Thr	Cys	Asp	Leu	Arg	Lys	Pro	Ala		
				120					125					130			
Arg	Ser	Lys	His	Cys	Ser	Val	Cys	Asn	Trp	Cys	Val	His	Arg	Phe	Asp		
			135					140					145				
His	His	Cys	Val	Trp	Val	Asn	Asn	Cys	Ile	Gly	Ala	Trp	Asn	Ile	Arg		
		150				155						160					
Tyr	Phe	Leu	Ile	Tyr	Val	Leu	Thr	Leu	Thr	Ala	Ser	Ala	Ala	Thr	Val		
	165					170					175						
Ala	Ile	Val	Ser	Thr	Thr	Phe	Leu	Val	His	Leu	Val	Val	Met	Ser	Asp		
180					185					190					195		
Leu	Tyr	Gln	Glu	Thr	Tyr	Ile	Asp	Asp	Leu	Gly	His	Leu	His	Val	Met		
				200					205					210			
Asp	Thr	Val	Phe	Leu	Ile	Gln	Tyr	Leu	Phe	Leu	Thr	Phe	Pro	Arg	Ile		
			215					220					225				

Val	Phe	Met	Leu	Gly	Phe	Val	Val	Val	Leu	Ser	Phe	Leu	Leu	Gly	Gly
		230					235					240			
Tyr	Leu	Leu	Phe	Val	Leu	Tyr	Leu	Ala	Ala	Thr	Asn	Gln	Thr	Thr	Asn
	245					250					255				
Glu	Trp	Tyr	Arg	Gly	Asp	Trp	Ala	Trp	Cys	Gln	Arg	Cys	Pro	Leu	Val
260					265					270					275
Ala	Trp	Pro	Pro	Ser	Ala	Glu	Pro	Gln	Val	His	Arg	Asn	Ile	His	Ser
				280					285					290	
His	Gly	Leu	Arg	Ser	Asn	Leu	Gln	Glu	Ile	Phe	Leu	Pro	Ala	Phe	Pro
			295					300					305		
Cys	His	Glu	Arg	Lys	Lys	Gln	Glu								
		310					315								

<210> 278

<211> 541

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28...-1

<400> 278

Met	Gly	Ser	Gln	Glu	Val	Leu	Gly	His	Ala	Ala	Arg	Leu	Ser	Ser	Ser
			-25					-20				-15			
Gly	Leu	Leu	Leu	Gln	Val	Leu	Phe	Arg	Leu	Ile	Thr	Phe	Val	Leu	Asn
	-10						-5					1			
Ala	Phe	Ile	Leu	Arg	Phe	Leu	Ser	Lys	Glu	Ile	Val	Gly	Val	Val	Asn
5					10					15					20
Val	Arg	Leu	Thr	Leu	Leu	Tyr	Ser	Thr	Thr	Leu	Phe	Leu	Ala	Arg	Glu
				25					30					35	
Ala	Phe	Arg	Arg	Ala	Cys	Leu	Ser	Gly	Gly	Thr	Gln	Arg	Asp	Trp	Ser
			40					45				50			
Gln	Thr	Leu	Asn	Leu	Leu	Trp	Leu	Thr	Val	Pro	Leu	Gly	Val	Phe	Trp
	55					60					65				
Ser	Leu	Phe	Leu	Gly	Trp	Ile	Trp	Leu	Gln	Leu	Leu	Glu	Val	Pro	Asp
	70					75				80					
Pro	Asn	Val	Val	Pro	His	Tyr	Ala	Thr	Gly	Val	Val	Leu	Phe	Gly	Leu
85					90				95						100
Ser	Ala	Val	Val	Glu	Leu	Leu	Gly	Glu	Pro	Phe	Trp	Val	Leu	Ala	Gln
				105				110						115	
Ala	His	Met	Phe	Val	Lys	Leu	Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val
			120					125					130		
Ile	Leu	Lys	Thr	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His
	135						140					145			
Trp	Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val
	150					155					160				
Leu	Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro
165					170					175					180
Glu	Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu
				185					190					195	
Leu	Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala
			200					205					210		
Lys	Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu
	215						220					225			
Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe
	230					235					240				
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val

Lys	Met	Asp	Glu	Leu	Tyr	Pro	Met	Glu	Pro	Glu	Glu	Glu	Ala	Asn	Gly
90						95					100				
Ser	Glu	Ile	Leu	Ala	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Lys	Lys	Asp	Ala
105					110					115					120
Glu	Glu	Asp	Asp	Ser	Leu	Ala	Asn	Ser	Ser	Asp	Leu	Leu	Lys	Glu	Leu
				125					130					135	
Leu	Glu	Thr	Gly	Asp	Asn	Arg	Glu	Arg	Ser	His	His	Gln	Asp	Gly	Ser
			140					145					150		
Asp	Asn	Glu	Glu	Glu	Val	Ser	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Arg	Gly
		155					160					165			
Leu	Lys	Arg	Ser	Pro	Gln	Leu	Glu	Asp	Glu	Ala	Lys	Glu	Leu	Gln	Lys
						175					180				
Arg	Tyr	Gly	Gly	Phe	Met	Arg	Arg	Val	Gly	Arg	Pro	Glu	Trp	Trp	Met
185					190					195					200
Asp	Tyr	Gln	Lys	Arg	Tyr	Gly	Gly	Phe	Leu	Lys	Arg	Phe	Ala	Glu	Ala
				205				210						215	
Leu	Pro	Ser	Asp	Glu	Glu	Gly	Glu	Ser	Tyr	Ser	Lys	Glu	Val	Pro	Glu
			220					225					230		
Met	Glu	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Arg	Phe					
		235					240								

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<210> 280
<211> 362
<212> PRT
<213> Homo sapiens
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<220>
<221> SIGNAL
<222> -40...-1
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<400>	280															
Met	Pro	Phe	Ala	Tyr	Phe	Phe	Thr	Glu	Ser	Glu	Gly	Phe	Ala	Gly	Ser	
-40					-35					-30					-25	
Arg	Lys	Gly	Val	Leu	Gly	Arg	Val	Tyr	Glu	Thr	Val	Val	Met	Leu	Met	
				-20					-15					-10		
Leu	Leu	Thr	Leu	Leu	Val	Leu	Gly	Met	Val	Trp	Val	Ala	Ser	Ala	Ile	
			-5					1				5				
Val	Asp	Lys	Asn	Lys	Ala	Asn	Arg	Glu	Ser	Leu	Tyr	Asp	Phe	Trp	Glu	
	10					15					20					
Tyr	Tyr	Leu	Pro	Tyr	Leu	Tyr	Ser	Cys	Ile	Ser	Phe	Leu	Gly	Val	Leu	
25				30						35					40	
Leu	Leu	Leu	Val	Cys	Thr	Pro	Leu	Gly	Leu	Ala	Arg	Met	Phe	Ser	Val	
				45					50					55		
Thr	Gly	Lys	Leu	Leu	Val	Lys	Pro	Arg	Leu	Leu	Glu	Asp	Leu	Glu	Glu	
			60					65					70			
Gln	Leu	Tyr	Cys	Ser	Ala	Phe	Glu	Glu	Ala	Ala	Leu	Thr	Arg	Arg	Ile	
		75					80					85				
Cys	Asn	Pro	Thr	Ser	Cys	Trp	Leu	Pro	Leu	Asp	Met	Glu	Leu	Leu	His	
	90					95				100						
Arg	Gln	Val	Leu	Ala	Leu	Gln	Thr	Gln	Arg	Val	Leu	Leu	Glu	Lys	Arg	
105					110					115					120	
Arg	Lys	Ala	Ser	Ala	Trp	Gln	Arg	Asn	Leu	Gly	Tyr	Pro	Leu	Ala	Met	
				125					130					135		
Leu	Cys	Leu	Leu	Val	Leu	Thr	Gly	Leu	Ser	Val	Leu	Ile	Val	Ala	Ile	
			140					145					150			
His	Ile	Leu	Glu	Leu	Leu	Ile	Asp	Glu	Ala	Ala	Met	Pro	Arg	Gly	Met	
		155					160					165				
Gln	Gly	Thr	Ser	Leu	Gly	Gln	Val	Ser	Phe	Ser	Lys	Leu	Gly	Ser	Phe	

170		175		180
Gly Ala Val Ile Gln Val Val Leu Ile Phe Tyr Leu Met Val Ser Ser				
185		190		195
Val Val Gly Phe Tyr Ser Ser Pro Leu Phe Arg Ser Leu Arg Pro Arg				200
	205		210	
Trp His Asp Thr Ala Met Thr Gln Ile Ile Gly Asn Cys Val Cys Leu				215
	220		225	
Leu Val Leu Ser Ser Ala Leu Pro Val Phe Ser Arg Thr Leu Gly Leu				230
	235		240	
Thr Arg Phe Asp Leu Leu Gly Asp Phe Gly Arg Phe Asn Trp Leu Gly				245
	250		255	
Asn Phe Tyr Ile Val Phe Leu Tyr Asn Ala Ala Phe Ala Gly Leu Thr				260
265		270		275
Thr Leu Tyr Leu Val Lys Thr Phe Thr Ala Ala Val Arg Ala Glu Leu				280
	285		290	
Ile Arg Ala Phe Gly Leu Asp Arg Leu Pro Leu Pro Val Ser Gly Phe				295
	300		305	
Pro Gln Ala Ser Arg Lys Thr Gln His Gln				310
	315		320	

<210> 281
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 281
Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu Thr
-20 -15 -10
Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp Gln Gln
-5 1 5 10
Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln Ile Arg Lys
15 20 25
Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile Leu Thr Glu Gln
30 35 40
Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala Lys Gly Ser Gln Lys
45 50 55
Ser
60

<210> 282
 <211> 541
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 282
Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser
-25 -20 -15
Gly Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn
-10 -5 1
Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn

470		475		480
Leu Gly Thr Ala Phe	Leu Thr Glu Thr Lys	Leu Ile His Phe	Leu Arg	
485	490	495	500	
Thr Gln Leu Gly Val	Pro Arg Arg Thr Asp	Lys Met Thr		
505	510			

<210> 283
 <211> 468
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 283

Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser	
-20	-15
Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Trp Arg Ala	
-5	1
Val Asp Val Val Leu Asp Cys Phe Leu Val Lys Asp Gly Ala His Arg	
15	20
Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg Ala Ser Leu Val Leu	
30	35
Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp	
45	50
Phe Gln Gly Gly Thr Leu Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu	
60	65
Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu Ala Leu Leu His	
80	85
Ala Asp Cys Ser Gly Lys Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe	
95	100
Leu Gln Met Thr Glu Thr Thr Val Lys Thr Ala Ala Trp Phe Met Ala	
110	115
Asn Val Gln Val Ser Gly Gly Gly Pro Ser Ile Ser Leu Val Met Lys	
125	130
Thr Pro Arg Val Ala Lys Asn Glu Val Leu Trp His Pro Thr Leu Asn	
140	145
Leu Pro Leu Ser Pro Gln Gly Thr Val Arg Thr Ala Val Glu Phe Gln	
160	165
Val Met Thr Gln Thr Gln Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala	
175	180
Ser Leu Asp Cys Gly Phe Ser Met Ala Pro Gly Leu Asp Leu Ile Ser	
190	195
Val Glu Trp Arg Leu Gln His Lys Gly Arg Gly Gln Leu Val Tyr Ser	
205	210
Trp Thr Ala Gly Gln Gly Gln Ala Val Arg Lys Gly Ala Thr Leu Glu	
220	225
Pro Ala Gln Leu Gly Met Ala Arg Asp Ala Ser Leu Thr Leu Pro Gly	
240	245
Leu Thr Ile Gln Asp Glu Gly Thr Tyr Ile Cys Gln Ile Thr Thr Ser	
255	260
Leu Tyr Arg Ala Gln Gln Ile Ile Gln Leu Asn Ile Gln Ala Ser Pro	
270	275
Lys Val Arg Leu Ser Leu Ala Asn Glu Ala Leu Leu Pro Thr Leu Ile	
285	290
Cys Asp Ile Ala Gly Tyr Tyr Pro Leu Asp Val Val Val Thr Trp Thr	
300	305
	310
	315

Arg Glu Glu Leu Gly Gly Ser Pro Ala Gln Val Ser Gly Ala Ser Phe
 320 325 330
 Ser Ser Leu Arg Gln Ser Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser
 335 340 345
 Leu Thr Ala Glu Pro Gly Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val
 350 355 360
 Thr His Ile Ser Leu Glu Glu Pro Leu Gly Ala Ser Thr Gln Val Val
 365 370 375
 Pro Pro Glu Arg Arg Thr Ala Leu Gly Val Ile Phe Ala Ser Ser Leu
 380 385 390 395
 Phe Leu Leu Ala Leu Met Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro
 400 405 410
 Thr Gly Leu Gly Leu Leu Gln Ala Glu Arg Trp Glu Thr Thr Ser Cys
 415 420 425
 Ala Asp Thr Gln Ser Ser His Leu His Glu Asp Arg Thr Ala Arg Val
 430 435 440
 Ser Gln Pro Ser
 445

<210> 284

<211> 406

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -31...-1

<400> 284

Met Val Arg Ile Gln Arg Arg Lys Leu Leu Ala Ser Cys Leu Cys Val
 -30 -25 -20
 Thr Ala Thr Val Phe Leu Leu Val Thr Leu Gln Ala Leu Asp Thr Val
 -15 -10 -5 1
 Glu Asn Leu Met Lys Val Thr Gly Pro Pro Gln Gly Val Thr Asp Ser
 5 10 15
 Met Gln Cys Phe Asn Asp Gln Trp Pro Leu Ser Asn Thr Arg Ser Ser
 20 25 30
 Glu His Ile Lys Glu Val Met Val Glu Leu Gly Lys Phe Glu Arg Lys
 35 40 45
 Glu Phe Lys Ser Ser Ser Leu Gln Asp Gly His Thr Lys Met Glu Glu
 50 55 60 65
 Ala Pro Thr His Leu Asn Ser Phe Leu Lys Lys Glu Gly Leu Thr Phe
 70 75 80
 Asn Arg Lys Arg Lys Trp Glu Leu Asp Ser Tyr Pro Ile Met Leu Trp
 85 90 95
 Trp Ser Pro Leu Thr Gly Glu Thr Gly Arg Leu Gly Gln Cys Gly Ala
 100 105 110
 Asp Ala Cys Phe Phe Thr Ile Asn Arg Thr Tyr Leu His His His Met
 115 120 125
 Thr Lys Ala Phe Leu Phe Tyr Gly Thr Asp Phe Asn Ile Asp Ser Leu
 130 135 140 145
 Pro Leu Pro Arg Lys Ala His His Asp Trp Ala Val Phe His Glu Glu
 150 155 160
 Ser Pro Lys Asn Asn Tyr Lys Leu Phe His Lys Pro Val Ile Thr Leu
 165 170 175
 Phe Asn Tyr Thr Ala Thr Phe Ser Arg His Ser His Leu Pro Leu Thr
 180 185 190
 Thr Gln Tyr Leu Glu Ser Ile Glu Val Leu Lys Ser Leu Arg Tyr Leu

195	200	205
Val Pro Leu Gln Ser Lys	Asn Lys Leu Arg Lys	Arg Leu Ala Pro Leu
210	215	220
Val Tyr Val Gln Ser Tyr	Cys Asp Pro Pro Ser	Asp Arg Asp Ser Tyr
	230	235
Val Arg Glu Leu Met Thr Tyr	Ile Glu Val Asp Ser Tyr	Gly Glu Cys
	245	250
Leu Arg Asn Lys Asp Leu Pro	Gln Gln Leu Lys Asn Pro	Ala Ser Met
	260	265
Asp Ala Asp Gly Phe Tyr Arg	Ile Ile Ala Gln Tyr Lys	Phe Ile Leu
	275	280
Ala Phe Glu Asn Ala Val Cys	Asp Asp Tyr Ile Thr Glu	Lys Phe Trp
290	295	300
Arg Pro Leu Lys Leu Gly Val	Val Val Pro Val Tyr Tyr	Gly Ser Pro Ser
	310	315
Ile Thr Asp Trp Leu Pro Ser	Asn Lys Ser Ala Ile Leu	Val Ser Glu
	325	330
Phe Ser His Pro Arg Glu Leu	Ala Ser Tyr Ile Arg Arg	Leu Asp Ser
	340	345
Asp Asp Arg Leu Tyr Glu Ala	Tyr Val Glu Trp Lys Leu	Lys Gly Arg
	355	360
Ser Leu Thr Ser Asp Phe		
370	375	

<210> 285
 <211> 305
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 285
Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
-25 -20 -15
Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
-10 -5 1 5
Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
10 15 20
Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
25 30 35
Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly
40 45 50
Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg
55 60 65 70
Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu
75 80 85
Val Ile Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly
90 95 100
Gly Lys Met Ser Gln Tyr Leu Asp Ser Leu Lys Val Gly Asp Val Val
105 110 115
Glu Phe Arg Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His
120 125 130
Phe Asn Ile Gln Pro Asn Lys Lys Ser Pro Pro Glu Pro Arg Val Ala
135 140 145 150
Lys Lys Leu Gly Met Ile Ala Gly Gly Thr Gly Ile Thr Pro Met Leu
155 160 165

Gln Leu Ile Arg Ala Ile Leu Lys Val Pro Glu Asp Pro Thr Gln Cys
 170 175 180
 Phe Leu Leu Phe Ala Asn Gln Thr Glu Lys Asp Ile Ile Leu Arg Glu
 185 190 195
 Asp Leu Glu Glu Leu Gln Ala Arg Tyr Pro Asn Arg Phe Lys Leu Trp
 200 205 210
 Phe Thr Leu Asp His Pro Pro Lys Asp Trp Ala Tyr Ser Lys Gly Phe
 215 220 225 230
 Val Thr Ala Asp Met Ile Arg Glu His Leu Pro Ala Pro Gly Asp Asp
 235 240 245
 Val Leu Val Leu Leu Cys Gly Pro Pro Pro Met Val Gln Leu Ala Cys
 250 255 260
 His Pro Asn Leu Asp Lys Leu Gly Tyr Ser Gln Lys Met Arg Phe Thr
 265 270 275
 Tyr

<210> 286
 <211> 442
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

 <220>
 <221> UNSURE
 <222> 132
 <223> Xaa = Pro,Arg

<400> 286
 Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser
 -20 -15 -10
 Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Leu Arg Ala
 -5 1 5 10
 Val Asp Val Val Leu Asp Cys Phe Leu Ala Lys Asp Gly Ala His Arg
 15 20 25
 Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg Ala Ser Leu Val Leu
 30 35 40
 Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp
 45 50 55
 Phe Gln Gly Gly Thr Leu Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu
 60 65 70 75
 Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu Ala Leu Leu His
 80 85 90
 Ala Asp Cys Ser Gly Lys Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe
 95 100 105
 Leu Gln Met Thr Glu Thr Thr Val Lys Thr Ala Ala Trp Phe Met Ala
 110 115 120
 Asn Met Gln Val Ser Gly Gly Gly Xaa Ser Ile Ser Leu Val Met Lys
 125 130 135
 Thr Pro Arg Val Thr Lys Asn Glu Ala Leu Trp His Pro Thr Leu Asn
 140 145 150 155
 Leu Pro Leu Ser Pro Gln Gly Thr Val Arg Thr Ala Val Glu Phe Gln
 160 165 170
 Val Met Thr Gln Thr Gln Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala
 175 180 185
 Ser Leu Asp Cys Gly Phe Ser Met Ala Pro Gly Leu Asp Leu Ile Ser

Gly Phe Leu Gly Cys Leu Val Asn Leu Gln Ala Gly His Tyr Leu Ala
 100 105 110
 Met Thr Thr Leu Leu Leu Glu Met Ser Thr Pro Phe Thr Cys Val Ser
 115 120 125
 Trp Met Leu Leu Lys Ala Gly Trp Ser Glu Ser Leu Phe Trp Lys Leu
 130 135 140
 Asn Gln Trp Leu Met Ile His Met Phe His Cys Arg Met Val Leu Thr
 145 150 155 160
 Tyr His Met Trp Trp Val Cys Phe Trp His Trp Asp Gly Leu Val Ser
 165 170 175
 Ser Leu Tyr Leu Pro His Leu Thr Leu Phe Leu Val Gly Leu Ala Leu
 180 185 190
 Leu Thr Leu Ile Ile Asn Pro Tyr Trp Thr His Lys Lys Thr Gln Gln
 195 200 205
 Leu Leu Asn Pro Val Asp Trp Asn Phe Ala Gln Pro Glu Ala Lys Ser
 210 215 220
 Arg Pro Glu Gly Asn Gly Gln Leu Leu Arg Lys Lys Arg Pro
 225 230 235

<210> 288
 <211> 398
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 288
 Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln Glu Val
 -20 -15 -10
 Gly Gln Val Leu Ala Gly Arg Ala Arg Arg Leu Leu Leu Gln Phe Gly
 -5 1 5 10
 Val Leu Phe Cys Thr Ile Leu Leu Leu Leu Trp Val Ser Val Phe Leu
 15 20 25
 Tyr Gly Ser Phe Tyr Tyr Ser Tyr Met Pro Thr Val Ser His Leu Ser
 30 35 40
 Pro Val His Phe Tyr Tyr Arg Thr Asp Cys Asp Ser Ser Thr Thr Ser
 45 50 55
 Leu Cys Ser Phe Pro Val Ala Asn Val Ser Leu Thr Lys Gly Gly Arg
 60 65 70 75
 Asp Arg Val Leu Met Tyr Gly Gln Pro Tyr Arg Val Thr Leu Glu Leu
 80 85 90
 Glu Leu Pro Glu Ser Pro Val Asn Gln Asp Leu Gly Met Phe Leu Val
 95 100 105
 Thr Ile Ser Cys Tyr Thr Arg Gly Gly Arg Ile Ile Ser Thr Ser Ser
 110 115 120
 Arg Ser Val Met Leu His Tyr Arg Ser Asp Leu Leu Gln Met Leu Asp
 125 130 135
 Thr Leu Val Phe Ser Ser Leu Leu Leu Phe Gly Phe Ala Glu Gln Lys
 140 145 150 155
 Gln Leu Leu Glu Val Glu Leu Tyr Ala Asp Tyr Arg Glu Asn Ser Tyr
 160 165 170
 Val Pro Thr Thr Gly Ala Ile Ile Glu Ile His Ser Lys Arg Ile Gln
 175 180 185
 Leu Tyr Gly Ala Tyr Leu Arg Ile His Ala His Phe Thr Gly Leu Arg
 190 195 200
 Tyr Leu Leu Tyr Asn Phe Pro Met Thr Cys Ala Phe Ile Gly Val Ala

205						210						215			
Ser	Asn	Phe	Thr	Phe	Leu	Ser	Val	Ile	Val	Leu	Phe	Ser	Tyr	Met	Gln
220					225					230					235
Trp	Val	Trp	Gly	Gly	Ile	Trp	Pro	Arg	His	Arg	Phe	Ser	Leu	Gln	Val
				240						245				250	
Asn	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Arg	Lys	Glu	Val	Gln	Arg	Arg	Ile
			255					260					265		
Ser	Ala	His	Gln	Pro	Gly	Pro	Glu	Gly	Gln	Glu	Glu	Ser	Thr	Pro	Gln
		270				275						280			
Ser	Asp	Val	Thr	Glu	Asp	Gly	Glu	Ser	Pro	Glu	Asp	Pro	Ser	Gly	Thr
285					290					295					
Glu	Gly	Gln	Leu	Ser	Glu	Glu	Glu	Lys	Pro	Asp	Gln	Gln	Pro	Leu	Ser
300					305				310						315
Gly	Glu	Glu	Glu	Leu	Glu	Pro	Glu	Ala	Ser	Asp	Gly	Ser	Gly	Ser	Trp
				320					325					330	
Glu	Asp	Ala	Ala	Leu	Leu	Thr	Glu	Ala	Asn	Leu	Pro	Ala	Pro	Ala	Pro
			335					340					345		
Ala	Ser	Ala	Ser	Ala	Pro	Val	Leu	Glu	Thr	Leu	Gly	Ser	Ser	Glu	Pro
		350					355					360			
Ala	Gly	Gly	Ala	Leu	Arg	Gln	Arg	Pro	Thr	Cys	Ser	Ser	Ser		
365						370					375				

<210> 289
 <211> 130
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 289															
Met	Arg	Gln	Lys	Ala	Val	Ser	Leu	Phe	Phe	Cys	Tyr	Leu	Leu	Leu	Phe
-20					-15					-10					-5
Thr	Cys	Ser	Gly	Val	Glu	Ala	Gly	Lys	Lys	Lys	Cys	Ser	Glu	Ser	Ser
			1				5					10			
Asp	Ser	Gly	Ser	Gly	Phe	Trp	Lys	Ala	Leu	Thr	Phe	Met	Ala	Val	Gly
		15				20					25				
Gly	Gly	Leu	Ala	Val	Ala	Gly	Leu	Pro	Ala	Leu	Gly	Phe	Thr	Gly	Ala
		30				35					40				
Gly	Ile	Ala	Ala	Asn	Ser	Val	Ala	Ala	Ser	Leu	Met	Ser	Trp	Ser	Ala
45				50						55					60
Ile	Leu	Asn	Gly	Gly	Gly	Val	Pro	Ala	Gly	Gly	Leu	Val	Ala	Thr	Leu
			65						70					75	
Gln	Ser	Leu	Gly	Ala	Gly	Gly	Ser	Ser	Val	Val	Ile	Gly	Asn	Ile	Gly
			80				85					90			
Ala	Leu	Met	Gly	Tyr	Ala	Thr	His	Lys	Tyr	Leu	Asp	Ser	Glu	Glu	Asp
		95					100					105			
Glu	Glu														
110															

<210> 290
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

<222> -20...-1

<400> 290

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Met Ala Val Gly Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly
-20                               -15           -10           -5
Phe Thr Gly Ala Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met
                               1             5             10
Ser Trp Ser Ala Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu
          15             20             25
Val Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile
          30             35             40
Gly Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp
45                               55                               60
Ser Glu Glu Asp Glu Glu
                               65
```

<210> 291

<211> 207

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23...-1

<400> 291

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Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp
                               -20           -15           -10
Leu Ile Ala Pro Ser Arg Ala Cys Thr Cys Val Pro Pro His Pro Gln
          -5             1             5
Thr Ala Phe Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly
10                               15             20             25
Thr Pro Glu Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys
          30             35             40
Met Thr Lys Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp
          45             50             55
Ile Arg Phe Val Tyr Thr Pro Ala Met Glu Ser Val Cys Gly Tyr Phe
          60             65             70
His Arg Ser His Asn Arg Ser Glu Glu Phe Leu Ile Ala Gly Lys Leu
          75             80             85
Gln Asp Gly Leu Leu His Ile Thr Thr Cys Ser Phe Val Ala Pro Trp
90                               95             100           105
Asn Ser Leu Ser Leu Ala Gln Arg Arg Gly Phe Thr Lys Thr Tyr Thr
          110           115           120
Val Gly Cys Glu Glu Cys Thr Val Phe Pro Cys Leu Ser Phe Pro Cys
          125           130           135
Lys Leu Gln Ser Gly Thr His Cys Leu Trp Thr Asp Gln Leu Leu Gln
          140           145           150
Gly Ser Glu Lys Gly Phe Gln Ser Arg His Leu Ala Cys Leu Pro Arg
          155           160           165
Glu Pro Gly Leu Cys Thr Trp Gln Ser Leu Arg Ser Gln Ile Ala
170                               175           180
```

<210> 292

<211> 111

<212> PRT

<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 292
 Met Lys Tyr Asp Cys Pro Phe Ser Gly Thr Ser Phe Val Val Phe Ser
 -20 -15 -10
 Leu Phe Leu Ile Cys Ala Met Ala Gly Asp Val Val Tyr Ala Asp Ile
 -5 1 5
 Lys Thr Val Arg Thr Ser Pro Leu Glu Leu Ala Phe Pro Leu Gln Arg
 10 15 20
 Ser Val Ser Phe Asn Phe Ser Thr Val His Lys Ser Cys Pro Ala Lys
 25 30 35 40
 Asp Trp Lys Val His Lys Gly Lys Cys Tyr Trp Ile Ala Glu Thr Lys
 45 50 55
 Lys Ser Trp Asn Lys Ser Gln Asn Asp Cys Ala Ile Asn Asn Ser Tyr
 60 65 70
 Leu Met Val Ile Gln Asp Ile Thr Ala Met Val Arg Phe Asn Ile
 75 80 85

<210> 293
 <211> 139
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 293
 Met Glu Ala Val Val Phe Val Phe Ser Leu Leu Asp Cys Cys Ala Leu
 -15 -10 -5 1
 Ile Phe Leu Ser Val Tyr Phe Ile Ile Thr Leu Ser Asp Leu Glu Cys
 5 10 15
 Asp Tyr Ile Asn Ala Arg Ser Cys Cys Ser Lys Leu Asn Lys Trp Val
 20 25 30
 Ile Pro Glu Leu Ile Gly His Thr Ile Val Thr Val Leu Leu Leu Met
 35 40 45
 Ser Leu His Trp Phe Ile Phe Leu Leu Asn Leu Pro Val Ala Thr Trp
 50 55 60 65
 Asn Ile Tyr Arg Tyr Ile Met Val Pro Ser Gly Asn Met Gly Val Phe
 70 75 80
 Asp Pro Thr Glu Ile His Asn Arg Gly Gln Leu Lys Ser His Met Lys
 85 90 95
 Glu Ala Met Ile Lys Leu Gly Phe His Leu Leu Cys Phe Phe Met Tyr
 100 105 110
 Leu Tyr Ser Met Ile Leu Ala Leu Ile Asn Asp
 115 120

<210> 294
 <211> 160
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 294
Met Gln Arg Val Ser Gly Leu Leu Ser Trp Thr Leu Ser Arg Val Leu
-25 -20 -15
Trp Leu Ser Gly Leu Ser Glu Pro Gly Ala Ala Arg Gln Pro Arg Ile
-10 -5 1 5
Met Glu Glu Lys Ala Leu Glu Val Tyr Asp Leu Ile Arg Thr Ile Arg
10 15 20
Asp Pro Glu Lys Pro Asn Thr Leu Glu Glu Leu Glu Val Val Ser Glu
25 30 35
Ser Cys Val Glu Val Gln Glu Ile Asn Glu Glu Glu Tyr Leu Val Ile
40 45 50
Ile Arg Phe Thr Pro Thr Val Pro His Cys Ser Leu Ala Thr Leu Ile
55 60 65
Gly Leu Cys Leu Arg Val Lys Leu Gln Arg Cys Leu Pro Phe Lys His
70 75 80 85
Lys Leu Glu Ile Tyr Ile Ser Glu Gly Thr His Ser Thr Glu Glu Asp
90 95 100
Ile Asn Lys Gln Ile Asn Asp Lys Glu Arg Val Ala Ala Ala Met Glu
105 110 115
Asn Pro Asn Leu Arg Glu Ile Val Glu Gln Cys Val Leu Glu Pro Asp
120 125 130

<210> 295
<211> 181
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16...-1

<400> 295
Met Pro Pro Phe Leu Leu Leu Thr Cys Leu Phe Ile Thr Gly Thr Ser
-15 -10 -5
Val Ser Pro Val Ala Leu Asp Pro Cys Ser Ala Tyr Ile Ser Leu Asn
1 5 10 15
Glu Pro Trp Arg Asn Thr Asp His Gln Leu Asp Glu Ser Gln Gly Pro
20 25 30
Pro Leu Cys Asp Asn His Val Asn Gly Glu Trp Tyr His Phe Thr Gly
35 40 45
Met Ala Gly Asp Ala Met Pro Thr Phe Cys Ile Pro Glu Asn His Cys
50 55 60
Gly Thr His Ala Pro Val Trp Leu Asn Gly Ser His Pro Leu Glu Gly
65 70 75 80
Asp Gly Ile Val Gln Arg Gln Ala Cys Ala Ser Phe Asn Gly Asn Cys
85 90 95
Cys Leu Trp Asn Thr Thr Val Glu Val Lys Ala Cys Pro Gly Gly Tyr
100 105 110
Tyr Val Tyr Arg Leu Thr Lys Pro Ser Val Cys Phe His Val Tyr Cys
115 120 125
Gly Arg Glu Tyr Leu Pro Cys Ala Leu Phe Leu His Gln Gln Gly His
130 135 140
Arg Trp Ser Pro Lys Val Pro Asn Tyr Arg Ile Cys Ser Tyr Ser Gly
145 150 155 160
Asn Tyr Ile Ser Ile
165

<210> 296

<211> 247
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 296
 Met Gly Leu Pro Gly Leu Phe Cys Leu Ala Val Leu Ala Ala Ser Ser
 -15 -10 -5
 Phe Ser Lys Ala Arg Glu Glu Glu Ile Thr Pro Val Val Ser Ile Ala
 1 5 10
 Tyr Lys Val Leu Glu Val Phe Pro Lys Gly Arg Trp Val Leu Ile Thr
 15 20 25 30
 Cys Cys Ala Pro Gln Pro Pro Pro Ile Thr Tyr Ser Leu Cys Gly
 35 40 45
 Thr Lys Asn Ile Lys Val Ala Lys Lys Val Val Lys Thr His Glu Pro
 50 55 60
 Ala Ser Phe Asn Leu Asn Val Thr Leu Lys Ser Ser Pro Asp Leu Leu
 65 70 75
 Thr Tyr Phe Cys Arg Ala Ser Ser Thr Ser Gly Ala His Val Asp Ser
 80 85 90
 Ala Arg Leu Gln Met His Trp Glu Leu Trp Ser Lys Pro Val Ser Glu
 95 100 105 110
 Leu Arg Ala Asn Phe Thr Leu Gln Asp Arg Gly Ala Gly Pro Arg Val
 115 120 125
 Glu Met Ile Cys Gln Ala Ser Ser Gly Ser Pro Pro Ile Thr Asn Ser
 130 135 140
 Leu Ile Gly Lys Asp Gly Gln Val His Leu Gln Gln Arg Pro Cys His
 145 150 155
 Arg Gln Pro Ala Asn Phe Ser Phe Leu Pro Ser Gln Thr Ser Asp Trp
 160 165 170
 Phe Trp Cys Gln Ala Ala Asn Asn Ala Asn Val Gln His Ser Ala Leu
 175 180 185 190
 Thr Val Val Pro Pro Gly Gly Leu Pro Arg Ala Pro Thr Ile Val Leu
 195 200 205
 Val Gly Ser Leu Ala Ser Thr Ala Ala Ile Thr Ser Arg Met Leu Gly
 210 215 220
 Trp Thr Thr Trp Ala Arg Trp
 225

<210> 297
 <211> 132
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41...-1

<400> 297
 Met Glu Gly Gly Ala Tyr Gly Ala Gly Lys Ala Gly Gly Ala Phe Asp
 -40 -35 -30
 Pro Tyr Thr Leu Val Arg Gln Pro His Thr Ile Leu Arg Val Val Ser
 -25 -20 -15 -10
 Trp Leu Phe Ser Ile Val Val Phe Gly Ser Ile Val Asn Glu Gly Tyr
 -5 1 5

Leu Asn Ser Ala Ser Glu Gly Glu Gln Phe Cys Ile Tyr Asn Arg Asn
 10 15 20
 Pro Asn Ala Cys Ser Tyr Gly Val Ala Val Gly Val Leu Ala Phe Leu
 25 30 35
 Thr Cys Leu Leu Tyr Leu Ala Leu Asp Val Tyr Phe Pro Gln Ile Ser
 40 45 50 55
 Ser Val Lys Asp Arg Lys Lys Ala Val Leu Ser Asp Ile Gly Val Ser
 60 65 70
 Gly Glu Pro His Pro Ala Gly Thr Pro Cys Thr Glu Ser Thr Glu Gly
 75 80 85
 Cys Pro Gly Pro
 90

<210> 298
 <211> 251
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 298
 Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser Val
 -20 -15 -10
 Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro Leu Leu
 -5 1 5
 Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg
 10 15 20
 Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala
 25 30 35 40
 Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala
 45 50 55
 Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met
 60 65 70
 Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn
 75 80 85
 Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His
 90 95 100
 Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala
 105 110 115 120
 Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg
 125 130 135
 Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg
 140 145 150
 His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val
 155 160 165
 Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln
 170 175 180
 Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu
 185 190 195 200
 Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
 205 210 215
 Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
 220 225

<210> 299
 <211> 137

<212> PRT
 <213> Homo sapiens

<220>
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 <222> -22...-1

<400> 299
 Met Leu Ser Gly Arg Leu Val Leu Gly Leu Val Ser Met Ala Gly Arg
 -20 -15 -10
 Val Cys Leu Cys Gln Gly Ser Ala Gly Ser Gly Ala Ile Gly Pro Val
 -5 1 5 10
 Glu Ala Ala Ile Arg Thr Lys Leu Glu Glu Ala Leu Ser Pro Glu Val
 15 20 25
 Leu Glu Leu Arg Asn Glu Ser Gly Gly His Ala Val Pro Pro Gly Ser
 30 35 40
 Glu Thr His Phe Arg Val Ala Val Val Ser Ser Arg Phe Glu Gly Leu
 45 50 55
 Ser Pro Leu Gln Arg His Arg Leu Val His Ala Ala Leu Ala Glu Glu
 60 65 70
 Leu Gly Gly Pro Val His Ala Leu Ala Ile Gln Ala Arg Thr Pro Ala
 75 80 85 90
 Gln Trp Arg Glu Asn Ser Gln Leu Asp Thr Ser Pro Pro Cys Leu Gly
 95 100 105
 Gly Asn Lys Lys Thr Leu Gly Thr Pro
 110 115

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 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -28...-1

<400> 300
 Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser
 -25 -20 -15
 Gly Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn
 -10 -5 1
 Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn
 5 10 15 20
 Val Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu
 25 30 35
 Ala Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser
 40 45 50
 Gln Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp
 55 60 65
 Ser Leu Phe Leu Gly Trp Ile Trp Leu Gln Leu Leu Glu Val Pro Asp
 70 75 80
 Pro Asn Val Val Pro His Tyr Ala Thr Gly Val Val Leu Phe Gly Leu
 85 90 95 100
 Ser Ala Val Val Glu Leu Leu Gly Glu Pro Phe Trp Val Leu Ala Gln
 105 110 115
 Ala His Met Phe Val Lys Leu Lys Val Ile Ala Glu Ser Leu Ser Val
 120 125 130
 Ile Leu Lys Ser Val Leu Thr Ala Phe Leu Val Leu Trp Leu Pro His

Met Glu Leu Glu Arg Ile Val Ser Ala Ala Leu Leu Ala Phe Val Gln
 -15 -10 -5
 Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp Glu Val Ile Phe
 1 5 10 15
 Ser Tyr Val Leu Gly Val Leu Glu Asp Leu Gly Pro Ser Gly Pro Ser
 20 25 30
 Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met Met Glu Ala Tyr
 35 40 45
 Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile Gly Asp Met Met
 50 55 60
 Gln Lys Leu Ser Gly Gln Leu Ser Asp Ala Arg Asn Lys Glu Asn Leu
 65 70 75
 Gln Pro Gln Ser Ser Gly Val Gln Gly Gln Val Pro Ile Ser Pro Glu
 80 85 90 95
 Pro Leu Gln Arg Pro Glu Met Leu Lys Glu Glu Thr Arg Ser Ser Ala
 100 105 110
 Ala Ala Ala Ala Asp Thr Gln Asp Glu Ala Thr Gly Ala Glu Glu Glu
 115 120 125
 Leu Leu Pro Gly Val Asp Val Leu Leu Glu Val Phe Pro Thr Cys Ser
 130 135 140
 Val Glu Gln Ala Gln Trp Val Leu Ala Lys Ala Arg Gly Asp Leu Glu
 145 150 155
 Glu Ala Val Gln Met Leu Val Glu Gly Lys Glu Glu Gly Pro Ala Ala
 160 165 170 175
 Trp Glu Gly Pro Asn Gln Asp Leu Pro Arg Arg Leu Arg Gly Pro Gln
 180 185 190
 Lys Asp Glu Leu Lys Ser Phe Ile Leu Gln Lys Tyr Met Met Val Asp
 195 200 205
 Ser Ala Glu Asp Gln Lys Ile His Arg Pro Met Ala Pro Lys Glu Ala
 210 215 220
 Pro Lys Lys Leu Ile Arg Tyr Ile Asp Asn Gln Val Val Ser Thr Lys
 225 230 235
 Gly Glu Arg Phe Lys Asp Val Arg Asn Pro Glu Ala Glu Glu Met Lys
 240 245 250 255
 Ala Thr Tyr Ile Asn Leu Lys Pro Ala Arg Lys Tyr Arg Phe His
 260 265 270

<210> 302

<211> 165

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -35...-1

<400> 302

Met Met Arg Cys Cys Arg Arg Arg Cys Cys Cys Arg Gln Pro Pro His
 -35 -30 -25 -20
 Ala Leu Arg Pro Leu Leu Leu Pro Leu Val Leu Leu Pro Pro Leu
 -15 -10 -5
 Ala Ala Ala Ala Ala Gly Pro Asn Arg Cys Asp Thr Ile Tyr Gln Gly
 1 5 10
 Phe Ala Glu Cys Leu Ile Arg Leu Gly Asp Ser Met Gly Arg Gly Gly
 15 20 25
 Glu Leu Glu Thr Ile Cys Arg Ser Trp Asn Tyr Phe His Ala Cys Ala
 30 35 40 45
 Ser Gln Val Leu Ser Gly Cys Pro Glu Glu Ala Ala Ala Val Trp Glu

				50					55				60			
Ser	Leu	Gln	Gln	Glu	Ala	Arg	Gln	Ala	Pro	Arg	Pro	Asn	Asn	Leu	His	
			65					70					75			
Thr	Leu	Cys	Gly	Ala	Pro	Val	His	Val	Arg	Glu	Arg	Gly	Thr	Gly	Ser	
		80					85					90				
Glu	Thr	Asn	Gln	Glu	Thr	Leu	Arg	Ala	Thr	Ala	Pro	Ala	Leu	Pro	Met	
	95					100					105					
Ala	Pro	Ala	Pro	Pro	Leu	Leu	Ala	Ala	Ala	Leu	Ala	Leu	Ala	Tyr	Leu	
110					115					120					125	
Leu	Arg	Pro	Leu	Ala												
				130												

<210> 303
 <211> 148
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -25..-1

<400> 303																
Met	Ala	Ser	Val	Val	Leu	Ala	Leu	Arg	Thr	Arg	Thr	Ala	Val	Thr	Ser	
-25					-20					-15					-10	
Leu	Leu	Ser	Pro	Thr	Pro	Ala	Thr	Ala	Leu	Ala	Val	Arg	Tyr	Ala	Ser	
				-5					1				5			
Lys	Lys	Ser	Gly	Gly	Ser	Ser	Lys	Asn	Leu	Gly	Gly	Lys	Ser	Ser	Gly	
	10						15					20				
Arg	Arg	Gln	Gly	Ile	Lys	Lys	Met	Glu	Gly	His	Tyr	Val	His	Ala	Gly	
25					30						35					
Asn	Ile	Ile	Ala	Thr	Gln	Arg	His	Phe	Arg	Trp	His	Pro	Gly	Ala	His	
40					45				50						55	
Val	Gly	Val	Gly	Lys	Asn	Lys	Cys	Leu	Tyr	Ala	Leu	Glu	Glu	Gly	Ile	
				60					65					70		
Val	Arg	Tyr	Thr	Lys	Glu	Val	Tyr	Val	Pro	His	Pro	Arg	Asn	Thr	Glu	
			75					80					85			
Ala	Val	Asp	Leu	Ile	Thr	Arg	Leu	Pro	Lys	Gly	Ala	Val	Leu	Tyr	Lys	
	90						95				100					
Thr	Phe	Val	His	Val	Val	Pro	Ala	Lys	Pro	Glu	Gly	Thr	Phe	Lys	Leu	
105					110						115					
Val	Ala	Met	Leu													
120																

<210> 304
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34..-1

<400> 304																
Met	Glu	Ser	Glu	Arg	Ser	Lys	Arg	Met	Gly	Asn	Ala	Cys	Ile	Pro	Leu	
				-30					-25					-20		
Lys	Arg	Ile	Ala	Tyr	Phe	Leu	Cys	Leu	Leu	Ser	Ala	Leu	Leu	Leu	Thr	
			-15					-10						-5		
Glu	Gly	Lys	Lys	Pro	Ala	Lys	Pro	Lys	Cys	Pro	Ala	Val	Cys	Thr	Cys	

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30..-1

<400> 306
 Met Ala Ala Thr Ser Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val
 -30 -25 -20 -15
 Ser Val Ala His Ala Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Asp
 -10 -5 1
 Pro Asp Ile Glu Met Ala Trp Ala Met Arg Ala Met Gln His Ala Glu
 5 10 15
 Val Tyr Tyr Lys Leu Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu
 20 25 30
 Thr Lys Val Asp Asp Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu
 35 40 45 50
 Thr Leu Arg Ile Asp Val Leu Asp Pro Glu Glu Leu Lys Ser Glu Ser
 55 60 65
 Ala Lys Glu Lys Trp Arg Pro Phe Cys Leu Lys Phe Asn Gly Ile Val
 70 75 80
 Glu Asp Phe Asn Tyr Gly Thr Leu Leu Arg Leu Asp Cys Ser Gln Gly
 85 90 95
 Tyr Thr Glu Glu Asn Thr Ile Phe Ala Pro Arg Ile Gln Phe Phe Ala
 100 105 110
 Ile Glu Ile Ala Arg Asn Arg Glu Gly Tyr Asn Lys Ala Val Tyr Ile
 115 120 125 130
 Ser Val Gln Asp Lys Glu Gly Glu Lys Gly Val Asn Asn Gly Gly Glu
 135 140 145
 Lys Arg Ala Asp Ser Gly Glu Glu Glu Asn Thr Lys Asn Gly Gly Glu
 150 155 160
 Lys Gly Ala Asp Ser Gly Glu Glu Lys Glu Glu Gly Ile Asn Arg Glu
 165 170 175
 Asp Lys Thr Asp Lys Gly Gly Glu Lys Gly Lys Glu Ala Asp Lys Glu
 180 185 190
 Ile Asn Lys Ser Gly Glu Lys Ala Met
 195 200

<210> 307
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 307
 Met Arg Gln Lys Ala Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe
 -20 -15 -10 -5
 Thr Cys Ser Gly Val Glu Ala Gly Lys Lys Cys Ser Glu Ser Ser
 1 5 10
 Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly
 15 20 25
 Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala
 30 35 40
 Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

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<220>
<221> SIGNAL
<222> -43..-1
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<210> 309
<211> 291
<212> PRT
<213> Homo sapiens
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304

				115				120					125				
Gly	Leu	Asp	Ser	Leu	Thr	Asn	Val	Asp	Leu	Arg	Gly	Asn	Ser	Phe	Asn		
				130				135					140				
Cys	Asp	Cys	Lys	Leu	Lys	Trp	Leu	Val	Glu	Trp	Leu	Gly	His	Thr	Asn		
		145					150					155					
Ala	Thr	Val	Glu	Asp	Ile	Tyr	Cys	Glu	Gly	Pro	Pro	Glu	Tyr	Lys	Lys		
	160					165					170						
Arg	Lys	Ile	Asn	Ser	Leu	Ser	Ser	Lys	Asp	Phe	Asp	Cys	Ile	Ile	Thr		
175					180					185					190		
Glu	Phe	Ala	Lys	Ser	Gln	Asp	Leu	Pro	Tyr	Gln	Ser	Leu	Ser	Ile	Asp		
				195				200						205			
Thr	Phe	Ser	Tyr	Leu	Asn	Asp	Glu	Tyr	Val	Val	Ile	Ala	Gln	Pro	Phe		
			210					215					220				
Thr	Gly	Lys	Cys	Ile	Phe	Leu	Glu	Trp	Asp	His	Val	Glu	Lys	Thr	Phe		
		225					230					235					
Arg	Asn	Tyr	Asp	Asn	Ile	Thr	Val	Leu	Arg	Glu	Ile	His	Arg	Phe	Thr		
	240					245					250						
Asn	Met	Ser															
255																	

<210> 310

<211> 426

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28...-1

<400> 310

Met	Ser	Pro	Ala	Phe	Arg	Ala	Met	Asp	Val	Glu	Pro	Arg	Ala	Lys	Gly		
			-25					-20					-15				
Val	Leu	Leu	Glu	Pro	Phe	Val	His	Gln	Val	Gly	Gly	His	Ser	Cys	Val		
		-10					-5					1					
Leu	Arg	Phe	Asn	Glu	Thr	Thr	Leu	Cys	Lys	Pro	Leu	Val	Pro	Arg	Glu		
5					10					15					20		
His	Gln	Phe	Tyr	Glu	Thr	Leu	Pro	Ala	Glu	Met	Arg	Lys	Phe	Thr	Pro		
				25					30					35			
Gln	Tyr	Lys	Gly	Val	Val	Ser	Val	Arg	Phe	Glu	Glu	Asp	Glu	Asp	Arg		
			40					45					50				
Asn	Leu	Cys	Leu	Ile	Ala	Tyr	Pro	Leu	Lys	Gly	Asp	His	Gly	Ile	Val		
	55						60					65					
Asp	Ile	Val	Asp	Asn	Ser	Asp	Cys	Glu	Pro	Lys	Ser	Lys	Leu	Leu	Arg		
	70					75					80						
Trp	Thr	Thr	Asn	Lys	Lys	His	His	Val	Leu	Glu	Thr	Glu	Lys	Thr	Pro		
85					90					95					100		
Lys	Asp	Trp	Val	Arg	Gln	His	Arg	Lys	Glu	Glu	Lys	Met	Lys	Ser	His		
				105					110					115			
Lys	Leu	Glu	Glu	Glu	Phe	Glu	Trp	Leu	Lys	Lys	Ser	Glu	Val	Leu	Tyr		
			120					125					130				
Tyr	Thr	Val	Glu	Lys	Lys	Gly	Asn	Ile	Ser	Ser	Gln	Leu	Lys	His	Tyr		
		135					140					145					
Asn	Pro	Trp	Ser	Met	Lys	Cys	His	Gln	Gln	Gln	Leu	Gln	Arg	Met	Lys		
	150				155						160						
Glu	Asn	Ala	Lys	His	Arg	Asn	Gln	Tyr	Lys	Phe	Ile	Leu	Leu	Glu	Asn		
165					170					175					180		
Leu	Thr	Ser	Arg	Tyr	Glu	Val	Pro	Cys	Val	Leu	Asp	Leu	Lys	Met	Gly		
				185					190					195			

Thr	Arg	Gln	His	Gly	Asp	Asp	Ala	Ser	Glu	Glu	Lys	Ala	Ala	Asn	Gln
			200					205					210		
Ile	Arg	Lys	Cys	Gln	Gln	Ser	Thr	Ser	Ala	Val	Ile	Gly	Val	Arg	Val
		215					220					225			
Cys	Gly	Met	Gln	Val	Tyr	Gln	Ala	Gly	Ser	Gly	Gln	Leu	Met	Phe	Met
	230					235					240				
Asn	Lys	Tyr	His	Gly	Arg	Lys	Leu	Ser	Met	Gln	Gly	Phe	Lys	Glu	Ala
245					250					255					260
Leu	Phe	Gln	Phe	Phe	His	Asn	Gly	Arg	Tyr	Leu	Arg	Arg	Glu	Leu	Leu
			265					270						275	
Gly	Pro	Val	Leu	Lys	Lys	Leu	Thr	Glu	Leu	Lys	Ala	Val	Leu	Glu	Arg
		280					285						290		
Gln	Glu	Ser	Tyr	Arg	Phe	Tyr	Ser	Ser	Ser	Leu	Leu	Val	Ile	Tyr	Asp
	295						300					305			
Gly	Lys	Glu	Arg	Pro	Glu	Val	Val	Leu	Asp	Ser	Asp	Ala	Glu	Asp	Leu
	310				315						320				
Glu	Asp	Leu	Ser	Glu	Glu	Ser	Ala	Asp	Glu	Ser	Ala	Gly	Ala	Tyr	Ala
325					330					335					340
Tyr	Lys	Pro	Ile	Gly	Ala	Ser	Ser	Val	Asp	Val	Arg	Met	Ile	Asp	Phe
			345					350						355	
Ala	His	Thr	Thr	Cys	Arg	Leu	Tyr	Gly	Glu	Asp	Thr	Val	Val	His	Glu
			360					365					370		
Gly	Gln	Asp	Ala	Gly	Tyr	Ile	Phe	Gly	Leu	Gln	Ser	Leu	Ile	Asp	Ile
		375				380						385			
Val	Thr	Glu	Ile	Ser	Glu	Glu	Ser	Gly	Glu						
	390					395									

<210> 311
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 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -16...-1

<400> 311															
Met	Gly	Leu	Tyr	Ala	Ala	Ala	Ala	Gly	Val	Leu	Ala	Gly	Val	Glu	Ser
	-15					-10					-5				
Arg	Gln	Gly	Ser	Ile	Lys	Gly	Leu	Val	Tyr	Ser	Ser	Asn	Phe	Gln	Asn
1			5					10					15		
Val	Lys	Gln	Leu	Tyr	Ala	Leu	Val	Cys	Glu	Thr	Gln	Arg	Tyr	Ser	Ala
		20					25					30			
Val	Leu	Asp	Ala	Val	Ile	Ala	Ser	Ala	Gly	Leu	Leu	Arg	Ala	Glu	Lys
	35					40					45				
Lys	Leu	Arg	Pro	His	Leu	Ala	Lys	Val	Leu	Val	Tyr	Glu	Leu	Leu	Leu
	50				55						60				
Gly	Lys	Gly	Phe	Arg	Gly	Gly	Gly	Gly	Arg	Trp	Lys	Ala	Leu	Leu	Gly
65				70				75						80	
Arg	His	Gln	Ala	Arg	Leu	Lys	Ala	Glu	Leu	Ala	Arg	Leu	Lys	Val	His
			85					90					95		
Arg	Gly	Val	Ser	Arg	Asn	Glu	Asp	Leu	Leu	Glu	Val	Gly	Ser	Arg	Pro
		100						105					110		
Gly	Pro	Ala	Ser	Gln	Leu	Pro	Arg	Phe	Val	Arg	Val	Asn	Thr	Leu	Lys
	115						120					125			
Thr	Cys	Ser	Asp	Asp	Val	Val	Asp	Tyr	Phe	Lys	Arg	Gln	Gly	Phe	Ser
	130					135					140				
Tyr	Gln	Gly	Arg	Ala	Ser	Ser	Leu	Asp	Asp	Leu	Arg	Ala	Leu	Lys	Gly

145					150					155					160
Lys	His	Phe	Leu	Leu	Asp	Pro	Leu	Met	Pro	Glu	Leu	Leu	Val	Phe	Pro
				165					170					175	
Ala	Gln	Thr	Asp	Leu	His	Glu	His	Pro	Leu	Tyr	Arg	Ala	Gly	His	Leu
			180					185					190		
Ile	Leu	Gln	Asp	Arg	Ala	Ser	Cys	Leu	Pro	Ala	Met	Leu	Leu	Asp	Pro
		195					200					205			
Pro	Pro	Gly	Ser	His	Val	Ile	Asp	Ala	Cys	Ala	Ala	Pro	Gly	Asn	Lys
	210					215				220					
Thr	Ser	His	Leu	Ala	Ala	Leu	Leu	Lys	Asn	Gln	Gly	Lys	Ile	Phe	Ala
225					230					235				240	
Phe	Asp	Leu	Asp	Ala	Lys	Arg	Leu	Ala	Ser	Met	Ala	Thr	Leu	Leu	Ala
				245				250						255	
Arg	Ala	Gly	Val	Ser	Cys	Cys	Glu	Leu	Ala	Glu	Glu	Asp	Phe	Leu	Ala
			260				265					270			
Val	Ser	Pro	Ser	Asp	Pro	Arg	Tyr	His	Glu	Val	His	Tyr	Ile	Leu	Leu
	275						280				285				
Asp	Pro	Ser	Cys	Ser	Gly	Ser	Gly	Met	Pro	Ser	Arg	Gln	Leu	Glu	Glu
	290					295			300						
Pro	Gly	Ala	Gly	Thr	Pro	Ser	Pro	Val	Arg	Leu	His	Ala	Leu	Ala	Gly
305					310				315					320	
Phe	Gln	Gln	Arg	Ala	Leu	Cys	His	Ala	Leu	Thr	Phe	Pro	Ser	Leu	Gln
				325					330					335	
Arg	Leu	Val	Tyr	Ser	Thr	Cys	Ser	Leu	Cys	Gln	Glu	Glu	Asn	Glu	Asp
		340						345					350		
Val	Val	Arg	Asp	Ala	Leu	Gln	Gln	Asn	Pro	Gly	Ala	Phe	Arg	Leu	Ala
	355						360				365				
Pro	Ala	Leu	Pro	Ala	Trp	Pro	His	Arg	Gly	Leu	Ser	Thr	Phe	Pro	Gly
	370				375				380						
Ala	Glu	His	Cys	Leu	Arg	Ala	Ser	Pro	Glu	Thr	Thr	Leu	Ser	Ser	Gly
385					390				395					400	
Phe	Phe	Val	Ala	Val	Ile	Glu	Arg	Val	Glu	Val	Pro	Ser	Ser	Ala	Ser
				405					410					415	
Gln	Ala	Lys	Ala	Ser	Ala	Pro	Glu	Arg	Thr	Pro	Ser	Pro	Ala	Pro	Lys
			420				425					430			
Arg	Lys	Lys	Arg	Gln	Gln	Arg	Ala	Ala	Ala	Gly	Ala	Cys	Thr	Pro	Pro
		435				440					445				
Cys	Thr														
	450														

<210> 312
 <211> 382
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 312
 Met Gly Leu Tyr Ala Ala Ala Ala Gly Val Leu Ala Gly Val Glu Ser
 -15 -10 -5
 Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser Ser Asn Phe Gln Asn
 1 5 10 15
 Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr Gln Arg Tyr Ser Ala
 20 25 30
 Val Leu Asp Ala Val Ile Ala Ser Ala Gly Leu Leu Arg Ala Glu Lys
 35 40 45

Lys Leu Arg Pro His Leu Ala Lys Val Leu Val Tyr Glu Leu Leu Leu
 50 55 60
 Gly Lys Gly Phe Arg Gly Gly Gly Arg Trp Lys Ala Leu Leu Gly
 65 70 75 80
 Arg His Gln Ala Arg Leu Lys Ala Glu Leu Ala Arg Leu Lys Val His
 85 90 95
 Arg Gly Val Ser Arg Asn Glu Asp Leu Leu Glu Val Gly Ser Arg Pro
 100 105 110
 Gly Pro Ala Ser Gln Leu Pro Arg Phe Val Arg Val Asn Thr Leu Lys
 115 120 125
 Thr Cys Ser Asp Asp Val Val Asp Tyr Phe Lys Arg Gln Gly Phe Ser
 130 135 140
 Tyr Gln Gly Arg Ala Ser Ser Leu Asp Asp Leu Arg Ala Leu Lys Gly
 145 150 155 160
 Lys His Phe Leu Leu Asp Pro Leu Met Pro Glu Leu Leu Val Phe Pro
 165 170 175
 Ala Gln Thr Asp Leu His Glu His Pro Leu Tyr Arg Ala Gly His Leu
 180 185 190
 Ile Leu Gln Asp Arg Ala Ser Cys Leu Pro Ala Met Leu Leu Asp Pro
 195 200 205
 Pro Pro Gly Ser His Val Ile Asp Ala Cys Ala Ala Pro Gly Asn Lys
 210 215 220
 Thr Ser His Leu Ala Ala Leu Leu Lys Asn Gln Gly Lys Ile Phe Ala
 225 230 235 240
 Phe Asp Leu Asp Ala Lys Arg Leu Ala Ser Met Ala Thr Leu Leu Ala
 245 250 255
 Arg Ala Gly Val Ser Cys Cys Glu Leu Ala Glu Glu Asp Phe Leu Ala
 260 265 270
 Val Ser Pro Ser Asp Pro Arg Tyr His Glu Val His Tyr Ile Leu Leu
 275 280 285
 Asp Pro Ser Cys Ser Gly Ser Gly Met Pro Ser Arg Gln Leu Glu Glu
 290 295 300
 Pro Gly Ala Gly Thr Pro Ser Pro Val Arg Leu His Ala Leu Ala Ala
 305 310 315 320
 Ser Ser Ser Glu Pro Cys Ala Thr Arg Ser Leu Ser Leu Pro Cys Ser
 325 330 335
 Gly Ser Ser Thr Pro Arg Ala Pro Ser Ala Arg Arg Arg Met Lys Thr
 340 345 350
 Trp Cys Glu Met Arg Cys Ser Arg Thr Arg Ala Pro Ser Gly
 355 360 365

<210> 313
 <211> 258
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36..-1

<400> 313
 Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Glu Leu Arg Leu Cys Phe
 -35 -30 -25
 Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp Ala
 -20 -15 -10 -5
 Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro Val
 1 5 10
 Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro Gly

<400> 316
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ser Leu Val Leu
 -15 -10 -5
 Cys Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala Phe Asp
 1 5 10 15
 Glu Leu Arg Thr Asp Phe Lys Ser Pro Ile Asp Gln Cys Asn Pro Val
 20 25 30
 His Ala Arg Glu Arg Leu Arg Asn Ile Glu Arg Ile Cys Phe Leu Leu
 35 40 45
 Arg Lys Leu Val Leu Pro Glu Tyr Ser Ile His Ser Leu Phe Cys Ile
 50 55 60
 Met Phe Leu Cys Ala Gln Glu Trp Leu Thr Leu Gly Leu Asn Val Pro
 65 70 75
 Leu Leu Phe Tyr His Phe Trp Arg Tyr Phe His Cys Pro Ala Asp Ser
 80 85 90 95
 Ser Glu Leu Ala Tyr Asp Pro Pro Val Val Met Asn Pro Asp Thr Leu
 100 105 110
 Ser Tyr Cys Cln Lys Glu Ala Trp Cys Lys Leu Ala Phe Tyr Leu Leu
 115 120 125
 Ser Phe Phe Tyr Tyr Leu Tyr Cys Met Ile Tyr Thr Leu Val Ser Ser
 130 135 140

<210> 317
 <211> 426
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

<400> 317
 Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly
 -25 -20 -15
 Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val
 -10 -5 1
 Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu
 5 10 15 20
 His Gln Phe Tyr Glu Thr Leu Pro Ser Glu Met Arg Lys Phe Thr Pro
 25 30 35
 Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg
 40 45 50
 Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val
 55 60 65
 Asp Ile Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg
 70 75 80
 Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro
 85 90 95 100
 Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His
 105 110 115
 Lys Leu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr
 120 125 130
 Tyr Thr Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr
 135 140 145
 Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys
 150 155 160
 Glu Asn Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn
 165 170 175 180

Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly
 185 190 195
 Thr Arg Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala Ala Asn Gln
 200 205 210
 Ile Arg Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly Val Arg Val
 215 220 225
 Cys Gly Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu Met Phe Met
 230 235 240
 Asn Lys Tyr His Gly Arg Lys Leu Ser Val Gln Gly Phe Lys Glu Ala
 245 250 255 260
 Leu Phe Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg Glu Leu Leu
 265 270 275
 Gly Pro Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val Leu Glu Arg
 280 285 290
 Gln Glu Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val Ile Tyr Asp
 295 300 305
 Gly Lys Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala Glu Asp Leu
 310 315 320
 Glu Asp Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly Ala Tyr Ala
 325 330 335 340
 Tyr Lys Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met Ile Asp Phe
 345 350 355
 Ala His Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val Val His Glu
 360 365 370
 Gly Gln Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu Ile Asp Ile
 375 380 385
 Val Thr Glu Ile Ser Glu Glu Ser Gly Glu
 390 395

<210> 318
 <211> 301
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 318
 Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val
 -20 -15 -10 -5
 Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln
 1 5 10
 Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg
 15 20 25
 Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile
 30 35 40
 Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu
 45 50 55 60
 Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Leu Ser Phe Val Phe
 65 70 75
 Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met
 80 85 90
 Lys Ser Val Leu Trp Trp Leu Pro Val Glu Lys Ala Phe Trp Arg Gln
 95 100 105
 Pro Ala Gly Pro Gly Ser Gly Ile Arg Glu Arg Leu Glu His Pro Val
 110 115 120
 Leu His Val Ser Trp Asn Asp Ala Arg Ala Tyr Cys Ala Trp Arg Gly

125					130					135					140
Lys	Arg	Leu	Pro	Thr	Glu	Glu	Glu	Trp	Glu	Phe	Ala	Ala	Arg	Gly	Gly
				145					150					155	
Leu	Lys	Gly	Gln	Val	Tyr	Pro	Trp	Gly	Asn	Trp	Phe	Gln	Pro	Asn	Arg
			160					165					170		
Thr	Asn	Leu	Trp	Gln	Gly	Lys	Phe	Pro	Lys	Gly	Asp	Lys	Ala	Glu	Asp
		175					180					185			
Gly	Phe	His	Gly	Val	Ser	Pro	Val	Asn	Ala	Phe	Pro	Ala	Gln	Asn	Asn
	190					195					200				
Tyr	Gly	Leu	Tyr	Asp	Leu	Leu	Gly	Asn	Val	Trp	Glu	Trp	Thr	Ala	Ser
205					210					215					220
Pro	Tyr	Gln	Ala	Ala	Glu	Gln	Asp	Met	Arg	Val	Leu	Arg	Gly	Ala	Ser
			225						230					235	
Trp	Ile	Asp	Thr	Ala	Asp	Gly	Ser	Ala	Asn	His	Arg	Ala	Arg	Val	Thr
			240					245					250		
Thr	Arg	Met	Gly	Asn	Thr	Pro	Asp	Ser	Ala	Ser	Asp	Asn	Leu	Gly	Phe
		255					260					265			
Arg	Cys	Ala	Ala	Asp	Ala	Gly	Arg	Pro	Pro	Gly	Glu	Leu			
	270					275					280				

<210> 319

<211> 119

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17...-1

<400> 319

Met	Gly	Ser	Gly	Trp	Leu	Thr	Ala	Val	Ala	Ser	Leu	Leu	Pro	Ser	Pro
		-15					-10					-5			
Gly	Asn	Ser	Glu	Leu	Pro	Val	Gln	Ala	Leu	Gly	Arg	Arg	Gly	Gly	Arg
	1				5					10				15	
Asp	Trp	Ala	Arg	Asn	Glu	Ala	Gly	Arg	Asp	Leu	Glu	Lys	Pro	Pro	Arg
				20				25					30		
Leu	His	Cys	Ser	Gly	Arg	Gly	Arg	Leu	Glu	Glu	Pro	Val	Pro	Pro	Asn
			35				40						45		
His	Leu	Pro	Val	Gly	Leu	Ser	Val	Arg	Gly	Ser	Gln	Val	Leu	Ser	Ser
		50					55				60				
Ala	Gly	Pro	Arg	Arg	Cys	Arg	Leu	Thr	Gly	Thr	Arg	Asn	Pro	Val	Arg
	65				70					75					
Gly	Pro	Arg	Arg	Val	Glu	Gln	Ile	Ala	Arg	Gly	Gly	Pro	Glu	Ala	Arg
80					85					90					95
Arg	Gln	Ala	Gly	Asp	Ser	Cys									
				100											

<210> 320

<211> 95

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -39...-1

<400> 320

Met Asp Tyr Ser Arg Val Phe Gln Gly Val Phe Phe Thr Phe Lys His

				-35					-30					-25			
Ala	Phe	Ala	Asp	Gly	Ala	Trp	Asp	Leu	Ser	Phe	Leu	Cys	Ala	Leu	Cys		
			-20					-15					-10				
Ser	Phe	Cys	Pro	Ile	Ser	Ala	Ala	Ser	Gly	Arg	Pro	Tyr	Arg	Tyr	Leu		
		-5					1				5						
Glu	Phe	Trp	Arg	Leu	Tyr	Leu	Ser	Pro	Ser	Ser	Met	Glu	Asn	Gly	Val		
10				15					20						25		
Gln	Lys	Phe	His	Glu	Thr	Phe	Phe	Ile	Val	Phe	Leu	Leu	Leu	Phe	Asp		
			30					35						40			
Ile	Glu	Arg	Lys	Gly	Lys	Ser	Ser	Val	Cys	Pro	Phe	Cys	Tyr	Arg			
			45					50					55				

<210> 321
 <211> 191
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39...-1

<400> 321																	
Met	Met	Thr	Ile	Thr	Phe	Leu	Pro	Tyr	Thr	Phe	Ser	Leu	Met	Val	Thr		
			-35					-30					-25				
Phe	Pro	Asp	Val	Pro	Leu	Gly	Ile	Phe	Leu	Phe	Cys	Val	Cys	Val	Ile		
		-20					-15				-10						
Ala	Ile	Gly	Val	Val	Gln	Ala	Leu	Ile	Val	Gly	Tyr	Ala	Phe	His	Phe		
		-5				1				5							
Pro	His	Leu	Leu	Ser	Pro	Gln	Ile	Gln	Arg	Ser	Ala	His	Arg	Ala	Leu		
10				15				20						25			
Tyr	Arg	Arg	His	Val	Leu	Gly	Ile	Val	Leu	Gln	Gly	Pro	Ala	Leu	Cys		
			30				35						40				
Phe	Ala	Ala	Ala	Ile	Phe	Ser	Leu	Phe	Phe	Val	Pro	Leu	Ser	Tyr	Leu		
			45				50					55					
Leu	Met	Val	Thr	Val	Ile	Leu	Leu	Pro	Tyr	Val	Ser	Lys	Val	Thr	Gly		
		60				65					70						
Trp	Cys	Arg	Asp	Arg	Leu	Leu	Gly	His	Arg	Glu	Pro	Ser	Ala	His	Pro		
	75				80				85								
Val	Glu	Val	Phe	Ser	Phe	Asp	Leu	His	Glu	Pro	Leu	Ser	Lys	Glu	Arg		
90				95				100						105			
Val	Glu	Ala	Phe	Ser	Asp	Gly	Val	Tyr	Ala	Ile	Val	Ala	Thr	Leu	Leu		
			110				115						120				
Ile	Leu	Asp	Ile	Cys	Pro	Ser	Cys	Ser	Leu	Trp	Leu	Ala	Val	Ala	Ser		
		125				130						135					
Phe	Gln	Arg	Leu	Leu	Leu	Arg	Gly	Leu	Ile	Cys	Leu	Phe	Val	Cys			
		140				145					150						

<210> 322
 <211> 89
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41...-1

<400> 322
 Met Pro Pro Thr Arg Asp Pro Phe Gln Gln Pro Thr Leu Asp Asn Asp

-40 -35 -30
 Asp Ser Tyr Leu Gly Glu Leu Arg Ala Ser Lys Val Leu Trp Phe Leu
 -25 -20 -15 -10
 Ala Gln Ile Pro Ser Arg Val Ala Gly Ser Leu Leu Ser Val Cys Val
 -5 1 5
 Met Ser Arg Asp Gly Asn Ile Lys Asp Ser Gly Glu Asp Thr Gln Ser
 10 15 20
 Gly Thr Arg Glu Val Cys Phe Leu Pro Ala Ser Leu Ser Pro Tyr Ser
 25 30 35
 Ser Arg Leu Thr Phe Gln Arg Arg Phe
 40 45

<210> 323
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -38...-1

<400> 323
 Met Ser Ser Pro Gln Leu Pro Ala Phe Leu Trp Asp Lys Gly Thr Leu
 -35 -30 -25
 Thr Thr Ala Ile Ser Asn Pro Ala Cys Leu Val Asn Val Leu Phe Phe
 -20 -15 -10
 Phe Thr Pro Leu Met Thr Leu Val Thr Leu Leu Ile Leu Val Trp Lys
 -5 1 5 10
 Val Thr Lys Asp Lys Ser Asn Lys Asn Arg Glu Thr His Pro Arg Lys
 15 20 25
 Glu Ala Thr Trp Leu Pro
 30

<210> 324
 <211> 168
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 324
 Met Arg Gly Pro Thr Ala Gly Pro Ser Val Leu Ser Ala Ala His Leu
 -25 -20 -15 -10
 Leu Val Val Ile Leu Pro Ala Asn Ala Ala Leu Lys Leu Leu Ser Trp
 -5 1 5
 Glu Arg Leu Ala Ala Pro Ala Ile Glu Val Glu Val Pro Ser Lys Glu
 10 15 20
 Val Leu Ala Ala Pro Thr Lys Ala Lys Leu Ile Pro Ser Glu Asp Met
 25 30 35
 Leu Ala Ala Pro Ala Met Asp Leu Leu Asp Ser Phe Ser Pro Gly Phe
 40 45 50 55
 Leu Ile Ala Ala Pro Ala Ser Ala Val Ile Thr Trp Pro Gly Pro Ala
 60 65 70
 Asp Leu Val Val Ala Met Leu Ile Ala Pro Val Ala Gly Leu Ile Ala
 75 80 85
 Ala Pro Ala Ile Ala Thr Ser Val Leu Gly Pro Val Ala Val Pro Ala

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          90          95          100
Thr Ala Met Pro Pro Ala Val Leu Ala Ala Pro Pro Ser Ala Ala Pro
    105          110          115
Gly Val Leu Val Asp Gly Glu Ala Ala Leu Ala Val Pro Trp Glu Ala
    120          125          130          135
Cys Trp Ile Pro Ser Pro Pro Ala
          140

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<210> 325
 <211> 166
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

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<400> 325
Met Leu Pro Leu Leu Ile Ile Cys Leu Leu Pro Ala Ile Glu Gly Lys
-15          -10          -5          1
Asn Cys Leu Arg Cys Trp Pro Glu Leu Ser Ala Leu Ile Asp Tyr Asp
          5          10          15
Leu Gln Ile Leu Trp Val Thr Pro Gly Pro Pro Thr Glu Leu Ser Gln
          20          25          30
Asn Arg Asp His Leu Glu Glu Glu Thr Ala Lys Phe Phe Thr Gln Val
          35          40          45
His Gln Ala Ile Lys Thr Leu Arg Asp Asp Lys Thr Val Leu Leu Glu
          50          55          60          65
Glu Ile Tyr Thr His Lys Asn Leu Phe Thr Glu Arg Leu Asn Lys Ile
          70          75          80
Ser Asp Gly Leu Lys Glu Lys Asp Ile Gln Ser Thr Leu Lys Val Thr
          85          90          95
Ser Cys Ala Asp Cys Arg Thr His Phe Leu Ser Cys Asn Asp Pro Thr
          100          105          110
Phe Cys Pro Ala Arg Asn Arg Arg Thr Ser Leu Trp Ala Val Ser Leu
          115          120          125
Ser Ser Ala Leu Leu Leu Ala Ile Ala Gly Asp Val Ser Phe Thr Gly
          130          135          140          145
Lys Gly Arg Arg Arg Gln
          150

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<210> 326
 <211> 156
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

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<400> 326
Met Asn Ile Leu Met Leu Thr Phe Ile Ile Cys Gly Leu Leu Thr Arg
-15          -10          -5          1
Val Thr Lys Gly Ser Phe Glu Pro Gln Lys Cys Trp Lys Asn Asn Val
          5          10          15
Gly His Cys Arg Arg Arg Cys Leu Asp Thr Glu Arg Tyr Ile Leu Leu
          20          25          30
Cys Arg Asn Lys Leu Ser Cys Cys Ile Ser Ile Ile Ser His Glu Tyr

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35		40		45												
Thr	Arg	Arg	Pro	Ala	Phe	Pro	Val	Ile	His	Leu	Glu	Asp	Ile	Thr	Leu	
50					55					60					65	
Asp	Tyr	Ser	Asp	Val	Asp	Ser	Phe	Thr	Gly	Ser	Pro	Val	Ser	Met	Leu	
			70						75					80		
Asn	Asp	Leu	Ile	Thr	Phe	Asp	Thr	Thr	Lys	Phe	Gly	Glu	Thr	Met	Thr	
			85					90					95			
Pro	Glu	Thr	Asn	Thr	Pro	Glu	Thr	Thr	Met	Pro	Pro	Ser	Glu	Ala	Thr	
		100					105					110				
Thr	Pro	Glu	Thr	Thr	Met	Pro	Pro	Ser	Glu	Thr	Ala	Thr	Ser	Glu	Thr	
	115					120					125					
Met	Pro	Pro	Pro	Ser	Gln	Thr	Ala	Leu	Thr	His	Asn					
130					135					140						

<210> 327
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32..-1

<400> 327																
Met	Ala	Lys	Met	Phe	Asp	Leu	Arg	Thr	Lys	Ile	Met	Ile	Gly	Ile	Glu	
	-30					-25					-20					
Ser	Ser	Leu	Leu	Val	Ala	Ala	Met	Val	Leu	Leu	Ser	Val	Val	Phe	Cys	
	-15				-10						-5					
Leu	Tyr	Phe	Lys	Val	Ala	Lys	Ala	Leu	Lys	Ala	Ala	Lys	Asp	Pro	Asp	
1			5					10					15			
Ala	Val	Ala	Val	Lys	Asn	His	Asn	Pro	Asp	Lys	Val	Cys	Trp	Ala	Thr	
		20					25					30				
Asn	Ser	Gln	Ala	Lys	Ala	Thr	Thr	Met	Glu	Ser	Cys	Pro	Ser	Leu	Gln	
	35					40					45					
Cys	Cys	Glu	Gly	Cys	Arg	Met	His	Ala	Ser	Ser	Asp	Ser	Leu	Pro	Pro	
	50				55						60					
Cys	Cys	Cys	Asp	Ile	Asn	Glu	Gly	Leu								
65				70												

<210> 328
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

<400> 328																
Met	Ser	Asp	Glu	Asp	Glu	Ser	Ser	Asp	Tyr	Leu	Cys	Leu	Ser	Ile	Leu	
	-25					-20					-15					
Gly	Leu	Phe	Cys	Cys	Leu	Pro	Leu	Ala	Ile	Pro	Ala	Val	Ile	Phe	Ser	
	-10				-5					1				5		
Cys	Leu	Thr	Lys	Asn	Tyr	Asn	Lys	Ser	Ser	Asp	Tyr	Glu	Leu	Ala	Ala	
			10					15					20			
Lys	Thr	Ser	Lys	Gln	Ala	Tyr	Tyr	Trp	Ala	Ile	Ala	Ser	Ile	Thr	Val	
		25					30					35				
Gly	Ile	Leu	Gly	Thr	Ile	Leu	Tyr	Thr	Tyr	Leu	Ile	Tyr	Leu	Leu	Arg	

40 45 50
 Leu
 <210> 329
 <211> 95
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -27..-1
 <400> 329
 Met Thr Asp Gln Asp Arg Ile Ile Asn Leu Val Val Gly Ser Leu Thr
 -25 -20 -15
 Ser Leu Leu Ile Leu Val Thr Leu Ile Ser Ala Phe Val Phe Pro Gln
 -10 -5 1 5
 Leu Pro Pro Lys Pro Leu Asn Ile Phe Phe Ala Val Cys Ile Ser Leu
 10 15 20
 Ser Ser Ile Thr Ala Cys Ile Ile Tyr Trp Tyr Arg Gln Gly Asp Leu
 25 30 35
 Glu Pro Lys Phe Arg Lys Leu Ile Tyr Tyr Ile Ile Phe Ser Ile Ile
 40 45 50
 Met Leu Cys Ile Cys Ala Asn Leu Tyr Phe His Asp Val Gly Arg
 55 60 65
 <210> 330
 <211> 84
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -20..-1
 <400> 330
 Met Ala Ala Ala Val Pro Ser Leu Leu Leu Ser Leu Pro Pro His
 -20 -15 -10 -5
 Gln Gly Leu Thr Phe Ser Asn Lys Ile Gln Pro Phe Gly Ala Gln Gly
 1 5 10
 Val Leu His Pro Glu Pro Gly Leu Arg Asp Trp Leu Leu Pro Thr Cys
 15 20 25
 Ser Arg Gln Leu Arg Val Ala Leu Pro Glu Lys Gly Ser Glu Gly Ser
 30 35 40
 Leu Cys Gln Thr Gln Leu Pro Ala Thr Pro Cys Phe Leu Pro Ser Asn
 45 50 55 60
 Thr Val Arg Thr
 <210> 331
 <211> 124
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> SIGNAL
 <222> -32..-1
 <400> 331

Met Val Val Val Glu Pro Gly Ala Ser Leu Phe Pro Asn Gly Val Pro
-30 -25 -20
Trp Leu Tyr Ala Val Phe Ala Val Leu Phe Val Phe Phe Leu Phe Ala
-15 -10 -5
Met Leu Ser Pro Phe Leu Leu Glu Ile Asp Gln His Ile Lys Lys Phe
1 5 10 15
Leu Ile Arg Cys Arg Tyr Ser Leu His Asn Thr Val His Lys Asp Lys
20 25 30
Lys Asn Ser Glu Ile Lys Met Asp His Leu Glu Arg Pro Gly Cys Pro
35 40 45
Leu Glu Ser Pro Arg Arg Gly Val Leu Gly Gly Lys Lys Asn Gly Met
50 55 60
Gly Asn Asp Pro Leu Leu Phe Val Lys Val Thr Lys Glu Pro Arg Asp
65 70 75 80
Ser Glu Ala Glu Ile Tyr Thr Pro Gly Pro Ser Val
85 90

<210> 332
<211> 62
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -46...-1

<400> 332
Met Asp Gln Leu Val Phe Lys Glu Thr Ile Trp Asn Asp Ala Phe Trp
-45 -40 -35
Gln Asn Pro Trp Asp Gln Gly Gly Leu Ala Val Ile Ile Leu Phe Ile
-30 -25 -20 -15
Thr Ala Val Leu Leu Leu Ile Leu Phe Ala Ile Val Phe Gly Leu Leu
-10 -5 1
Thr Ser Thr Glu Asn Thr Gln Cys Glu Ala Gly Glu Glu Glu
5 10 15

<210> 333
<211> 150
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23...-1

<400> 333
Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile Cys
-20 -15 -10
Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr Lys
-5 1 5
Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Gly Cys
10 15 20 25
Leu Tyr Leu Ile Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe
30 35 40
Val Leu Ser Val His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys
45 50 55
Lys Leu Lys Lys Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu
60 65 70

Ser Pro Leu Ile Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr
 75 80 85
 Thr Ala Ser Val Ile Tyr Lys Ile Trp Glu His Arg Ser His His Pro
 90 95 100 105
 Ser Ser Lys Lys Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu
 110 115 120
 Glu Gly Ala Arg Arg Tyr
 125

<210> 334
 <211> 198
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<400> 334
 Met Leu Leu Gly Arg Leu Thr Ser Gln Leu Leu Arg Ala Val Pro Trp
 -10 -5 1
 Ala Gly Gly Arg Pro Pro Trp Pro Val Ser Gly Val Leu Gly Ser Arg
 5 10 15
 Val Cys Gly Pro Leu Tyr Ser Thr Ser Pro Ala Gly Pro Gly Arg Ala
 20 25 30 35
 Ala Ser Leu Pro Arg Lys Gly Ala Gln Leu Glu Leu Glu Glu Met Val
 40 45 50
 Pro Arg Lys Met Ser Val Ser Pro Leu Glu Ser Trp Leu Thr Ala Arg
 55 60 65
 Cys Phe Leu Pro Arg Leu Asp Thr Gly Thr Ala Gly Thr Val Ala Pro
 70 75 80
 Pro Gln Ser Tyr Gln Cys Pro Pro Ser Gln Ile Gly Glu Gly Ala Glu
 85 90 95
 Gln Gly Asp Glu Gly Val Ala Asp Ala Pro Gln Ile Gln Cys Lys Asn
 100 105 110 115
 Val Leu Lys Ile Arg Arg Arg Lys Met Asn His His Lys Tyr Arg Lys
 120 125 130
 Leu Val Lys Lys Thr Arg Phe Leu Arg Arg Lys Val Gln Glu Gly Arg
 135 140 145
 Leu Arg Arg Lys Gln Ile Lys Phe Glu Lys Asp Leu Arg Arg Ile Trp
 150 155 160
 Leu Lys Ala Gly Leu Lys Glu Ala Pro Glu Gly Trp Gln Thr Pro Lys
 165 170 175
 Ile Tyr Leu Arg Gly Lys
 180 185

<210> 335
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 335
 Met Val Pro Leu Pro Lys Gln Ser Leu Lys Phe Phe Cys Ala Leu Glu
 -20 -15 -10

Val Val Leu Pro Ser Cys Asp Cys Arg Ser Pro Gly Ile Gly Leu Val
 -5 1 5
 Glu Glu Pro Met Asp Lys Val Glu Glu Gly Pro Leu Ser Phe Leu Met
 10 15 20
 Lys Arg Lys Thr Ala Gln Lys Leu Ala Ile Gln Lys Ala Leu Ser Asp
 25 30 35 40
 Ala Phe Gln Lys Leu Leu Ile Val Val Leu Gly Lys Thr Val Leu Ile
 45 50 55
 Ile Leu Glu Val Leu Gln Phe Gln
 60

<210> 336
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -45...-1

<400> 336
 Met Val Leu Met Trp Thr Ser Gly Asp Ala Phe Lys Thr Ala Tyr Phe
 -45 -40 -35 -30
 Leu Leu Lys Gly Ala Pro Leu Gln Phe Ser Val Cys Gly Leu Leu Gln
 -25 -20 -15
 Val Leu Val Asp Leu Ala Ile Leu Gly Gln Ala Tyr Ala Phe Ala Pro
 -10 -5 1
 Pro Pro Glu Ala Gly Ala Pro Arg Arg Ala Pro His Trp His Gln Gly
 5 10 15
 Pro Leu Thr Val Gly Arg Thr Arg Met Trp Asp Arg Gln Pro Arg Ala
 20 25 30 35
 Leu Val Gly Pro Asp Leu Pro Ala Gly Arg Val Gly Ala Val Ala Pro
 40 45 50
 Ala Gly Val Ala Glu Met Gly His Gly His Trp Gly Leu His Gln Pro
 55 60 65
 Leu Trp Gly Val Ser Gly Trp Ala Val Gly Val Gly Leu Gly Arg Cys
 70 75 80
 Leu Cys Ser Ala Gly Thr Ala Arg Val Asp Leu Ala Pro Arg Val Leu
 85 90 95
 Asp Val Phe Arg Met Thr
 100 105

<210> 337
 <211> 142
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<400> 337
 Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn Gly Gln
 -15 -10 -5
 Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Phe Tyr Cys Lys Tyr
 1 5 10
 Cys Phe Val Tyr Gly Gln Asp Trp Ala Pro Thr Ala Gly Leu Glu Glu
 15 20 25

Gly	Ile	Ser	Gln	Ile	Thr	Ser	Lys	Ser	Gln	Asp	Val	Arg	Gln	Ala	Leu
30					35					40					45
Val	Trp	Asn	Phe	Pro	Ile	Asp	Val	Thr	Phe	Lys	Ser	Thr	Asn	Pro	Tyr
				50					55					60	
Gly	Trp	Pro	Gln	Ile	Val	Leu	Ser	Val	Tyr	Gly	Pro	Asp	Val	Phe	Gly
			65					70					75		
Asn	Asp	Val	Val	Arg	Gly	Tyr	Gly	Ala	Val	His	Val	Pro	Phe	Ser	Pro
		80					85					90			
Gly	Arg	His	Lys	Arg	Thr	Ile	Pro	Met	Phe	Val	Pro	Glu	Ser	Thr	Ser
	95					100					105				
Lys	Leu	Gln	Lys	Phe	Thr	Arg	Ser	Ala	Ser	Cys	Ser	Thr	His		
110					115					120					

<210> 338
 <211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<220>
 <221> UNSURE
 <222> 21
 <223> Xaa = Ala,Pro

Thr	Ser	Glu	Glu	Arg	Thr	Ala	Met	Lys	Arg	Glu	Gly	Gly	Ala	Ala	His
		-25					-20					-15			
Leu	Cys	Ser	Asp	Ser	Leu	Pro	Glu	Ser	Gln	Gln	Gln	Asp	Gly	Asn	His
	-10					-5				1				5	
Ala	Pro	Asn	Phe	Ser	Ser	His	Gly	Ser	Cys	Arg	Arg	Arg	Gln	Arg	Xaa
				10					15					20	
Asp	Met	Thr	Arg	Arg	Cys	Met	Pro	Ala	Arg	Pro	Gly	Phe	Pro	Ser	Ser
		25						30				35			
Pro	Ala	Pro	Gly	Ser	Ser	Pro	Pro	Arg	Cys	His	Leu	Arg	Pro	Gly	Ser
		40					45					50			
Thr	Ala	His	Ala	Ala	Ala	Gly	Lys	Arg	Thr	Glu	Ser	Pro	Gly	Asp	Arg
	55					60					65				
Tyr	Arg	Ala	Glu	Gly	Leu	Arg	Arg	Gly	Arg	Val	Ala	Gly	Ala	Arg	Val
70					75					80					85

<210> 339
 <211> 90
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

Met	Pro	Cys	Leu	Asp	Gln	Gln	Leu	Thr	Val	His	Ala	Leu	Pro	Cys	Pro
		-30					-25					-20			
Ala	Gln	Pro	Ser	Ser	Leu	Ala	Phe	Cys	Gln	Val	Gly	Phe	Leu	Thr	Ala
	-15					-10					-5				
Gln	Pro	Ser	Pro	Pro	Arg	Arg	Arg	Asn	Gly	Lys	Asp	Arg	Tyr	Thr	Leu

Year	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

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<220>  
<221> SIGNAL  
<222> -35..-1
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<210> 341
<211> 131
<212> PRT
<213> Homo sapiens
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<220>  
<221> SIGNAL  
<222> -15..-1
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323

<210> 342
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39...-1

<400> 342
 Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser
 -35 -30 -25
 Ile Phe Gly Tyr Lys Arg Arg Gly Gly Val Pro Ser Leu Ile Ala Gly
 -20 -15 -10
 Leu Phe Val Gly Cys Leu Ala Gly Tyr Gly Ala Tyr Arg Val Ser Asn
 -5 1 5
 Asp Lys Arg Asp Val Lys Val Ser Leu Phe Thr Ala Phe Phe Leu Ala
 10 15 20 25
 Thr Ile Met Gly Val Arg Phe Lys Arg Ser Lys Lys Ile Met Pro Ala
 30 35 40
 Gly Leu Val Ala Gly Leu Ser Leu Met Met Ile Leu Arg Leu Val Leu
 45 50 55
 Leu Leu Leu
 60

<210> 343
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43...-1

<400> 343
 Met Cys Glu Thr Leu Leu Thr Ser Lys Trp Ala Ser Val Ser Pro Ile
 -40 -35 -30
 Pro Ala Leu Leu Gln Glu Gly Glu Asn Arg Asp Ser Arg Arg Leu Gly
 -25 -20 -15
 Asp Ala Leu Leu Phe Leu Arg Pro Ala Gly Ser Cys Ala Leu Gln Val
 -10 -5 1 5
 Ser Trp Pro Ala Ala Leu Ala Gly Pro Arg Ser His Thr Gly Gln Leu
 10 15 20
 Thr Gln His Phe Cys His Leu Lys Asn Asp Thr Cys Ile Pro Pro Ser
 25 30 35
 Leu Gly Pro Pro Arg Asn Ser Gly Ser Leu Glu Ser Leu Arg Ser Lys
 40 45 50
 Arg Tyr
 55

<210> 344
 <211> 217
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<220>
 <221> UNSURE
 <222> 185
 <223> Xaa = Phe,Val

<400> 344
 Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser Leu
 -15 -10 -5
 Cys Cys Ser Ser Tyr Val Pro Ser Val Ala Pro Thr Ala Ala His Ser
 1 5 10
 Val Arg Val Pro His Ser Ala Gly His Cys Gly Gln Arg Val Leu Ala
 15 20 25
 Cys Ser Leu Pro Gln Val Phe Leu Lys Pro Trp Ile Phe Val Glu His
 30 35 40 45
 Phe Ser Ser Trp Leu Ser Leu Glu Leu Phe Ser Phe Leu Arg Tyr Leu
 50 55 60
 Gly Thr Leu Leu Cys Ala Cys Gly His Arg Leu Arg Glu Gly Arg Leu
 65 70 75
 Leu Pro Cys Leu Leu Gly Val Gly Ser Trp Leu Leu Phe Asn Asn Trp
 80 85 90
 Thr Gly Gly Ser Trp Phe Ser Leu His Leu Gln Gln Val Ser Leu Ser
 95 100 105
 Gln Gly Ser His Val Ala Ala Phe Leu Pro Glu Ala Ile Gly Pro Gly
 110 115 120 125
 Val Pro Val Pro Val Ser Gly Glu Ser Thr Ser Ala Gln Gln Ser His
 130 135 140
 Ala Gly Trp Gln Leu Ser Ala Glu Ala Asp Ala Cys Pro Ser Val Leu
 145 150 155
 Tyr Ser Glu Val Leu Glu Trp Asn Lys Asn Ile Asn Thr Tyr Thr Ser
 160 165 170
 Phe His Asp Phe Cys Leu Ile Leu Gly Ile Phe Xaa Val Leu Phe Cys
 175 180 185
 Phe Gly Gly Asp Arg Leu Thr Leu His
 190 195

<210> 345
 <211> 183
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 345
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
 -20 -15 -10 -5
 Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
 1 5 10
 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
 15 20 25
 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
 30 35 40
 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
 45 50 55 60
 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 65 70 75

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
80 85 90
Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
95 100 105
Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser
110 115 120
Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
125 130 135 140
Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
145 150 155
Asp Arg His Lys Met Leu Ser
160

<210> 346
<211> 247
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13...-1

<400> 346
Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr
-10 -5 1
Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr
5 10 15
Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys
20 25 30 35
Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn Ala His Leu Arg Thr
40 45 50
Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val Glu Phe Gly Gly Arg
55 60 65
Met Asn Thr Val Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg
70 75 80
Thr Glu Val Gln Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln
85 90 95
Phe Leu Ile Pro Asn Leu Ala Leu Ile Asp Lys Gln Glu Ser Glu Ile
100 105 110 115
Thr Tyr Leu Val Pro Trp Cys Lys Leu Glu Lys Pro Pro Lys Glu Gly
120 125 130
Val Tyr Glu Leu Ala Thr Phe Gln Met Lys Pro Gly Gly Pro Ala Leu
135 140 145
Trp Gly Asp Ala Phe Lys Arg Ala Val His Ala His Val Asn Leu Gly
150 155 160
Tyr Thr Lys Leu Val Gly Val Phe His Thr Glu Tyr Gly Ala Leu Asn
165 170 175
Arg Val His Val Leu Trp Trp Asn Glu Ser Ala Asp Ser Arg Ala Ala
180 185 190 195
Gly Arg His Lys Ser His Glu Asp Pro Arg Val Val Ala Ala Val Arg
200 205 210
Glu Ser Val Asn Tyr Leu Val Ser Gln Gln Asn Met Leu Leu Ile Pro
215 220 225
Thr Ser Phe Ser Pro Leu Lys
230

<210> 347
<211> 104

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47...-1

<400> 347
 Met Phe Ser Pro Arg Gln Ala Leu Thr Pro Asp Pro Leu His Ser Pro
 -45 -40 -35
 Ala Tyr Ser Pro Val Leu Gly Gly Trp Ser Arg Phe Arg Ser Val Asp
 -30 -25 -20
 Phe Arg Phe Leu Tyr Leu Thr Leu Asn Gln Ser Cys Ile Phe Ala Asn
 -15 -10 -5 1
 Tyr Lys Glu Ala His Ala Asn Arg Tyr Cys Thr Glu Gly Arg Tyr Thr
 5 10 15
 Arg Glu Ile Gln Arg Leu Thr Ser Pro Ala Ala Trp Pro Thr Arg Asp
 20 25 30
 Lys Asn Arg Met Ile Ser Asn Gly Met Ala Leu Asn Ser Pro Ala Glu
 35 40 45
 Gly Leu Ala Phe Gln Cys Arg Phe
 50 55

<210> 348
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 348
 Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met Gly Val Gln Val Val
 -20 -15 -10
 Gly Arg Ala Phe Ala Arg Ala Leu Arg Gln Glu Phe Ala Ala Ser Arg
 -5 1 5 10
 Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His Arg Ser Ala Ala Ala
 15 20 25
 Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala Gln Gln Ile Leu Asn
 30 35 40
 Val Ser Lys Leu Ser Pro Glu Val Gln Lys Asn Tyr Glu His Leu
 45 50 55
 Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser Phe Tyr Leu Gln Ser
 60 65 70 75
 Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu Glu Leu Lys Ile Gln
 80 85 90
 Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro His Thr
 95 100

<210> 349
 <211> 302
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 349

Met	Ala	Pro	Asn	Ser	Ile	Thr	Leu	Leu	Gly	Leu	Ala	Val	Asn	Val	Val
			-15					-10					-5		
Thr	Thr	Leu	Val	Leu	Ile	Ser	Tyr	Cys	Pro	Thr	Ala	Thr	Glu	Glu	Ala
		1				5					10				
Pro	Tyr	Trp	Thr	Tyr	Leu	Leu	Cys	Ala	Leu	Gly	Leu	Phe	Ile	Tyr	Gln
15					20					25					30
Ser	Leu	Asp	Ala	Ile	Asp	Gly	Lys	Gln	Ala	Arg	Arg	Thr	Asn	Ser	Cys
				35					40					45	
Ser	Pro	Leu	Gly	Glu	Leu	Phe	Asp	His	Gly	Cys	Asp	Ser	Leu	Ser	Thr
			50					55					60		
Val	Phe	Met	Ala	Val	Gly	Ala	Ser	Ile	Ala	Ala	Arg	Leu	Gly	Thr	Tyr
		65					70					75			
Pro	Asp	Trp	Phe	Phe	Phe	Cys	Ser	Phe	Ile	Gly	Met	Phe	Val	Phe	Tyr
	80					85					90				
Cys	Ala	His	Trp	Gln	Thr	Tyr	Val	Ser	Gly	Met	Leu	Arg	Phe	Gly	Lys
95					100					105					110
Val	Asp	Val	Thr	Glu	Ile	Gln	Ile	Ala	Leu	Val	Ile	Val	Phe	Val	Leu
				115					120					125	
Ser	Ala	Phe	Gly	Gly	Ala	Thr	Met	Trp	Asp	Tyr	Thr	Gly	Thr	Ser	Val
			130					135					140		
Leu	Ser	Pro	Gly	Leu	His	Ile	Gly	Leu	Ile	Ile	Ile	Leu	Ala	Ile	Met
		145					150					155			
Ile	Tyr	Lys	Lys	Ser	Ala	Thr	Asp	Val	Phe	Glu	Lys	His	Pro	Cys	Leu
	160					165					170				
Tyr	Ile	Leu	Met	Phe	Gly	Cys	Val	Phe	Ala	Lys	Val	Ser	Gln	Lys	Leu
175					180					185					190
Val	Val	Ala	His	Met	Thr	Lys	Ser	Glu	Leu	Tyr	Leu	Gln	Asp	Thr	Val
				195					200					205	
Phe	Leu	Gly	Pro	Gly	Leu	Leu	Phe	Leu	Asp	Gln	Tyr	Phe	Asn	Asn	Phe
			210					215					220		
Ile	Asp	Glu	Tyr	Val	Val	Leu	Trp	Met	Ala	Met	Val	Ile	Ser	Ser	Phe
	225						230					235			
Asp	Met	Val	Ile	Tyr	Phe	Ser	Ala	Leu	Cys	Leu	Gln	Ile	Ser	Arg	His
	240					245					250				
Leu	His	Leu	Asn	Ile	Phe	Lys	Thr	Ala	Cys	His	Gln	Ala	Pro	Glu	Gln
255					260					265					270
Val	Gln	Val	Leu	Ser	Ser	Lys	Ser	His	Gln	Asn	Asn	Met	Asp		
				275					280						

<210> 350

<211> 107

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -14...-1

<400> 350

Met	Ile	Leu	Val	Thr	Val	Pro	Gly	Val	Cys	Pro	Ala	Gln	Cys	Cys	Trp
				-10					-5					1	
Ala	Glu	Gln	Arg	Gly	Arg	Gly	Ser	Gly	Met	Tyr	Phe	Ile	Asp	Lys	Trp
		5					10					15			
Ala	Arg	Pro	Ser	Trp	Val	Pro	His	Trp	Leu	Asn	Asp	Leu	Phe	Ile	Val
		20				25					30				
Lys	Ser	Gly	Tyr	Leu	Val	Cys	Ile	Arg	Thr	Thr	Val	Ile	Arg	Gln	Gly

35 40 45 50
 Ile Val Arg Ile Gly Arg Asn Lys Ile Ser Glu Ser Gly Arg Ser Ala
 55 60 65
 Leu Tyr Thr Ile Ala Lys Asn Lys Met Val Ile Phe Lys Val Pro Asp
 70 75 80
 Cys Met His Leu Asn Ala Asp Tyr Phe Gly Val
 85 90

<210> 351
 <211> 229
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 351
 Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
 -30 -25 -20
 Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu Ala
 -15 -10 -5
 Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
 1 5 10
 Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
 15 20 25 30
 Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
 35 40 45
 Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
 50 55 60
 Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
 65 70 75
 Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
 80 85 90
 Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
 95 100 105 110
 Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
 115 120 125
 Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
 130 135 140
 Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln
 145 150 155
 Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn
 160 165 170
 Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu
 175 180 185 190
 Ala Ser Glu Lys Lys
 195

<210> 352
 <211> 206
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 352
 Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
 -30 -25 -20
 Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu Ala
 -15 -10 -5
 Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
 1 5 10
 Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
 15 20 25 30
 Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
 35 40 45
 Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
 50 55 60
 Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
 65 70 75
 Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
 80 85 90
 Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
 95 100 105 110
 Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
 115 120 125
 Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
 130 135 140
 Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Ser Arg
 145 150 155
 Ala Phe Phe Leu Ser Thr Glu Lys Lys Asn Leu Glu Thr Lys
 160 165 170

<210> 353
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -44..-1

<400> 353
 Met Ala Ala Glu Gly Trp Ile Trp Arg Trp Gly Trp Gly Arg Arg Cys
 -40 -35 -30
 Leu Gly Arg Pro Gly Leu Leu Gly Pro Gly Pro Gly Pro Thr Thr Pro
 -25 -20 -15
 Leu Phe Leu Leu Leu Leu Gly Ser Val Thr Ala Asp Ile Thr Asp
 -10 -5 1
 Gly Asn Ile Glu His Leu Lys Arg Glu His Ser Leu Ile Lys Pro Tyr
 5 10 15 20
 Gln Gly Val Gly Ser Ser Ser Pro Ser Gly Thr Ser Arg Ala Ala Leu
 25 30 35
 Cys Ser Arg Ala Ser Thr Tyr Val
 40

<210> 354
 <211> 151
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

<222> -32...-1

<400> 354

Met Asp Ser Ala Ser Asn Pro Thr Asn Leu Val Ser Thr Ser Gln Arg
-30 -25 -20
His Arg Pro Leu Leu Ser Ser Cys Gly Leu Pro Pro Ser Thr Ala Ser
-15 -10 -5
Ala Val Arg Arg Leu Cys Ser Arg Gly Val Leu Lys Gly Ser Asn Glu
1 5 10 15
Arg Arg Asp Met Glu Ser Phe Trp Lys Leu Asn Arg Ser Pro Gly Ser
20 25 30
Asp Arg Tyr Leu Glu Ser Arg Asp Ala Ser Arg Leu Ser Gly Arg Asp
35 40 45
Pro Ser Ser Trp Thr Val Glu Asp Val Met Gln Phe Val Arg Glu Ala
50 55 60
Asp Pro Gln Leu Gly Pro His Ala Asp Leu Phe Arg Lys His Glu Ile
65 70 75 80
Asp Gly Lys Ala Leu Leu Leu Leu Arg Ser Asp Met Met Met Lys Tyr
85 90 95
Met Gly Leu Lys Leu Gly Pro Ala Leu Lys Leu Ser Tyr His Ile Asp
100 105 110
Arg Leu Lys Gln Gly Lys Phe
115

<210> 355

<211> 65

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16...-1

<400> 355

Met Ala Glu Leu Ala Cys Val Arg Glu Ser Thr Ser Val Ala Trp Ala
-15 -10 -5
Cys Lys Val Arg Gly Gly Thr Ala Pro Ser Pro Ser Gly Ala Glu Gly
1 5 10 15
His Val Met Leu Asn Lys Ser Arg Glu Val Glu Ser Pro Val Ser Ser
20 25 30
Arg Pro Arg Cys Gly Met Pro Thr Val Pro Pro Gly Ser Leu Lys Thr
35 40 45
Leu

<210> 356

<211> 189

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24...-1

<220>

<221> UNSURE

<222> 41

<223> Xaa = Ala,Gly

<400> 356
Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
-20 -15 -10
Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val
-5 1 5
Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu
10 15 20
Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys
25 30 35 40
Xaa Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln
45 50 55
Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu
60 65 70
Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala
75 80 85
Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly
90 95 100
Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg
105 110 115 120
Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr
125 130 135
His Gly Leu Ser Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly
140 145 150
Leu Cys Leu Ala Gly Leu Ala Leu Glu Ile Arg Ser Leu
155 160 165

<210> 357
<211> 183
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -47...-1

<400> 357
Met Thr Glu Cys Thr Ser Leu Gln Phe Val Ser Pro Phe Ala Phe Glu
-45 -40 -35
Ala Met Gln Lys Val Asp Val Val Cys Leu Ala Ser Leu Ser Asp Pro
-30 -25 -20
Glu Leu Arg Leu Leu Leu Pro Cys Leu Val Arg Met Ala Leu Cys Ala
-15 -10 -5 1
Pro Ala Asp Gln Ser Gln Ser Trp Ala Gln Asp Lys Lys Leu Ile Leu
5 10 15
Arg Leu Leu Ser Gly Val Glu Ala Val Asn Ser Ile Val Ala Leu Leu
20 25 30
Ser Val Asp Phe His Ala Leu Glu Gln Asp Ala Ser Lys Glu Gln Gln
35 40 45
Leu Arg Pro Ser Leu Ala Leu Leu Pro Arg Leu Glu Cys Gly Gly Val
50 55 60 65
Ile Ser Ala His Cys Asn Leu His Leu Leu Gly Ser Ser Asp Ser Ser
70 75 80
Ala Ser Val Ser Arg Val Asp Gly Thr Thr Gly Thr Arg His His Ala
85 90 95
Arg Leu Phe Cys Ile Ile Ser Arg Asp Glu Val Ser Pro Tyr Trp Pro
100 105 110
Gly Trp Ser Arg Thr Pro Asn Leu Val Ile His Leu Pro Gln Pro Pro
115 120 125

Lys Val Leu Gly Leu Pro Ala
130 135

<210> 358
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 358
Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
-10 -5 1
Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
5 10 15
Gln Asn Met Ile Arg Arg Leu Glu Ile Glu Ala Glu Asn His Tyr Trp
20 25 30
Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Ala
35 40 45 50
Val Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser
55 60 65
Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn
70 75 80
Val Thr Lys Lys Trp Ser
85

<210> 359
<211> 244
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 359
Met Glu Leu Thr Ile Phe Ile Leu Arg Leu Ala Ile Tyr Ile Leu Thr
-25 -20 -15
Phe Pro Leu Tyr Leu Leu Asn Phe Leu Gly Leu Trp Ser Trp Ile Cys
-10 -5 1
Lys Lys Trp Phe Pro Tyr Phe Leu Val Arg Phe Thr Val Ile Tyr Asn
5 10 15
Glu Gln Met Ala Ser Lys Lys Arg Glu Leu Phe Ser Asn Leu Gln Glu
20 25 30 35
Phe Ala Gly Pro Ser Gly Lys Leu Ser Leu Leu Glu Val Gly Cys Gly
40 45 50
Thr Gly Ala Asn Phe Lys Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys
55 60 65
Ile Asp Pro Asn Pro Asn Phe Glu Lys Phe Leu Ile Lys Ser Ile Ala
70 75 80
Glu Asn Arg His Leu Gln Phe Glu Arg Phe Val Val Ala Ala Gly Glu
85 90 95
Asn Met His Gln Val Ala Asp Gly Ser Val Asp Val Val Val Cys Thr
100 105 110 115
Leu Val Leu Cys Ser Val Lys Asn Gln Glu Arg Ile Leu Arg Glu Val
120 125 130

Cys	Arg	Val	Leu	Arg	Pro	Gly	Gly	Ala	Phe	Tyr	Phe	Met	Glu	His	Val
			135					140					145		
Ala	Ala	Glu	Cys	Ser	Thr	Trp	Asn	Tyr	Phe	Trp	Gln	Gln	Val	Leu	Asp
		150					155					160			
Pro	Ala	Trp	His	Leu	Leu	Phe	Asp	Gly	Cys	Asn	Leu	Thr	Arg	Glu	Ser
		165				170					175				
Trp	Lys	Ala	Leu	Glu	Arg	Ala	Ser	Phe	Ser	Lys	Leu	Lys	Leu	Gln	His
180					185					190					195
Ile	Gln	Ala	Pro	Leu	Ser	Trp	Glu	Leu	Val	Arg	Pro	His	Ile	Tyr	Gly
				200					205					210	
Tyr	Ala	Val	Lys												
			215												

<210> 360
 <211> 177
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23..-1

<400>	360															
Met	Ser	Asn	Gln	Arg	Leu	Pro	Leu	Ile	Phe	Ser	Leu	Leu	Phe	Ile	Cys	
			-20					-15					-10			
Phe	Phe	Gly	Glu	Ser	Phe	Cys	Ile	Cys	Asp	Gly	Thr	Val	Trp	Thr	Lys	
		-5					1				5					
Val	Gly	Trp	Glu	Ile	Leu	Pro	Glu	Glu	Val	His	Tyr	Trp	Lys	Val	Lys	
10					15					20					25	
Gly	Ser	Pro	Ser	His	Cys	Leu	Pro	Tyr	Leu	Asp	Lys	Leu	Cys	Cys		
				30					35					40		
Asp	Phe	Ala	Asn	Met	Asp	Ile	Phe	Gln	Gly	Cys	Leu	Tyr	Leu	Ile	Tyr	
			45					50					55			
Asn	Leu	Leu	Gln	Ala	Val	Phe	Phe	Val	Leu	Phe	Val	Leu	Ser	Val	His	
		60				65					70					
Tyr	Leu	Trp	Lys	Lys	Trp	Lys	Lys	His	Gln	Lys	Lys	Leu	Lys	Lys	Gln	
		75			80						85					
Ala	Ser	Leu	Glu	Lys	Pro	Gly	Asn	Asp	Leu	Glu	Ser	Pro	Leu	Ile	Asn	
90					95					100					105	
Asn	Ile	Asp	Gln	Thr	Leu	His	Arg	Val	Ala	Thr	Thr	Ala	Ser	Val	Ile	
				110					115					120		
Tyr	Lys	Ile	Trp	Glu	His	Arg	Ser	His	His	Pro	Ser	Ser	Lys	Lys	Ile	
			125					130					135			
Lys	His	Cys	Lys	Leu	Lys	Lys	Lys	Ser	Lys	Glu	Glu	Gly	Ala	Arg	Arg	
		140					145					150				
Tyr																

<210> 361
 <211> 158
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21..-1

<400> 361
 Met Ala Leu Cys Ala Leu Thr Arg Ala Leu Pro Ser Leu Asn Leu Ala

-20 -15 -10
 Pro Pro Thr Val Ala Ala Pro Ala Pro Ser Leu Phe Pro Ala Ala Gln
 -5 1 5 10
 Met Met Asn Asn Gly Leu Leu Gln Gln Pro Ser Ala Leu Met Leu Leu
 15 20 25
 Pro Cys Arg Pro Val Leu Thr Ser Val Ala Leu Asn Ala Asn Phe Val
 30 35 40
 Ser Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr Pro Val Lys Met Arg
 45 50 55
 Lys Ser Gly Gly Arg Asp His Thr Gly Ala Gly Asn Val Arg Arg Thr
 60 65 70 75
 Val Gly Arg Val Ser Asn Val Asp His Asn Lys Arg Val Ile Gly Lys
 80 85 90
 Ala Gly Arg Asn Arg Trp Leu Gly Lys Arg Pro Asn Ser Gly Arg Trp
 95 100 105
 His Arg Lys Gly Gly Trp Ala Gly Arg Lys Ile Arg Pro Leu Pro Pro
 110 115 120
 Met Lys Ser Tyr Val Lys Leu Pro Ser Ala Ser Ala Gln Ser
 125 130 135

<210> 362
 <211> 186
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<400> 362
 Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn Gly Gln
 -15 -10 -5
 Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Leu Tyr Cys Lys Tyr
 1 5 10
 Cys Phe Val Tyr Gly Gln Asp Trp Ala Pro Thr Ala Gly Leu Glu Glu
 15 20 25
 Gly Ile Ser Gln Ile Thr Ser Lys Ser Gln Asp Val Arg Gln Ala Leu
 30 35 40 45
 Val Trp Asn Phe Pro Ile Asp Val Thr Phe Lys Ser Thr Asn Pro Tyr
 50 55 60
 Gly Trp Pro Gln Ile Val Leu Ser Val Tyr Gly Pro Asp Val Phe Gly
 65 70 75
 Asn Asp Val Val Arg Gly Tyr Gly Ala Val His Val Pro Phe Ser Pro
 80 85 90
 Gly Arg His Lys Arg Thr Ile Pro Met Phe Val Pro Glu Ser Thr Ser
 95 100 105
 Lys Leu Gln Lys Phe Thr Ser Trp Phe Met Gly Arg Arg Pro Glu Tyr
 110 115 120 125
 Thr Asp Pro Lys Val Val Ala Gln Gly Glu Gly Arg Glu Ala Ile Thr
 130 135 140
 Ala Pro Arg Lys Ala Val Phe Ser Val His Gly Leu Thr Ser Pro Arg
 145 150 155
 Ala Leu Ala Leu Val His Ile Lys Gly Thr
 160 165

<210> 363
 <211> 150
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -47..-1

<400> 363

Met Gly Asp Arg Val Lys Gly Ser Lys Ser Arg Ala Phe Val Ser Pro
-45 -40 -35
Trp Pro His Thr Pro Met Ala Ser Gly Leu Arg Asp Pro Trp Leu Gln
-30 -25 -20
Pro Thr Ala Leu Gly Leu Ala Leu Cys Ser Thr Lys Ala Leu Ser Val
-15 -10 -5 1
Gly Ser Ala Pro Leu Pro Pro Arg Asn Ser Asn Thr Met Ala Ala Ala
5 10 15
Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu
20 25 30
Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu
35 40 45
Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg
50 55 60 65
Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val
70 75 80
Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg
85 90 95
Pro Gly Ile His Leu Cys
100

<210> 364

<211> 95

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -45..-1

<400> 364

Met Leu His His Val Ile Thr Ala Gly Pro Val Leu Leu Leu His Leu
-45 -40 -35 -30
Pro Arg Pro Asp Thr Ser Thr Arg Leu Leu Leu Thr Ser Val Ser Ala
-25 -20 -15
Phe Ile Leu Leu Leu Leu Ser Gly Pro Ala Glu Met Ser Ala Ser
-10 -5 1
Gln Glu Ser Phe Pro Gly Ser Leu Gln Gln Glu Ile Ala Ser Leu Ile
5 10 15
Thr Val Ala Leu Gly Ser Leu Ile Ser Leu Ser Cys Ser Thr Leu Leu
20 25 30 35
Tyr Phe Ser Cys Glu Leu Lys Ile Pro Cys Glu Asp Val Asn Leu
40 45 50

<210> 365

<211> 94

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26...-1

<400> 365

Met Ala Ala Ile Glu Ile Glu Val Lys Pro Asn Gln Gly Phe Cys Gly
-25 -20 -15
Ser Ala Cys Leu Leu Ala Val Ile Arg Ala Phe Phe Phe Lys Lys Asn
-10 -5 1 5
Ala Cys Leu Leu Arg Glu Ile Leu Gln Ser Lys Leu Gly Gly Met Gly
10 15 20
Pro Val Val Phe Ser Tyr Arg Gly Leu Pro Leu Trp Leu Phe Ala Trp
25 30 35
Leu Phe Pro Arg Cys Thr Val Pro Leu Thr Phe Gly Phe Glu Asn Met
40 45 50
Arg Gly Leu Gly Val Val Ala Tyr Ala Cys Asn Pro Ser Thr
55 60 65

<210> 366

<211> 140

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -40...-1

<400> 366

Met Thr Ser Met Thr Gln Ser Leu Arg Glu Val Ile Lys Ala Met Thr
-40 -35 -30 -25
Lys Ala Arg Asn Phe Glu Arg Val Leu Gly Lys Ile Thr Leu Val Ser
-20 -15 -10
Ala Ala Pro Gly Lys Val Ile Cys Glu Met Lys Val Glu Glu His
-5 1 5
Thr Asn Ala Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val
10 15 20
Asp Asn Ile Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro
25 30 35 40
Gly Val Ser Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu
45 50 55
Gly Glu Asp Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr
60 65 70
Leu Ala Phe Thr Ser Val Asp Leu Thr Asn Lys Ala Thr Gly Lys Leu
75 80 85
Ile Ala Gln Gly Arg His Thr Lys His Leu Gly Asn
90 95 100

<210> 367

<211> 39

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -35...-1

<400> 367

Met Asp Pro Gly Trp Pro His Phe Lys Leu Thr His Ser Arg Cys Met
-35 -30 -25 -20
Ala Val Leu Phe Leu Gly Thr Leu Pro Leu Cys Pro Val Thr Ser Pro

Val Trp Gly Trp Ser Pro Gly
 1

<210> 368
 <211> 78
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41..-1

<400> 368
 Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu Glu Tyr
 -40 -35 -30
 Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr Leu Leu
 -25 -20 -15 -10
 Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu Leu Val
 -5 1 5
 Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser Cys Val
 10 15 20
 Gly Ser Phe Ile Leu Ala Gly Ser Leu Phe Glu Phe Pro Gly
 25 30 35

<210> 369
 <211> 83
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40..-1

<400> 369
 Met Gly Leu Thr Ser Thr Trp Arg Tyr Gly Arg Gly Pro Gly Ile Gly
 -40 -35 -30 -25
 Thr Val Thr Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val
 -20 -15 -10
 Thr Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu
 -5 1 5
 Asp Thr Thr Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu
 10 15 20
 Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn
 25 30 35 40
 Lys Ser Lys

<210> 370
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 370
 Met Ala Val Leu Ala Gly Ser Leu Leu Gly Pro Thr Ser Arg Ser Ala

-15					-10					-5				1
Ala	Leu	Leu	Gly	Gly	Arg	Trp	Leu	Gln	Pro	Arg	Ala	Trp	Leu	Gly
		5						10					15	Phe
Pro	Asp	Ala	Trp	Gly	Leu	Pro	Thr	Pro	Gln	Gln	Ala	Arg	Gly	Lys
		20					25					30		Ala
Arg	Gly	Asn	Glu	Tyr	Gln	Pro	Ser	Asn	Ile	Lys	Arg	Lys	Asn	Lys
		35				40					45			His
Gly	Trp	Val	Arg	Arg	Leu	Ser	Thr	Pro	Ala	Gly	Val	Gln	Val	Ile
50					55					60				65
Arg	Arg	Met	Leu	Lys	Gly	Arg	Lys	Ser	Leu	Ser	His			
			70						75					

<210> 371
 <211> 279
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42...-1

<400> 371

Met	Ala	Ala	Pro	Val	Arg	Arg	Thr	Leu	Leu	Gly	Val	Ala	Gly	Gly	Trp
		-40					-35					-30			
Arg	Arg	Phe	Glu	Arg	Leu	Trp	Ala	Gly	Ser	Leu	Ser	Ser	Arg	Ser	Leu
		-25				-20					-15				
Ala	Leu	Ala	Ala	Ala	Pro	Ser	Ser	Asn	Gly	Ser	Pro	Trp	Arg	Leu	Leu
-10					-5					1				5	
Gly	Ala	Leu	Cys	Leu	Gln	Arg	Pro	Pro	Val	Val	Ser	Lys	Pro	Leu	Thr
		10					15					20			
Pro	Leu	Gln	Glu	Glu	Met	Ala	Ser	Leu	Leu	Gln	Gln	Ile	Glu	Ile	Glu
		25				30					35				
Arg	Ser	Leu	Tyr	Ser	Asp	His	Glu	Leu	Arg	Ala	Leu	Asp	Glu	Asn	Gln
		40				45					50				
Arg	Leu	Ala	Lys	Lys	Lys	Ala	Asp	Leu	His	Asp	Glu	Glu	Asp	Glu	Gln
				60						65					70
Asp	Ile	Leu	Leu	Ala	Gln	Asp	Leu	Glu	Asp	Met	Trp	Glu	Gln	Lys	Phe
			75					80						85	
Leu	Gln	Phe	Lys	Leu	Gly	Ala	Arg	Ile	Thr	Glu	Ala	Asp	Glu	Lys	Asn
		90					95					100			
Asp	Arg	Thr	Ser	Leu	Asn	Arg	Asn	Leu	Asp	Arg	Asn	Leu	Val	Leu	Leu
		105					110					115			
Val	Arg	Glu	Lys	Phe	Gly	Asp	Gln	Asp	Val	Trp	Ile	Leu	Pro	Gln	Ala
		120				125					130				
Glu	Trp	Gln	Pro	Gly	Glu	Thr	Leu	Arg	Gly	Thr	Ala	Glu	Arg	Thr	Leu
				140					145						150
Ala	Thr	Leu	Ser	Glu	Asn	Asn	Met	Glu	Ala	Lys	Phe	Leu	Gly	Asn	Ala
				155					160					165	
Pro	Cys	Gly	His	Tyr	Thr	Phe	Lys	Phe	Pro	Gln	Ala	Met	Arg	Thr	Glu
			170				175					180			
Ser	Asn	Leu	Gly	Ala	Lys	Val	Phe	Phe	Phe	Lys	Ala	Leu	Leu	Leu	Thr
		185				190					195				
Gly	Asp	Phe	Ser	Gln	Ala	Gly	Asn	Lys	Gly	His	His	Val	Trp	Val	Ile
	200					205					210				
Lys	Asp	Glu	Leu	Gly	Asp	Tyr	Leu	Lys	Pro	Lys	Tyr	Leu	Ala	Gln	Val
	215				220					225					230
Arg	Arg	Phe	Val	Ser	Asp	Leu									
					235										

<210> 372
 <211> 184
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 372
 Met Ala Cys Thr Thr Thr Ala Pro Ala Gln Glu His Met Leu Leu Thr
 -30 -25 -20
 Pro Leu Thr Ala Leu Met Val Gly Ala Ala Ser Leu Leu Glu Gly Arg
 -15 -10 -5 1
 Pro Gln Ile Ser Ala Pro Tyr Ser Arg Ala Ala Cys Cys Ser Pro Gly
 5 10 15
 Ala Leu Gly Cys Pro Ala Ala Arg Val Gly Ile Leu Asp Leu Met Tyr
 20 25 30
 Ser Trp Val Ala Arg Lys Val Leu Arg Cys Ser Asn Thr Gly Leu Gln
 35 40 45
 Gly Leu His Cys Ala Pro Ala Tyr Ala Ala Gln Leu Gly Met Asp Pro
 50 55 60 65
 Gly Arg Gly Gln Arg Ala Gly Gly Pro Val Glu Gln Thr Tyr Phe Ser
 70 75 80
 Pro Met Gly Lys Leu Pro Thr Leu Ser Trp Leu Glu Gly Cys Thr Ala
 85 90 95
 Val Met Thr Leu Ala Ser Ala Trp Leu Leu Gly Ser Pro Arg Glu Thr
 100 105 110
 Tyr Asn His Glu Lys Val Lys Glu Lys Gln Cys Pro Phe Ser Ser Met
 115 120 125
 Val Leu Gly Glu Tyr Gly Phe Leu Pro Thr Val Asp His Leu Ser Thr
 130 135 140 145
 Leu Gly Cys Asn Met Arg Glu Leu
 150

<210> 373
 <211> 101
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42..-1

<400> 373
 Met Ala His Val Ala Glu Lys Asp Gly Leu Asp Trp Ala Ser Gly Cys
 -40 -35 -30
 Ile Pro Gly Leu Gln Thr Gly Ile Cys Leu Phe Gly Ser Gln Leu Cys
 -25 -20 -15
 Phe His Leu Ser Trp Leu Tyr Ser Trp Ala Ser Gln Cys Gly Pro Thr
 -10 -5 1 5
 Ala Pro Val Ile Asp Lys Lys Ser Ser Pro Leu Leu Thr Glu Leu Leu
 10 15 20
 Asp Leu Val Leu Ile Gly Pro Asp Glu Glu Gly Ile Gln Pro Gln Val
 25 30 35
 Ile Ile Val Ala Arg Lys Met Glu Tyr Thr Lys Trp Thr Gly Leu Ala
 40 45 50

Cys Thr His Arg Asp
55

<210> 374
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20...-1

<400> 374
Met Gly Pro Asn Thr Lys Asn Leu Leu Leu Val Thr Leu Val Ala Ser
-20 -15 -10 -5
Thr Val Pro Gly Asn Ser Leu Gly Gln Asp Phe Thr Phe Ala His Leu
1 5 10
Glu Arg Ser Cys Thr Arg Glu Asn Arg Ser Pro Gly Glu Val Phe Gln
15 20 25
Gln Pro Cys Lys Ser Gly Gly Gly Gly Val Gly Glu Pro Asn Ala Gln
30 35 40
Gly Gln Leu Leu Ser Gln His Pro Leu Pro Ala Phe Ile Asn Cys Ser
45 50 55 60
His Gly Gln Ala Phe
65

<210> 375
<211> 90
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28...-1

<400> 375
Met Ala Phe Pro Gly Gln Ser Asp Thr Lys Met Gln Trp Pro Glu Val
-25 -20 -15
Pro Ala Leu Pro Leu Leu Ser Ser Leu Cys Met Ala Met Val Arg Lys
-10 -5 1
Ser Ser Ala Leu Gly Lys Glu Val Gly Arg Arg Val Lys Glu Met Val
5 10 15 20
Met Leu Val Ala Pro Phe Arg Gln Ser Ser Ser Leu Ser Arg Thr Phe
25 30 35
Ser Ser Arg Lys Val Val Lys Ala His Ala Ser Leu His Gly Ala Arg
40 45 50
Leu Ser Pro Leu Ser Arg Asn Ile Arg Gly
55 60

<210> 376
<211> 89
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33...-1

<220>
 <221> UNSURE
 <222> 47
 <223> Xaa = Ala,Pro,Ser,Thr

<400> 376
 Met Ala Gln Pro Ala Ala Pro Ser Leu Thr Arg Pro Phe Leu Ala Glu
 -30 -25 -20
 Ala Pro Thr Ala Leu Val Pro His Ser Pro Leu Pro Gly Ala Leu Ser
 -15 -10 -5
 Ser Ala Pro Gly Pro Lys Gln Pro Pro Thr Ala Ser Thr Gly Pro Glu
 1 5 10 15
 Leu Leu Leu Leu Pro Leu Ser Ser Phe Met Pro Cys Gly Ala Ala Ala
 20 25 30
 Pro Ala Arg Val Ser Ser Gln Arg Ala Thr Pro Arg Asp Lys Pro Xaa
 35 40 45
 Gly Pro Leu Ile Pro Gly Gln Cys Pro
 50 55

<210> 377
 <211> 132
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 377
 Met Asn Arg Val Leu Cys Ala Pro Ala Ala Gly Ala Val Arg Ala Leu
 -15 -10 -5 1
 Arg Leu Ile Gly Trp Ala Ser Arg Ser Leu His Pro Leu Pro Gly Ser
 5 10 15
 Arg Asp Arg Ala His Pro Ala Ala Glu Glu Glu Asp Asp Pro Asp Arg
 20 25 30
 Pro Ile Glu Phe Ser Ser Ser Lys Ala Asn Pro His Arg Trp Ser Val
 35 40 45
 Gly His Thr Met Gly Lys Gly His Gln Arg Pro Trp Trp Lys Val Leu
 50 55 60 65
 Pro Leu Ser Cys Phe Leu Val Ala Leu Ile Ile Trp Cys Tyr Leu Arg
 70 75 80
 Glu Glu Ser Glu Ala Asp Gln Trp Leu Arg Gln Val Trp Gly Glu Val
 85 90 95
 Pro Glu Pro Ser Asp Arg Ser Glu Glu Pro Glu Thr Pro Ala Ala Tyr
 100 105 110
 Arg Ala Arg Thr
 115

<210> 378
 <211> 102
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<220>

[illegible][illegible][illegible][illegible][illegible][illegible]

Arg Ala Leu Tyr Arg Arg His Val Leu Gly Ile Val Leu Gln Gly Pro
 25 30 35
 Ala Leu Cys Phe Ala Ala Ala Ile Phe Ser Leu Phe Phe Val Pro Leu
 40 45 50
 Ser Tyr Leu Leu Met Val Thr Val Ile Leu Leu Pro Tyr Val Ser Lys
 55 60 65 70
 Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His Arg Glu Pro Ser
 75 80 85
 Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His Glu Pro Leu Ser
 90 95 100
 Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile Val Ala
 105 110 115
 Thr Leu Leu Ile Leu Asp Ile Trp
 120 125

<210> 381
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 381
 Met Glu Met Leu Phe Asp Glu Arg Ala Pro Leu Leu Phe Ile Leu Phe
 -25 -20 -15
 Lys Phe Ser Leu Cys Pro Tyr Ala Ala Ala Leu Ser Lys Pro Ile Phe
 -10 -5 1 5
 Gly Ser Val Ala Cys Met Thr Lys Glu Ile Leu Ala Arg His Gly Gly
 10 15 20
 Ser Arg Leu
 25

<210> 382
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 382
 Met Leu Arg Pro Ala Leu Pro Trp Leu Tyr Leu Gly Leu Cys Ser Leu
 -20 -15 -10
 Leu Val Gly Glu Ala Glu Ala Pro Ser Pro Val Asp Pro Leu Glu Arg
 -5 1 5
 Ser Arg Pro Tyr Ala Val Leu Arg Gly Gln Asn Leu Val Leu Met Gly
 10 15 20 25
 Thr Ile Phe Ser Ile Leu Leu Val Thr Val Ile Leu Met Ala Phe Cys
 30 35 40
 Val Tyr Lys Pro Ile Arg Arg Arg
 45

<210> 383
 <211> 95
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -48...-1

<400> 383

Met	Ala	Ser	Ser	His	Trp	Asn	Glu	Thr	Thr	Thr	Ser	Val	Tyr	Gln	Tyr
			-45					-40					-35		
Leu	Gly	Phe	Gln	Val	Gln	Lys	Ile	Tyr	Pro	Phe	His	Asp	Asn	Trp	Asn
		-30				-25						-20			
Thr	Ala	Cys	Phe	Val	Ile	Leu	Leu	Leu	Phe	Ile	Phe	Thr	Val	Val	Ser
	-15				-10					-5					
Leu	Val	Val	Leu	Ala	Phe	Leu	Tyr	Glu	Val	Leu	Asp	Cys	Cys	Cys	Cys
1			5					10					15		
Val	Lys	Asn	Lys	Thr	Val	Lys	Asp	Leu	Lys	Ser	Glu	Pro	Asn	Pro	Leu
		20					25					30			
Arg	Ser	Met	Met	Asp	Asn	Ile	Arg	Lys	Arg	Glu	Thr	Glu	Val	Val	
		35					40					45			

<210> 384

<211> 150

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20...-1

<400> 384

Met	Ala	Arg	His	Gly	Leu	Pro	Leu	Leu	Pro	Leu	Leu	Ser	Leu	Leu	Val
-20				-15					-10						-5
Gly	Ala	Trp	Leu	Lys	Leu	Gly	Asn	Gly	Gln	Ala	Thr	Ser	Met	Val	Gln
			1				5					10			
Leu	Gln	Gly	Gly	Arg	Phe	Leu	Met	Gly	Thr	Asn	Ser	Pro	Asp	Ser	Arg
	15					20					25				
Asp	Gly	Glu	Gly	Pro	Val	Arg	Glu	Ala	Thr	Val	Lys	Pro	Phe	Ala	Ile
	30					35				40					
Asp	Ile	Phe	Pro	Val	Thr	Asn	Lys	Asp	Phe	Arg	Asp	Phe	Val	Arg	Glu
45					50				55						60
Lys	Lys	Tyr	Arg	Thr	Glu	Ala	Glu	Met	Phe	Gly	Trp	Ser	Phe	Val	Phe
				65				70						75	
Glu	Asp	Phe	Val	Ser	Asp	Glu	Leu	Arg	Asn	Lys	Ala	Thr	Gln	Pro	Met
			80				85						90		
Lys	Val	Lys	Phe	Thr	His	Gly	Gly	Thr	Gly	Ser	Ser	Gln	Thr	Ala	Pro
		95				100						105			
Thr	Cys	Gly	Arg	Glu	Ser	Ser	Pro	Arg	Glu	Thr	Lys	Leu	Arg	Met	Ala
	110					115					120				
Ser	Met	Glu	Ser	Pro	Gln										
125					130										

<210> 385

<211> 354

<212> PRT

<213> Homo sapiens

<400> 385

Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro

1				5					10					15		
Met	Pro	Thr	Cys	Arg	Val	Tyr	Gly	Thr	Val	Ala	His	Gln	Asp	Gly	His	
			20					25					30			
Leu	Leu	Val	Leu	Gly	Gly	Cys	Gly	Arg	Ala	Gly	Leu	Pro	Leu	Asp	Thr	
		35					40					45				
Ala	Glu	Thr	Leu	Asp	Met	Ala	Ser	His	Thr	Trp	Leu	Ala	Leu	Ala	Pro	
	50					55					60					
Leu	Pro	Thr	Ala	Arg	Ala	Gly	Ala	Ala	Ala	Val	Val	Leu	Gly	Lys	Gln	
65				70						75					80	
Val	Leu	Val	Val	Cys	Gly	Val	Asp	Glu	Val	Gln	Ser	Pro	Val	Ala	Ala	
			85					90						95		
Val	Glu	Ala	Phe	Leu	Met	Asp	Glu	Gly	Arg	Trp	Glu	Arg	Arg	Ala	Thr	
		100						105					110			
Leu	Pro	Gln	Ala	Ala	Met	Gly	Val	Ala	Thr	Val	Glu	Arg	Asp	Gly	Met	
	115						120						125			
Val	Tyr	Ala	Leu	Gly	Gly	Met	Gly	Pro	Asp	Thr	Ala	Pro	Gln	Ala	Gln	
	130					135					140					
Val	Arg	Val	Tyr	Asp	Pro	Arg	Arg	Asp	Cys	Trp	Leu	Ser	Leu	Pro	Ser	
145				150					155						160	
Met	Pro	Thr	Pro	Cys	Tyr	Gly	Ala	Ser	Thr	Phe	Leu	His	Gly	Asn	Lys	
			165						170					175		
Ile	Tyr	Val	Leu	Gly	Gly	Arg	Gln	Gly	Lys	Leu	Pro	Val	Thr	Ala	Phe	
		180						185					190			
Glu	Ala	Phe	Asp	Leu	Glu	Ala	Arg	Thr	Trp	Thr	Arg	His	Pro	Ser	Leu	
	195					200						205				
Pro	Ser	Arg	Arg	Ala	Phe	Ala	Gly	Cys	Ala	Met	Ala	Glu	Gly	Ser	Val	
	210					215					220					
Phe	Ser	Leu	Gly	Gly	Leu	Gln	Gln	Pro	Gly	Pro	His	Asn	Phe	Tyr	Ser	
225				230						235					240	
Arg	Pro	His	Phe	Val	Asn	Thr	Val	Glu	Met	Phe	Asp	Leu	Glu	His	Gly	
			245					250						255		
Ser	Trp	Thr	Lys	Leu	Pro	Arg	Ser	Leu	Arg	Met	Arg	Asp	Lys	Arg	Ala	
		260						265					270			
Asp	Phe	Val	Val	Gly	Ser	Leu	Gly	Gly	His	Ile	Val	Ala	Ile	Gly	Gly	
	275						280					285				
Leu	Gly	Asn	Gln	Pro	Cys	Pro	Leu	Gly	Ser	Val	Glu	Ser	Phe	Ser	Leu	
	290					295					300					
Ala	Arg	Arg	Arg	Trp	Glu	Ala	Leu	Pro	Ala	Met	Pro	Thr	Ala	Arg	Cys	
305				310						315					320	
Ser	Cys	Ser	Ser	Leu	Gln	Ala	Gly	Pro	Arg	Leu	Phe	Val	Ile	Gly	Gly	
			325					330						335		
Val	Ala	Gln	Gly	Pro	Ser	Gln	Ala	Val	Glu	Ala	Leu	Cys	Leu	Arg	Asp	
			340					345					350			

<210> 386

<211> 207

<212> PRT

<213> Homo sapiens

<400> 386

Met	Ala	Leu	Leu	Phe	Ala	Arg	Ser	Leu	Arg	Leu	Cys	Arg	Trp	Gly	Ala	
1				5				10					15			
Lys	Arg	Leu	Gly	Val	Ala	Ser	Thr	Glu	Ala	Gln	Arg	Gly	Val	Ser	Phe	
		20						25				30				
Lys	Leu	Glu	Glu	Lys	Thr	Ala	His	Ser	Ser	Leu	Ala	Leu	Phe	Arg	Asp	
	35					40					45					
Asp	Thr	Gly	Val	Lys	Tyr	Gly	Leu	Val	Gly	Leu	Glu	Pro	Thr	Lys	Val	

50		55		60
Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val Val Leu Ala Asp				
65		70		75
Thr Ala Val Thr Ser Gly Arg His Tyr Trp Glu Val Thr Val Lys Arg				80
	85		90	
Ser Gln Gln Phe Arg Ile Gly Val Ala Asp Val Asp Met Ser Arg Asp				95
	100		105	
Ser Cys Ile Gly Val Asp Asp Arg Ser Trp Val Phe Thr Tyr Ala Gln				110
	115		120	
Arg Lys Trp Tyr Thr Met Leu Ala Asn Glu Lys Ala Pro Val Glu Gly				125
	130		135	
Ile Gly Gln Pro Glu Lys Val Gly Leu Leu Leu Glu Tyr Glu Ala Gln				140
	145		150	
Lys Leu Ser Leu Val Asp Val Ser Gln Val Ser Val Val His Thr Leu				155
	165		170	
Gln Thr Asp Phe Arg Gly Pro Val Val Pro Ala Phe Ala Leu Trp Asp				175
	180		185	
Gly Glu Leu Leu Thr His Ser Gly Leu Glu Val Pro Glu Gly Leu				190
	195		200	
				205

<210> 387

<211> 210

<212> PRT

<213> Homo sapiens

<400> 387

Met Ala Ala Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly		
1	5	10
Gln Ala Leu Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg		15
	20	25
Phe Ser Val Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp		30
	35	40
Gln Asn Leu Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala		45
	50	55
Val Ala Ile Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala		60
	65	70
Pro Ala Pro Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val		75
	85	90
Val Asp Ala Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu		95
	100	105
Ser Gly Met Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu		110
	115	120
Pro Gly Phe Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala		125
	130	135
Ala Asn Tyr Ala Ser Val Lys Thr Pro Ala Leu Ile Val Tyr Gly Asp		140
	145	150
Gln Asp Pro Met Gly Gln Thr Ser Phe Glu His Leu Lys Gln Leu Pro		155
	165	170
Asn His Arg Val Leu Ile Met Lys Gly Ala Gly His Pro Cys Tyr Leu		175
	180	185
Asp Lys Pro Glu Glu Trp His Thr Gly Leu Leu Asp Phe Leu Gln Gly		190
	195	200
		205

Leu Gln
210

<210> 388

<211> 375

<212> PRT

<213> Homo sapiens

<400> 388

Met Ala Val Thr Glu Ala Ser Leu Leu Arg Gln Cys Pro Leu Leu Leu
1 5 10 15
Pro Gln Asn Arg Ser Lys Thr Val Tyr Glu Gly Phe Ile Ser Ala Gln
20 25 30
Gly Arg Asp Phe His Leu Arg Ile Val Leu Pro Glu Asp Leu Gln Leu
35 40 45
Lys Asn Ala Arg Leu Leu Cys Ile Trp Gln Leu Arg Thr Ile Leu Ser
50 55 60
Gly Tyr His Arg Ile Val Gln Gln Arg Met Gln His Ser Pro Asp Leu
65 70 75 80
Met Ser Phe Met Met Glu Leu Lys Met Leu Leu Glu Val Ala Leu Lys
85 90 95
Asn Arg Gln Glu Leu Tyr Ala Leu Pro Pro Pro Pro Gln Phe Tyr Ser
100 105 110
Ser Leu Ile Glu Glu Ile Gly Thr Leu Gly Trp Asp Lys Leu Val Tyr
115 120 125
Ala Asp Thr Cys Phe Ser Thr Ile Lys Leu Lys Ala Glu Asp Ala Ser
130 135 140
Gly Arg Glu His Leu Ile Thr Leu Lys Leu Lys Ala Lys Tyr Pro Ala
145 150 155 160
Glu Ser Pro Asp Tyr Phe Val Asp Phe Pro Val Pro Phe Cys Ala Ser
165 170 175
Trp Thr Pro Gln Ser Ser Leu Ile Ser Ile Tyr Ser Gln Phe Leu Ala
180 185 190
Ala Ile Glu Ser Leu Lys Ala Phe Trp Asp Val Met Asp Glu Ile Asp
195 200 205
Glu Lys Thr Trp Val Leu Glu Pro Glu Lys Pro Pro Arg Ser Ala Thr
210 215 220
Ala Arg Arg Ile Ala Leu Gly Asn Asn Val Ser Ile Asn Ile Glu Val
225 230 235 240
Asp Pro Arg His Pro Thr Met Leu Pro Glu Cys Phe Phe Leu Gly Ala
245 250 255
Asp His Val Val Lys Pro Leu Gly Ile Lys Leu Ser Arg Asn Ile His
260 265 270
Leu Trp Asp Pro Glu Asn Ser Val Leu Gln Asn Leu Lys Asp Val Leu
275 280 285
Glu Ile Asp Phe Pro Ala Arg Ala Ile Leu Glu Lys Ser Asp Phe Thr
290 295 300
Met Asp Cys Gly Ile Cys Tyr Ala Tyr Gln Leu Asp Gly Thr Ile Pro
305 310 315 320
Asp Gln Val Cys Asp Asn Ser Gln Cys Gly Gln Pro Phe His Gln Ile
325 330 335
Cys Leu Tyr Glu Trp Leu Arg Gly Leu Leu Thr Ser Arg Gln Ser Phe
340 345 350
Asn Ile Ile Phe Gly Glu Cys Pro Tyr Cys Ser Lys Pro Ile Thr Leu
355 360 365
Lys Met Ser Gly Arg Lys His
370 375

<210> 389

<211> 509

<212> PRT

<213> Homo sapiens

<400> 389

Met	Ala	Ala	Ile	Gly	Val	His	Leu	Gly	Cys	Thr	Ser	Ala	Cys	Val	Ala	1	5	10	15
Val	Tyr	Lys	Asp	Gly	Arg	Ala	Gly	Val	Val	Ala	Asn	Asp	Ala	Gly	Asp	20	25	30	
Arg	Val	Thr	Pro	Ala	Val	Val	Ala	Tyr	Ser	Glu	Asn	Glu	Glu	Ile	Val	35	40	45	
Gly	Leu	Ala	Ala	Lys	Gln	Ser	Arg	Ile	Arg	Asn	Ile	Ser	Asn	Thr	Val	50	55	60	
Met	Lys	Val	Lys	Gln	Ile	Leu	Gly	Arg	Ser	Ser	Ser	Asp	Pro	Gln	Ala	65	70	75	80
Gln	Lys	Tyr	Ile	Ala	Glu	Ser	Lys	Cys	Leu	Val	Ile	Glu	Lys	Asn	Gly	85	90	95	
Lys	Leu	Arg	Tyr	Glu	Ile	Asp	Thr	Gly	Glu	Glu	Thr	Lys	Phe	Val	Asn	100	105	110	
Pro	Glu	Asp	Val	Ala	Arg	Leu	Ile	Phe	Ser	Lys	Met	Lys	Glu	Thr	Ala	115	120	125	
His	Ser	Val	Leu	Gly	Ser	Asp	Ala	Asn	Asp	Val	Val	Ile	Thr	Val	Pro	130	135	140	
Phe	Asp	Phe	Gly	Glu	Lys	Gln	Lys	Asn	Ala	Leu	Gly	Glu	Ala	Ala	Arg	145	150	155	160
Ala	Ala	Gly	Phe	Asn	Val	Leu	Arg	Leu	Ile	His	Glu	Pro	Ser	Ala	Ala	165	170	175	
Leu	Leu	Ala	Tyr	Gly	Ile	Gly	Gln	Asp	Ser	Pro	Thr	Gly	Lys	Ser	Asn	180	185	190	
Ile	Leu	Val	Phe	Lys	Leu	Gly	Gly	Thr	Ser	Leu	Ser	Leu	Ser	Val	Met	195	200	205	
Glu	Val	Asn	Ser	Gly	Ile	Tyr	Arg	Val	Leu	Ser	Thr	Asn	Thr	Asp	Asp	210	215	220	
Asn	Ile	Gly	Gly	Ala	His	Phe	Thr	Glu	Thr	Leu	Ala	Gln	Tyr	Leu	Ala	225	230	235	240
Ser	Glu	Phe	Gln	Arg	Ser	Phe	Lys	His	Asp	Val	Arg	Gly	Asn	Ala	Arg	245	250	255	
Ala	Met	Met	Lys	Leu	Thr	Asn	Ser	Ala	Glu	Val	Ala	Lys	His	Ser	Leu	260	265	270	
Ser	Thr	Leu	Gly	Ser	Ala	Asn	Cys	Phe	Leu	Asp	Ser	Leu	Tyr	Glu	Gly	275	280	285	
Gln	Asp	Phe	Asp	Cys	Asn	Val	Ser	Arg	Ala	Arg	Phe	Glu	Leu	Leu	Cys	290	295	300	
Ser	Pro	Leu	Phe	Asn	Lys	Cys	Ile	Glu	Ala	Ile	Arg	Gly	Leu	Leu	Asp	305	310	315	320
Gln	Asn	Gly	Phe	Thr	Thr	Asp	Asp	Ile	Asn	Lys	Val	Val	Leu	Cys	Gly	325	330	335	
Gly	Ser	Ser	Arg	Ile	Pro	Lys	Leu	Gln	Leu	Ile	Lys	Asp	Leu	Phe		340	345	350	
Pro	Ala	Val	Glu	Leu	Leu	Asn	Ser	Ile	Pro	Pro	Asp	Glu	Val	Ile	Pro	355	360	365	
Ile	Gly	Ala	Ala	Ile	Glu	Ala	Gly	Ile	Leu	Ile	Gly	Lys	Glu	Asn	Leu	370	375	380	
Leu	Val	Glu	Asp	Ser	Leu	Met	Ile	Glu	Cys	Ser	Ala	Arg	Asp	Ile	Leu	385	390	395	400
Val	Lys	Gly	Val	Asp	Glu	Ser	Gly	Ala	Ser	Arg	Phe	Thr	Val	Leu	Phe	405	410	415	
Pro	Ser	Gly	Thr	Pro	Leu	Pro	Ala	Arg	Arg	Gln	His	Thr	Leu	Gln	Ala	420	425	430	
Pro	Gly	Ser	Ile	Ser	Ser	Val	Cys	Leu	Glu	Leu	Tyr	Glu	Ser	Asp	Gly	435	440	445	
Lys	Asn	Ser	Ala	Lys	Glu	Glu	Thr	Lys	Phe	Ala	Gln	Val	Val	Leu	Gln	450	455	460	

Asp Leu Asp Lys Lys Glu Asn Gly Leu Arg Asp Ile Leu Ala Val Leu
 465 470 475 480
 Thr Met Lys Arg Asp Gly Ser Leu His Val Thr Cys Thr Asp Gln Glu
 485 490 495
 Thr Gly Lys Cys Glu Ala Ile Ser Ile Glu Ile Ala Ser
 500 505

<210> 390
 <211> 78
 <212> PRT
 <213> Homo sapiens

<400> 390
 Met Tyr Asn Thr Gly Arg His Val Ser Leu Arg Leu Asp Lys Glu His
 1 5 10 15
 Leu Val Asn Ile Ser Gly Gly Pro Met Thr Tyr Ser His Arg Leu Glu
 20 25 30
 Glu Ile Arg Leu His Phe Gly Ser Glu Asp Ser Gln Gly Ser Glu His
 35 40 45
 Leu Leu Asn Gly Gln Ala Phe Ser Gly Glu Leu Gln Glu Arg Asp Leu
 50 55 60
 Phe Ile Leu Leu Thr Ser Val Ser Gly His Leu Pro Asp Thr
 65 70 75

<210> 391
 <211> 162
 <212> PRT
 <213> Homo sapiens

<400> 391
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
 1 5 10 15
 Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Ile Val
 20 25 30
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
 35 40 45
 Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
 50 55 60
 Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
 65 70 75 80
 Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
 85 90 95
 Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
 100 105 110
 Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
 115 120 125
 Thr Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
 130 135 140
 Ile Arg Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu
 145 150 155 160
 Leu Gly

<210> 392
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 392

Met Asn Ser Leu Leu His Phe Gly Ile Leu Leu Glu Leu Ser Leu Leu
1 5 10 15
Lys Gln Phe Lys Ser Val Tyr Val Pro Gly Asn His Thr His Gln Ala
20 25 30
Ser Tyr Lys Pro Leu Leu Lys Gln Val Val Glu Glu Ile Phe His Pro
35 40 45
Glu Arg Pro Asp Ser Val Asp Ile Glu His Met Ser Ser Gly Leu Thr
50 55 60
Asp Leu Leu Lys Thr Gly Phe Ser Met Phe Met Lys Val Ser Arg Pro
65 70 75 80
His Pro Ser Asp Tyr Pro Leu Leu Ile Leu Phe Val Val Gly Gly Val
85 90 95
Thr Val Ser Glu Val Lys Met Val Lys Asp Leu Val Ala Ser Leu Lys
100 105 110
Pro Gly Thr Gln Val Ile Val Leu Ser Thr Arg Leu Leu Lys Pro Leu
115 120 125
Asn Ile Pro Glu Leu Leu Phe Ala Thr Asp Arg Leu His Pro Asp Leu
130 135 140
Gly Phe
145

<210> 393

<211> 225

<212> PRT

<213> Homo sapiens

<400> 393

Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
1 5 10 15
Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val
20 25 30
Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
35 40 45
Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
50 55 60
Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
65 70 75 80
Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
85 90 95
Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
100 105 110
Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
115 120 125
Ala Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
130 135 140
Ile Arg Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu
145 150 155 160
Leu Gly Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile
165 170 175
Val Gly Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser
180 185 190
Ser Ser Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser
195 200 205
Tyr His Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr
210 215 220
Val
225

<210> 394
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 394
 Met Arg Leu Gln Asp Arg Ile Ala Thr Phe Phe Phe Pro Lys Gly Met
 1 5 10 15
 Met Leu Thr Thr Ala Ala Leu Met Leu Phe Phe Leu His Leu Gly Ile
 20 25 30
 Phe Ile Arg Asp Val His Asn Phe Cys Ile Thr Tyr His Tyr Asp His
 35 40 45
 Met Ser Phe His Tyr Thr Val Val Leu Met Phe Ser Gln Val Ile Ser
 50 55 60
 Ile Cys Trp Ala Ala Met Gly Ser Leu Tyr Ala Glu Met Thr Glu Asn
 65 70 75 80
 Asn Ala Gln Arg Ser His Val Leu Gln Pro Pro Val Leu Gly Val Ser
 85 90 95
 Gly His Arg Val Pro Gly Gly Ala Pro Leu Arg Pro Gly Glu Ser Glu
 100 105 110
 Gln Gly

<210> 395
 <211> 367
 <212> PRT
 <213> Homo sapiens

<400> 395
 Met Ala Thr Pro Asn Asn Leu Thr Pro Thr Asn Cys Ser Trp Trp Pro
 1 5 10 15
 Ile Ser Ala Leu Glu Ser Asp Ala Ala Lys Pro Ala Glu Ala Pro Asp
 20 25 30
 Ala Pro Glu Ala Ala Ser Pro Ala His Trp Pro Arg Glu Ser Leu Val
 35 40 45
 Leu Tyr His Trp Thr Gln Ser Phe Ser Ser Gln Lys Val Arg Leu Val
 50 55 60
 Ile Ala Glu Lys Gly Leu Val Cys Glu Glu Arg Asp Val Ser Leu Pro
 65 70 75 80
 Gln Ser Glu His Lys Glu Pro Trp Phe Met Arg Leu Asn Leu Gly Glu
 85 90 95
 Glu Val Pro Val Ile Ile His Arg Asp Asn Ile Ile Ser Asp Tyr Asp
 100 105 110
 Gln Ile Ile Asp Tyr Val Glu Arg Thr Phe Thr Gly Glu His Val Val
 115 120 125
 Ala Leu Met Pro Glu Val Gly Ser Leu Gln His Ala Arg Val Leu Gln
 130 135 140
 Tyr Arg Glu Leu Leu Asp Ala Leu Pro Met Asp Ala Tyr Thr His Gly
 145 150 155 160
 Cys Ile Leu His Pro Glu Leu Thr Thr Asp Ser Met Ile Pro Lys Tyr
 165 170 175
 Ala Thr Ala Glu Ile Arg Arg His Leu Ala Asn Ala Thr Thr Asp Leu
 180 185 190
 Met Lys Leu Asp His Glu Glu Glu Pro Gln Leu Ser Glu Pro Tyr Leu
 195 200 205
 Ser Lys Gln Lys Lys Leu Met Val Lys Ile Leu Glu His Asp Asp Val
 210 215 220
 Ser Tyr Leu Lys Lys Ile Leu Gly Glu Leu Ala Met Val Leu Asp Gln
 225 230 235 240

Ile Glu Ala Glu Leu Glu Lys Arg Lys Leu Glu Asn Glu Gly Gln Lys
245 250 255
Cys Glu Leu Trp Leu Cys Gly Cys Ala Phe Thr Leu Ala Asp Val Leu
260 265 270
Leu Gly Ala Thr Leu His Arg Leu Lys Phe Leu Gly Leu Ser Lys Lys
275 280 285
Tyr Trp Glu Asp Gly Ser Arg Pro Asn Leu Gln Ser Phe Phe Glu Arg
290 295 300
Val Gln Arg Arg Phe Ala Phe Arg Lys Val Leu Gly Asp Ile His Thr
305 310 315 320
Thr Leu Leu Ser Ala Val Ile Pro Asn Ala Phe Arg Leu Val Lys Arg
325 330 335
Lys Pro Pro Ser Phe Phe Gly Ala Ser Phe Leu Met Gly Ser Leu Gly
340 345 350
Gly Met Gly Tyr Phe Ala Tyr Trp Tyr Leu Lys Lys Lys Tyr Ile
355 360 365

<210> 396
<211> 279
<212> PRT
<213> Homo sapiens

<400> 396
Met Pro Val Cys Ala Pro Val Leu Trp Arg Ala Arg Arg Leu Cys Gly
1 5 10 15
Met Pro Val Cys Ala Pro Val Pro Trp Arg Ala Arg Arg Leu Cys Thr
20 25 30
Arg Ala Val Val Cys Pro Ser Ser Val Pro Phe Ile Ala Gly Gln Gly
35 40 45
Cys Thr His Met Cys Lys Pro Ala Thr Asp Pro Arg Phe Thr Arg Ser
50 55 60
Pro Leu Ala Gly Gly Val Ile Leu Gly Val Ala Leu Trp Leu Arg His
65 70 75 80
Asp Pro Gln Thr Thr Asn Leu Leu Tyr Leu Glu Leu Gly Asp Lys Pro
85 90 95
Ala Pro Asn Thr Phe Tyr Val Gly Ile Tyr Ile Leu Ile Ala Val Gly
100 105 110
Ala Val Met Met Phe Val Gly Phe Leu Gly Cys Tyr Gly Ala Ile Gln
115 120 125
Glu Ser Gln Cys Leu Leu Gly Thr Phe Phe Thr Cys Leu Val Ile Leu
130 135 140
Phe Ala Cys Glu Val Ala Ala Gly Ile Trp Gly Phe Val Asn Lys Asp
145 150 155 160
Gln Ile Ala Lys Asp Val Lys Gln Phe Tyr Asp Gln Ala Leu Gln Gln
165 170 175
Ala Val Val Asp Asp Ala Asn Asn Ala Lys Ala Val Val Lys Thr
180 185 190
Phe His Glu Thr Leu Asp Cys Cys Gly Ser Ser Thr Leu Thr Ala Leu
195 200 205
Thr Thr Ser Val Leu Lys Asn Asn Leu Cys Pro Ser Gly Ser Asn Ile
210 215 220
Ile Ser Asn Leu Phe Lys Glu Asp Cys His Gln Lys Ile Asp Asp Leu
225 230 235 240
Phe Ser Gly Lys Leu Tyr Leu Ile Gly Ile Ala Ala Ile Val Val Ala
245 250 255
Val Ile Met Ile Phe Glu Met Ile Leu Ser Met Val Leu Cys Cys Gly
260 265 270
Ile Arg Asn Ser Ser Val Tyr

275

<210> 397
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 397
 Met Cys Leu Leu Leu Gly Ala Thr Gly Val Gly Lys Thr Leu Leu Val
 1 5 10 15
 Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly Asp Leu Gly
 20 25 30
 Glu Pro Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu Thr Asp Ile
 35 40 45
 Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly Cys Met Gly
 50 55 60
 Pro Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu Leu Phe Val
 65 70 75 80
 Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Ser Cys Val Gln Leu
 85 90 95
 Leu Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser Val Leu Ile
 100 105 110
 Leu Phe Asn Lys Ile Asp Leu Pro Cys Tyr Met Ser Thr Glu Glu Met
 115 120 125
 Lys Ser Leu Ile Arg Leu Pro Asp Ile Ile Ala Cys Ala Lys Gln Asn
 130 135 140
 Ile Thr Thr Ala Glu Ile Ser Ala Arg Glu Gly Thr Gly Leu Ala Gly
 145 150 155 160
 Val Leu Ala Trp Leu Gln Ala Thr His Arg Ala Asn Asp
 165 170

<210> 398
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 398
 Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu Pro Gly Ser Ser
 1 5 10 15
 Val Leu Phe Leu Cys Asp Met Gln Glu Lys Phe Arg His Asn Ile Ala
 20 25 30
 Tyr Phe Pro Gln Ile Val Ser Val Ala Ala Arg Met Leu Lys Val Ala
 35 40 45
 Arg Leu Leu Glu Val Pro Val Met Leu Thr Glu Gln Tyr Pro Gln Gly
 50 55 60
 Leu Gly Pro Thr Val Pro Glu Leu Gly Thr Glu Gly Leu Arg Pro Leu
 65 70 75 80
 Ala Lys Thr Cys Phe Ser Met Val Pro Ala Leu Gln Gln Glu Leu Asp
 85 90 95
 Ser Arg Pro Gln Leu Arg Ser Val Leu Leu Cys Gly Ile Glu Ala Gln
 100 105 110
 Ala Cys Ile Leu Asn Thr Thr Leu Asp Leu Leu Asp Arg Gly Leu Gln
 115 120 125
 Val His Val Val Val Asp Ala Cys Ser Ser Arg Ser Gln Val Asp Arg
 130 135 140
 Leu Val Ala Leu Ala Arg Met Arg Gln Ser Gly Ala Phe Leu Ser Thr
 145 150 155 160
 Ser Glu Gly Leu Ile Leu Gln Leu Val Gly Asp Ala Val His Pro Gln

				165					170					175			
Phe	Lys	Glu	Ile	Gln	Lys	Leu	Ile	Lys	Glu	Pro	Ala	Pro	Asp	Ser	Gly		
			180					185					190				
Leu	Leu	Gly	Leu	Phe	Gln	Gly	Gln	Asn	Ser	Leu	Leu	His					
		195					200					205					

<210> 399
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 399

Met	Trp	Leu	Tyr	Arg	Asn	Pro	Tyr	Val	Glu	Ala	Glu	Tyr	Phe	Pro	Thr		
1			5						10					15			
Lys	Pro	Met	Phe	Val	Ile	Ala	Phe	Leu	Ser	Pro	Leu	Ser	Leu	Ile	Phe		
			20					25					30				
Leu	Ala	Lys	Phe	Leu	Lys	Lys	Ala	Asp	Thr	Arg	Asp	Ser	Arg	Gln	Ala		
		35					40					45					
Cys	Leu	Ala	Ala	Ser	Leu	Ala	Leu	Ala	Leu	Asn	Gly	Val	Phe	Thr	Asn		
	50					55					60						
Thr	Ile	Lys	Leu	Ile	Val	Gly	Arg	Pro	Arg	Pro	Asp	Phe	Phe	Tyr	Arg		
65					70					75					80		
Cys	Phe	Pro	Asp	Gly	Leu	Ala	His	Ser	Asp	Leu	Met	Cys	Thr	Gly	Asp		
				85					90					95			
Lys	Asp	Val	Val	Asn	Glu	Gly	Arg	Lys	Ser	Phe	Pro	Ser	Gly	His	Ser		
			100					105					110				
Ser	Phe	Ala	Phe	Ala	Gly	Leu	Ala	Phe	Ala	Ser	Phe	Tyr	Leu	Ala	Gly		
		115				120						125					
Lys	Leu	His	Cys	Phe	Thr	Pro	Gln	Gly	Arg	Gly	Lys	Ser	Trp	Arg	Phe		
	130					135					140						
Cys	Ala	Phe	Leu	Ser	Pro	Leu	Leu	Phe	Ala	Ala	Val	Ile	Ala	Leu	Ser		
145					150				155						160		
Arg	Thr	Cys	Asp	Tyr	Lys	His	His	Trp	Gln	Asp	Leu	Leu	Lys	Cys	Thr		
				165					170					175			
Asn	Thr	Ala	Lys														
			180														

<210> 400
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 400

Met	Cys	Thr	Ala	Leu	Leu	Leu	Leu	Tyr	Leu	Arg	Trp	Cys	Phe	Asn	Leu		
1				5					10					15			
Lys	Leu	Val	Asn	Val	Lys	Tyr	Glu	Pro	Lys	Asp	Ser	Leu	Gly	Pro	Glu		
			20					25					30				
Met	Thr	Phe	Val	Ala	Asp	Ala	Ala	Arg	Gly	Pro	Leu	Leu	Ser	Ser	Leu		
		35					40					45					
Asp	Ser	Pro	Ala	Asn	Leu	Met	Ser	Thr	Ala	Ser	Val	Cys	Ile	Ser	Leu		
	50					55					60						
Pro	Glu	Gly	Cys	Ser	Gly	Gly	Arg	Ser	Pro	Cys	Tyr	Ser	Gln	Lys	Trp		
65					70					75					80		
Pro	Pro	Glu	Val	Pro	Glu	Lys	Leu	Thr	Ser	Leu	Gly	Gln	Gln	Ser	Ser		
				85					90					95			
Thr	Ser	Ser	Leu	Thr	Asp	Thr	Asp	Val	Gln	Val	Ser	Pro	Met	Leu	Val		
			100					105					110				
Ala	Gly	Val	Asn	His	Ser	Ser	Ser	Leu	Leu	Asp	Asn	Ile	Pro	Phe	Thr		

130		135		140											
Thr	Glu	Cys	Gly	Gln	Asp	Phe	Ala	Gln	Glu	Ala	Gly	Leu	His	Gln	His
145					150					155					160
Tyr	Ile	Arg	His	Ala	Arg	Gly	Glu	Leu							
				165											

<210> 403
 <211> 367
 <212> PRT
 <213> Homo sapiens

<400> 403

Met	Ala	Thr	Pro	Asn	Asn	Leu	Thr	Pro	Thr	Asn	Cys	Ser	Trp	Trp	Pro
1				5					10					15	
Ile	Ser	Ala	Leu	Glu	Ser	Asp	Ala	Ala	Lys	Pro	Ala	Glu	Ala	Pro	Asp
			20					25					30		
Ala	Pro	Glu	Ala	Ala	Ser	Pro	Ala	His	Trp	Pro	Arg	Glu	Ser	Leu	Val
		35					40					45			
Leu	Tyr	His	Trp	Thr	Gln	Ser	Phe	Ser	Ser	Gln	Lys	Val	Arg	Leu	Val
	50					55					60				
Ile	Ala	Glu	Lys	Gly	Leu	Val	Cys	Glu	Glu	Arg	Asp	Val	Ser	Leu	Pro
65					70					75					80
Gln	Ser	Glu	His	Lys	Glu	Pro	Trp	Phe	Met	Arg	Leu	Asn	Leu	Gly	Glu
				85					90					95	
Glu	Val	Pro	Val	Ile	Ile	His	Arg	Asp	Asn	Ile	Ile	Ser	Asp	Tyr	Asp
			100					105					110		
Gln	Ile	Ile	Asp	Tyr	Val	Glu	Arg	Thr	Phe	Thr	Gly	Glu	His	Val	Val
	115						120					125			
Ala	Leu	Met	Pro	Glu	Val	Gly	Ser	Leu	Gln	His	Ala	Arg	Val	Leu	Gln
	130					135					140				
Tyr	Arg	Glu	Leu	Leu	Asp	Ala	Leu	Pro	Met	Asp	Ala	Tyr	Thr	His	Gly
145					150					155					160
Cys	Ile	Leu	His	Leu	Glu	Leu	Thr	Thr	Asp	Ser	Met	Ile	Pro	Lys	Tyr
				165					170					175	
Ala	Thr	Ala	Glu	Ile	Arg	Arg	His	Leu	Ala	Asn	Ala	Thr	Thr	Asp	Leu
			180					185					190		
Met	Lys	Leu	Asp	His	Glu	Glu	Glu	Pro	Gln	Leu	Ser	Glu	Pro	Tyr	Leu
	195						200						205		
Ser	Lys	Gln	Lys	Lys	Leu	Met	Ala	Lys	Ile	Leu	Glu	His	Asp	Asp	Val
	210					215					220				
Ser	Tyr	Leu	Lys	Lys	Ile	Leu	Gly	Glu	Leu	Ala	Met	Val	Leu	Asp	Gln
225					230					235					240
Ile	Glu	Ala	Glu	Leu	Glu	Lys	Arg	Lys	Leu	Glu	Asn	Glu	Gly	Gln	Lys
			245						250					255	
Cys	Glu	Leu	Trp	Leu	Cys	Gly	Cys	Ala	Phe	Thr	Leu	Ala	Asp	Val	Leu
		260						265					270		
Leu	Gly	Ala	Thr	Leu	His	Arg	Leu	Lys	Phe	Leu	Gly	Leu	Ser	Lys	Lys
	275						280					285			
Tyr	Trp	Glu	Asp	Gly	Ser	Arg	Pro	Asn	Leu	Gln	Ser	Phe	Phe	Glu	Arg
	290					295					300				
Val	Gln	Arg	Arg	Phe	Ala	Phe	Arg	Lys	Val	Leu	Gly	Asp	Ile	His	Thr
305					310					315					320
Thr	Leu	Leu	Ser	Ala	Val	Ile	Pro	Asn	Ala	Phe	Arg	Leu	Val	Lys	Arg
				325					330					335	
Lys	Pro	Pro	Ser	Phe	Phe	Gly	Ala	Ser	Phe	Leu	Met	Gly	Ser	Leu	Gly
			340					345					350		
Gly	Met	Gly	Tyr	Phe	Ala	Tyr	Trp	Tyr	Leu	Lys	Lys	Lys	Tyr	Ile	
		355					360					365			

<210> 404
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 404
 Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu Pro Gly Ser Ser
 1 5 10 15
 Pro Val Pro Val
 20

<210> 405
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 405
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
 1 5 10 15
 Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val
 20 25 30
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
 35 40 45
 Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
 50 55 60
 Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
 65 70 75 80
 Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
 85 90 95
 Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
 100 105 110
 Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
 115 120 125
 Thr Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
 130 135 140
 Ile Arg Asp Phe Tyr Asn Ser Ile Val Asn Val Ala Gln Lys Arg Glu
 145 150 155 160
 Leu Gly Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile
 165 170 175
 Val Gly Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser
 180 185 190
 Ser Ser Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser
 195 200 205
 Tyr His Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr
 210 215 220
 Val
 225

<210> 406
 <211> 378
 <212> PRT
 <213> Homo sapiens

<400> 406
 Met Asp Pro Gly Asp Asp Trp Leu Val Glu Ser Leu Arg Leu Tyr Gln
 1 5 10 15
 Asp Phe Tyr Ala Phe Asp Leu Ser Gly Ala Thr Arg Val Leu Glu Trp

<210> 408
 <211> 345
 <212> PRT
 <213> Homo sapiens

<400> 408

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Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly Cys Gly Gln Ala
1      5      10      15
Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu Leu Thr Ala Val
      20      25      30
Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn Phe Phe Ile Gln
      35      40      45
Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val Glu Pro Arg Arg
      50      55      60
Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg Ser Ala Leu Ile
65      70      75      80
Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro Tyr Pro Ile Arg
      85      90      95
Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe Thr Gly Cys Ala
      100     105     110
Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu Lys Ser Arg Val
      115     120     125
Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu Asp Ser Ile Arg
      130     135     140
Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn Lys Trp Trp Asn
145     150     155     160
Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile Ile Ala Ala Asn
      165     170     175
Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu Gln Arg Thr Met
      180     185     190
Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val Leu Cys Ser Pro
      195     200     205
Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe His Met Ala Ala
210     215     220
Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile Val Asn Ile Leu
225     230     235     240
Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala Gly Val Ile Ser
      245     250     255
Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly Arg Tyr Gly Pro
      260     265     270
Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met Asp Thr Ala Gly
      275     280     285
Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly
      290     295     300
Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp
305     310     315     320
Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn
      325     330     335
Gly Pro Lys Lys Gly Gly Gly Ser Lys
      340     345

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<210> 409
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 409

[illegible]

$\langle 211 \rangle$ 121

<213> Homo sapiens

Met	Asn	Thr	Glu	Ala	Glu	Gln	Gln	Leu	Leu	His	His	Ala	Arg	Asn	Gly
1				5					10					15	
Asn	Ala	Glu	Glu	Val	Arg	Gln	Leu	Leu	Glu	Thr	Met	Ala	Ser	Asn	Glu
			20					25					30		
Val	Ile	Ala	Asp	Ile	Asn	Cys	Lys	Gly	Arg	Ser	Lys	Ser	Asn	Leu	Gly
			35				40					45			
Trp	Thr	Pro	Leu	His	Leu	Ala	Cys	Tyr	Phe	Gly	His	Arg	Gln	Val	Val
	50					55					60				
Gln	Asp	Leu	Leu	Lys	Ala	Gly	Ala	Glu	Val	Asn	Val	Leu	Asn	Asp	Met
65				70						75				80	
Gly	Asp	Thr	Pro	Leu	His	Arg	Ala	Ala	Phe	Thr	Gly	Arg	Lys	Val	Lys
				85					90				95		
Ile	Ile	Leu	Cys	Ser	Met	Phe	Val	Ser	Glu	Val	Phe	Gly	Gly	Val	Val
			100					105					110		
Thr	Ile	Val	Phe	Ser	Val	Ile	Thr	Ile							
			115				120								

<211> 170

<213> Homo sapiens

<400> 411
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro
 1 5 10 15
 Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
 20 25 30
 Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
 35 40 45
 Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
 50 55 60
 Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
 65 70 75 80
 Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
 85 90 95
 Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
 100 105 110
 Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
 115 120 125
 Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
 130 135 140
 Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
 145 150 155 160
 His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 165 170

<210> 412
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 412
 Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys
 1 5 10 15
 Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His Thr Ala
 20 25 30
 Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu
 35 40 45
 Ser Val Leu Lys Leu His His Ser Leu Gln Gln Ser Glu Pro Asp Leu
 50 55 60
 Arg His Leu Val Leu Val Val Asn Thr Leu Arg Arg Ile Gln Ala Ser
 65 70 75 80
 Met Ala Pro Ala Ala Ala Leu Pro Pro Val Pro Ser Pro Pro Ala Ala
 85 90 95
 Pro Ser Val Ala Asp Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser
 100 105 110
 Ala Ser Met Ala Ser Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu
 115 120 125
 Ser Gln Ala Pro Gln Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser
 130 135 140
 Ile Gly Gly Ala Ala Pro Ser Leu Gly Ala Leu Asp Leu Leu Gly Pro
 145 150 155 160
 Ala Thr Gly Cys Leu Leu Asp Asp Gly Leu Glu Gly Leu Phe Glu Asp
 165 170 175
 Ile Asp Thr Ser Met Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu
 180 185 190
 Gly Leu Lys Pro Gly Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro
 195 200 205
 Glu Leu Asp Glu Ala Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly

210 215 220
 Thr Gln Ala Leu Glu Arg Pro Pro Gly Pro Gly Arg
 225 230 235

<210> 413
 <211> 191
 <212> PRT
 <213> Homo sapiens

<400> 413
 Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile Thr
 1 5 10 15
 Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp Asn Phe
 20 25 30
 Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn Thr Lys
 35 40 45
 Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val Gly Arg
 50 55 60
 Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser Phe Phe
 65 70 75 80
 Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser Glu Asp
 85 90 95
 Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu Val His
 100 105 110
 Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile Arg Asp
 115 120 125
 Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu Ser Pro
 130 135 140
 Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly Thr Ile
 145 150 155 160
 Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Phe Gln Gln His
 165 170 175
 Ala Ala Leu Lys Ile Ser Ser Ala Leu Lys Asp Ser Asp Leu Pro
 180 185 190

<210> 414
 <211> 389
 <212> PRT
 <213> Homo sapiens

<400> 414
 Met Ala Glu Pro Asp Pro Ser His Pro Leu Glu Thr Gln Ala Gly Lys
 1 5 10 15
 Val Gln Glu Ala Gln Asp Ser Asp Ser Asp Ser Glu Gly Gly Ala Ala
 20 25 30
 Gly Gly Glu Ala Asp Met Asp Phe Leu Arg Asn Leu Phe Ser Gln Thr
 35 40 45
 Leu Ser Leu Gly Ser Gln Lys Glu Arg Leu Leu Asp Glu Leu Thr Leu
 50 55 60
 Glu Gly Val Ala Arg Tyr Met Gln Ser Glu Arg Cys Arg Arg Val Ile
 65 70 75 80
 Cys Leu Val Gly Ala Gly Ile Ser Thr Ser Ala Gly Ile Pro Asp Phe
 85 90 95
 Arg Ser Pro Ser Thr Gly Leu Tyr Asp Asn Leu Glu Lys Tyr His Leu
 100 105 110
 Pro Tyr Pro Glu Ala Ile Phe Glu Ile Ser Tyr Phe Lys Lys His Pro
 115 120 125
 Glu Pro Phe Phe Ala Leu Ala Lys Glu Leu Tyr Pro Gly Gln Phe Lys

130		135		140
Pro Thr Ile Cys His Tyr Phe Met Arg Leu Leu Lys Asp Lys Gly Leu				
145		150		155
Leu Leu Arg Cys Tyr Thr Gln Asn Ile Asp Thr Leu Glu Arg Ile Ala				160
	165		170	
Gly Leu Glu Gln Glu Asp Leu Val Glu Ala His Gly Thr Phe Tyr Thr				175
	180		185	
Ser His Cys Val Ser Ala Ser Cys Arg His Glu Tyr Pro Leu Ser Trp				190
	195		200	
Met Lys Glu Lys Ile Phe Ser Glu Val Thr Pro Lys Cys Glu Asp Cys				205
	210		215	
Gln Ser Leu Val Lys Pro Asp Ile Val Phe Phe Gly Glu Ser Leu Pro				220
225		230		235
Ala Arg Phe Phe Ser Cys Met Gln Ser Asp Phe Leu Lys Val Asp Leu				240
	245		250	
Leu Leu Val Met Gly Thr Ser Leu Gln Val Gln Pro Phe Ala Ser Leu				255
	260		265	
Ile Ser Lys Ala Pro Leu Ser Thr Pro Arg Leu Leu Ile Asn Lys Glu				270
	275		280	
Lys Ala Gly Gln Ser Asp Pro Phe Leu Gly Met Ile Met Gly Leu Gly				285
	290		295	
Gly Gly Met Asp Phe Asp Ser Lys Lys Ala Tyr Arg Asp Val Ala Trp				300
305		310		315
Leu Gly Glu Cys Asp Gln Gly Cys Leu Ala Leu Ala Glu Leu Leu Gly				320
	325		330	
Trp Lys Lys Glu Leu Glu Asp Leu Val Arg Arg Glu His Ala Ser Ile				335
	340		345	
Asp Ala Gln Ser Gly Ala Gly Val Pro Asn Pro Ser Thr Ser Ala Ser				350
	355		360	
Pro Lys Lys Ser Pro Pro Pro Ala Lys Asp Glu Ala Arg Thr Thr Glu				365
	370		375	
Arg Glu Lys Pro Gln				380
385				

<210> 415

<211> 481

<212> PRT

<213> Homo sapiens

<400> 415

Met Ser Leu Asn Leu Pro Glu Ala Ser Leu Leu Ser Arg Ala Ser Trp	
1	5
Pro Glu Gln Ala Lys Glu Pro Arg Arg Glu Gly His Thr Asp Lys Gln	10
	20
Gln Thr Glu Asp Val Leu Ala Ala Gly Leu Arg Cys Leu Pro His Leu	25
	30
Pro Ala Ile Cys Ala Arg Arg Met Ser Pro Ala Phe Arg Ala Met Asp	35
	40
Val Glu Pro Arg Ala Lys Gly Val Leu Leu Glu Pro Phe Val His Gln	45
	50
Val Gly Gly His Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys	55
	60
Lys Pro Leu Val Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ala	65
	70
Glu Met Arg Lys Phe Thr Pro Gln Tyr Lys Gly Val Val Ser Val Arg	75
	80
Phe Glu Glu Asp Glu Asp Arg Asn Leu Cys Leu Ile Ala Tyr Pro Leu	85
	90
	95
	100
	105
	110
	115
	120
	125
	130
	135
	140

Lys	Gly	Asp	His	Gly	Ile	Val	Asp	Ile	Val	Asp	Asn	Ser	Asp	Cys	Glu
145					150					155					160
Pro	Lys	Ser	Lys	Leu	Leu	Arg	Trp	Thr	Thr	Asn	Lys	Lys	His	His	Val
				165						170					175
Leu	Glu	Thr	Glu	Lys	Thr	Pro	Lys	Asp	Trp	Val	Arg	Gln	His	Arg	Lys
			180					185					190		
Glu	Glu	Lys	Met	Lys	Ser	His	Lys	Leu	Glu	Glu	Glu	Phe	Glu	Trp	Leu
		195					200					205			
Lys	Lys	Ser	Glu	Val	Leu	Tyr	Tyr	Thr	Val	Glu	Lys	Lys	Gly	Asn	Ile
	210					215					220				
Ser	Ser	Gln	Leu	Lys	His	Tyr	Asn	Pro	Trp	Ser	Met	Lys	Cys	His	Gln
225					230					235					240
Gln	Gln	Leu	Gln	Arg	Met	Lys	Glu	Asn	Ala	Lys	His	Arg	Asn	Gln	Tyr
				245				250						255	
Lys	Phe	Ile	Leu	Leu	Glu	Asn	Leu	Thr	Ser	Arg	Tyr	Glu	Val	Pro	Cys
			260					265					270		
Val	Leu	Asp	Leu	Lys	Met	Gly	Thr	Arg	Gln	His	Gly	Asp	Asp	Ala	Ser
		275					280					285			
Glu	Glu	Lys	Ala	Ala	Asn	Gln	Ile	Arg	Lys	Cys	Gln	Gln	Ser	Thr	Ser
	290					295					300				
Ala	Val	Ile	Gly	Val	Arg	Val	Cys	Gly	Met	Gln	Val	Tyr	Gln	Ala	Gly
305					310					315					320
Ser	Gly	Gln	Leu	Met	Phe	Met	Asn	Lys	Tyr	His	Gly	Arg	Lys	Leu	Ser
				325					330					335	
Val	Gln	Gly	Phe	Lys	Glu	Ala	Leu	Phe	Gln	Phe	Phe	His	Asn	Gly	Arg
			340					345					350		
Tyr	Leu	Arg	Arg	Glu	Leu	Leu	Gly	Pro	Val	Leu	Lys	Lys	Leu	Thr	Glu
	355						360					365			
Leu	Lys	Ala	Val	Leu	Glu	Arg	Gln	Glu	Ser	Tyr	Arg	Phe	Tyr	Ser	Ser
	370					375					380				
Ser	Leu	Leu	Val	Ile	Tyr	Asp	Gly	Lys	Glu	Arg	Pro	Glu	Val	Val	Leu
385					390					395					400
Asp	Ser	Asp	Ala	Glu	Asp	Leu	Glu	Asp	Leu	Ser	Glu	Glu	Ser	Ala	Asp
				405					410					415	
Glu	Ser	Ala	Gly	Ala	Tyr	Ala	Tyr	Lys	Pro	Ile	Gly	Ala	Ser	Ser	Val
			420					425					430		
Asp	Val	Arg	Met	Ile	Asp	Phe	Ala	His	Thr	Thr	Cys	Arg	Leu	Tyr	Gly
	435					440						445			
Glu	Asp	Thr	Val	Val	His	Glu	Gly	Gln	Asp	Ala	Gly	Tyr	Ile	Phe	Gly
	450					455					460				
Leu	Gln	Ser	Leu	Ile	Asp	Ile	Val	Thr	Glu	Ile	Ser	Glu	Glu	Ser	Gly
465					470					475					480
Glu															

<210> 416
 <211> 354
 <212> PRT
 <213> Homo sapiens

<400> 416
 Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro
 1 5 10 15
 Met Pro Thr Cys Arg Val Tyr Gly Thr Val Ala His Gln Asp Gly His
 20 25 30
 Leu Leu Val Leu Gly Gly Cys Gly Arg Ala Gly Leu Pro Leu Asp Thr
 35 40 45
 Ala Glu Thr Leu Asp Met Ala Ser His Thr Trp Leu Ala Leu Ala Pro
 50 55 60

Leu Pro Thr Ala Arg Ala Gly Ala Ala Ala Val Val Leu Gly Lys Gln
 65 70 75 80
 Val Leu Val Val Gly Gly Val Asp Glu Val Gln Ser Pro Val Ala Ala
 85 90 95
 Val Glu Ala Phe Leu Met Asp Glu Gly Arg Trp Glu Arg Arg Ala Thr
 100 105 110
 Leu Pro Gln Ala Ala Met Gly Val Ala Thr Val Glu Arg Asp Gly Met
 115 120 125
 Val Tyr Ala Leu Gly Gly Met Gly Pro Asp Thr Ala Pro Gln Ala Gln
 130 135 140
 Val Arg Val Tyr Glu Pro Arg Arg Asp Cys Trp Leu Ser Leu Pro Ser
 145 150 155 160
 Met Pro Thr Pro Cys Tyr Gly Ala Ser Thr Phe Leu His Gly Asn Lys
 165 170 175
 Ile Tyr Val Leu Gly Gly Arg Gln Gly Lys Leu Pro Val Thr Ala Phe
 180 185 190
 Glu Ala Phe Asp Leu Glu Ala Arg Thr Trp Thr Arg His Pro Ser Leu
 195 200 205
 Pro Ser Arg Arg Ala Phe Ala Gly Cys Ala Met Ala Glu Gly Ser Val
 210 215 220
 Phe Ser Leu Gly Gly Leu Gln Gln Pro Gly Pro His Asn Phe Tyr Ser
 225 230 235 240
 Arg Pro His Phe Val Asn Thr Val Glu Met Phe Asp Leu Glu His Gly
 245 250 255
 Ser Trp Thr Lys Leu Pro Arg Ser Leu Arg Met Arg Asp Lys Arg Ala
 260 265 270
 Asp Phe Val Val Gly Ser Leu Gly Gly His Ile Val Ala Ile Gly Gly
 275 280 285
 Leu Gly Asn Gln Pro Cys Pro Leu Gly Ser Val Glu Ser Phe Ser Leu
 290 295 300
 Ala Arg Arg Arg Trp Glu Ala Leu Pro Ala Met Pro Thr Ala Arg Cys
 305 310 315 320
 Ser Cys Ser Ser Leu Gln Ala Gly Pro Arg Leu Phe Val Ile Gly Gly
 325 330 335
 Val Ala Gln Gly Pro Ser Gln Ala Val Glu Ala Leu Cys Leu Arg Asp
 340 345 350
 Gly Val

<210> 417

<211> 20

<212> PRT

<213> Homo sapiens

<400> 417

Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile Thr
 1 5 10 15

Phe Val Phe Gln
 20

<210> 418

<211> 320

<212> PRT

<213> Homo sapiens

<400> 418

Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile Thr
 1 5 10 15

Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp Asn Phe

Cys Ala Ala Leu Trp Trp His Lys Lys Gly Leu Ala Val Leu Phe Cys
 115 120 125
 Ile Leu Gln Phe Leu Ser Met Thr Trp Tyr Ser Leu Ser Tyr Ile Pro
 130 135 140
 Tyr Ala Arg Asp Ala Val Ile Lys Cys Cys Ser Ser Leu Leu Ser
 145 150 155

<210> 420
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 420
 Met Glu Gln Arg Leu Ala Glu Phe Arg Ala Ala Arg Lys Arg Ala Gly
 1 5 10 15
 Leu Ala Ala Gln Pro Pro Ala Ala Ser Gln Gly Ala Gln Thr Pro Gly
 20 25 30
 Glu Lys Ala Glu Ala Ala Ala Thr Leu Lys Ala Ala Pro Gly Trp Leu
 35 40 45
 Lys Arg Phe Leu Val Trp Lys Pro Arg Pro Ala Ser Ala Arg Ala Gln
 50 55 60
 Pro Gly Leu Val Gln Glu Ala Ala Gln Pro Gln Gly Ser Thr Ser Glu
 65 70 75 80
 Thr Pro Trp Asn Thr Ala Ile Pro Leu Pro Ser Cys Trp Asp Gln Ser
 85 90 95
 Phe Leu Thr Asn Ile Thr Phe Leu Lys Val Leu Leu Trp Leu Val Leu
 100 105 110
 Leu Gly Leu Phe Val Glu Leu Glu Phe Gly Leu Ala Tyr Phe Val Leu
 115 120 125
 Ser Leu Phe Tyr Trp Met Tyr Val Gly Thr Arg Gly Pro Glu Glu Lys
 130 135 140
 Lys Glu Gly Glu Lys Ser Ala Tyr Ser Val Phe Asn Pro Gly Cys Glu
 145 150 155 160
 Ala Ile Gln Gly Thr Leu Thr Ala Glu Gln Leu Glu Arg Glu Leu Gln
 165 170 175
 Leu Arg Pro Leu Ala Gly Arg
 180

<210> 421
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 421
 Met Ala Ala Pro Arg Arg Gly Arg Gly Ser Ser Thr Val Leu Ser Ser
 1 5 10 15
 Val Pro Leu Gln Met Leu Phe Tyr Leu Ser Gly Thr Tyr Tyr Ala Leu
 20 25 30
 Tyr Phe Leu Ala Thr Leu Leu Met Ile Thr Tyr Lys Ser Gln Val Phe
 35 40 45
 Ser Tyr Pro His Arg Tyr Leu Val Leu Asp Leu Ala Leu Leu Phe Leu
 50 55 60
 Met Gly Ile Leu Glu Ala Val Arg Leu Tyr Leu Gly Thr Arg Gly Asn
 65 70 75 80
 Leu Thr Glu Ala Glu Arg Pro Leu Ala Ala Ser Leu Ala Leu Thr Ala
 85 90 95
 Gly Thr Ala Leu Leu Ser Ala His Phe Leu Leu Trp Gln Ala Leu Val
 100 105 110

Leu Trp Ala Asp Trp Ala Leu Ser Ala Thr Leu Leu Ala Leu His Gly
115 120 125
Leu Glu Ala Val Leu Gln Val Val Ala Ile Ala Ala Phe Thr Arg
130 135 140

<210> 422
<211> 73
<212> PRT
<213> Homo sapiens

<400> 422
Met Ser Gly Val Pro Ala Glu Met Thr Gly Ala Val Glu Ala Phe Leu
1 5 10 15
Pro Val Val Ser Ser Arg Arg Leu Pro Arg Phe Val His Met Val
20 25 30
Ala Gly Val Ser Ser Lys Gln Glu Arg Ala Arg Ser Asn Thr Glu Ala
35 40 45
Leu Phe Lys Leu Cys Phe His His Ile Cys Gln Cys Leu Thr Asp Glu
50 55 60
His Lys Phe His Gly Gln Val Gln Phe
65 70

<210> 423
<211> 142
<212> PRT
<213> Homo sapiens

<400> 423
Met Pro Pro Phe Gly Gly His Pro Leu Ser Gln Glu Glu Asp Gly Ser
1 5 10 15
Gln Arg Cys Cys Cys Leu Ser Ser Leu Arg Ser Val Asp Asp Ser Asn
20 25 30
Gly Glu Thr Val Val Ile Met Ala Leu Phe Leu Ala Val Ser Tyr His
35 40 45
His Lys Thr Gln Ser Lys Arg Trp Pro Gly Leu Thr Pro Pro His Ser
50 55 60
Ser Leu Leu Cys Arg Pro Leu Gln Leu Ser Phe Leu Val Ile Gln Ser
65 70 75 80
Val Arg Met Arg Ala Cys Gly Cys Asp Ser Gly His Cys Arg Ile Leu
85 90 95
Gly Arg Tyr Ser Leu Leu Gly Trp Ser Gln Gly His Arg Ala Arg Gly
100 105 110
Arg Gly Gly Val Ser Leu Arg Asp Asn Thr Phe Phe Gln Glu Ala Ser
115 120 125
Glu Gly Gln Gly Gln Trp Leu Met Pro Val Ile Pro Ala Phe
130 135 140

<210> 424
<211> 149
<212> PRT
<213> Homo sapiens

<400> 424
Met Leu Ser Ile Leu Lys Pro Arg Arg Ser Gln Glu Trp Arg Thr Ala
1 5 10 15
Leu Arg Arg Tyr Cys Cys Pro Thr Asp Leu Gln Ala Pro Arg Ser Pro
20 25 30
Val Pro Pro Ile Arg Lys Val Gly Ile Ser Asp Val Ile Val His Ala

Leu Ile Arg His Leu Arg Thr Phe Ser Ala Ala Ala Ala Leu Ala Pro
 20 25 30
 Arg Tyr Pro Thr Arg Leu Pro Ser Ser Leu Leu Leu Trp His Leu Cys
 35 40 45
 Gln Cys Leu His Leu Leu Tyr Ala Val Ser Thr Ser Cys Asn Ser His
 50 55 60
 Gly Lys Arg Ser Ala Ala Trp Ala Met Thr Arg Thr Glu Asp Thr Asp
 65 70 75 80
 Ala Leu Thr Asp Ser Phe Asp Asp Ser Phe Ile Ser Ser Ala Asp
 85 90 95

<210> 430

<211> 99

<212> PRT

<213> Homo sapiens

<400> 430

Met Lys Lys Lys Glu Glu Thr Thr Leu Ser Glu Met Glu Pro Val Glu
 1 5 10 15
 Pro Gln Tyr Gln Leu Val Asn Ala Glu Ser Thr Ser Pro Phe Leu His
 20 25 30
 Cys Leu Arg Glu Val Ile Gly Glu Tyr Ser Val His Glu Phe Ser Leu
 35 40 45
 Leu Gly Lys Thr Glu Ser Gln Gly Ile Gly Leu Trp Ile Ala Leu Val
 50 55 60
 Val Phe Leu Ser Phe Leu Ile Phe Ser Thr Ser Phe Tyr Ile Ser Asn
 65 70 75 80
 Ala Glu Gln Pro Phe Phe Lys Glu Pro Pro Thr Glu Ala Ala Lys Glu
 85 90 95
 Leu Ser Leu

<210> 431

<211> 122

<212> PRT

<213> Homo sapiens

<400> 431

Ile Arg Ala Thr Met Val Ala Arg Val Trp Ser Leu Met Arg Phe Leu
 1 5 10 15
 Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp Gln
 20 25 30
 Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys Ala
 35 40 45
 Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr Val Cys
 50 55 60
 Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys Ile
 65 70 75 80
 Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr Val Met
 85 90 95
 Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser Lys Glu
 100 105 110
 Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys
 115 120

<210> 432

<211> 118

<212> PRT

<213> Homo sapiens

<400> 432

Met Gln Pro Ser Leu Leu Arg Ser Tyr Arg Leu Lys Ala Gln Leu Ser
1 5 10 15
Leu Ser Ser Thr Val Pro Arg Arg Ile Thr Asp Lys Pro Ala Thr Lys
20 25 30
Ser Trp Glu Gly Gly Arg Arg Glu Leu Cys Pro Arg Val Leu Phe Thr
35 40 45
Gln Leu Leu Leu Trp Val Trp Pro Gly Asp Pro Gly Pro Glu Leu Gln
50 55 60
Glu Thr Gly Phe Pro Gly Pro Pro Arg Pro Ala His Leu Lys Thr Asp
65 70 75 80
Arg Ala Ile Met Val Gly Val Lys Gly Ile Glu Glu Lys Ser Gly Ile
85 90 95
Gly Ala Gly Val Cys Arg Val Ser Val Glu Lys Leu Ala Ser Thr Gln
100 105 110
Glu Arg Thr Ser Ser Leu
115

<210> 433

<211> 49

<212> PRT

<213> Homo sapiens

<400> 433

Met Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Pro
1 5 10 15
Val Phe Pro His Leu Thr Val Val Leu Ala Ile Gly Met Phe Phe
20 25 30
Thr Ala Trp Phe Phe Val Tyr Pro Phe Thr Glu Gln Pro Glu Asp Gln
35 40 45
His

<210> 434

<211> 89

<212> PRT

<213> Homo sapiens

<400> 434

Met Leu Ala Leu Phe His Phe His Leu Pro Pro Trp Asp Asp Ala Val
1 5 10 15
Arg Arg Pro Ser Val Asp Ala Ser Pro Ser Thr Leu Asn Phe Pro Asp
20 25 30
Ala Glu Leu Tyr Ala Ser Ile Phe Leu Cys Cys Met Ala Pro Gly Glu
35 40 45
Ile Leu Ile Ser Phe Leu Thr Leu Val Gln Ile Ala His Ala Asn Gly
50 55 60
Arg Gly Cys Asn Thr Pro Ala Cys Gly Ala Ala Ala Cys Val Trp His
65 70 75 80
Glu Asn Ser Gln Glu Glu Arg Lys Tyr
85

<210> 435

<211> 87

<212> PRT

<213> Homo sapiens

<400> 435

Met Ser Gln Gln His Arg Arg Lys Arg Pro Ser Ser Glu Arg Lys Ser
 1 5 10 15
 Thr Arg Lys Met Asp Thr Trp Gln Ser Leu Lys Val Lys Glu Val Phe
 20 25 30
 Cys Lys His Asn Ser Ser Tyr Glu Cys Leu Leu Tyr Lys Glu Val Glu
 35 40 45
 Ala Arg Gln Val Ser Lys Thr Ala Thr Asp Gly Ser Tyr Leu Leu Val
 50 55 60
 Phe Thr Ser Tyr Val Ile Ser Ser Pro Val Trp Thr Gly Pro Gly Asp
 65 70 75 80
 Leu Leu Pro Val Asn Arg Ile
 85

<210> 436

<211> 45

<212> PRT

<213> Homo sapiens

<400> 436

Met Pro Arg Ser Ser Arg Ser Pro Gly Asp Pro Gly Ala Leu Leu Glu
 1 5 10 15
 Asp Gly Pro Gln Ser Gln Thr Pro Glu Asp Cys Pro Ala Arg Pro Glu
 20 25 30
 His Gln Gln Asp Gly Arg Gly His Leu Pro Lys His Glu
 35 40 45

<210> 437

<211> 65

<212> PRT

<213> Homo sapiens

<400> 437

Met Ala Tyr Leu Asp Asp Lys Gly Ser Leu Leu Ala Ile His Ser His
 1 5 10 15
 Ala Arg Gln His Ser His Glu Thr Asn Gln Val His Gln Trp Leu Pro
 20 25 30
 Arg Asn Thr Phe Ala Phe Leu Ile Lys Glu Asp Arg Cys Ser Cys Arg
 35 40 45
 Ser Thr Cys Ala Ser Phe Ser Phe Ser Ser Ser Phe Ser Phe Leu Ile
 50 55 60
 Ser
 65

<210> 438

<211> 112

<212> PRT

<213> Homo sapiens

<400> 438

Met Arg Lys Lys Cys Lys Cys Phe Thr Ile Lys Lys Thr Asn Thr Tyr
 1 5 10 15
 Glu Glu Ser Asn Ala Gly Asn Glu Gly Gln Lys Glu Ala Ile Ser Ile
 20 25 30
 Cys Ile Cys Arg Arg Asp Gly Leu Leu Pro Leu Trp Val Thr Arg Leu
 35 40 45
 Ser Asp Leu Val Phe Ser Lys Glu Lys Ala His Gly Met Ile Pro Leu
 50 55 60
 Leu Gly Ser His Arg Glu Lys Lys Thr Ser Lys Glu Met Lys Thr Ser

65					70					75					80
Ser	Arg	Asn	Leu	Arg	Tyr	Phe	Ile	Val	Cys	Arg	Asp	Ala	Ser	Ser	Tyr
				85					90					95	
Thr	Pro	Gln	Ser	Leu	Ile	Ser	Gly	Tyr	Ile	Gly	Pro	Cys	Gln	His	Gln
			100					105					110		

<210> 439
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 439															
Met	Val	Phe	Gly	Ala	Met	Val	Leu	Leu	Val	Gly	Leu	Glu	Glu	Leu	Thr
1			5						10					15	
Asn	Ile	Arg	Asn	Val	Glu	Arg	Leu	Lys	Lys	Asp	Leu	Arg	Ala	Ser	Tyr
			20					25					30		
Cys	Leu	Ile	Asp	Ser	Phe	Leu	Gly	Asp	Ser	Glu	Leu	Ile	Gly	Asp	Leu
		35					40					45			
Thr	Gln	Cys	Val	Asp	Cys	Val	Ile	Pro	Pro	Glu	Gly	Ser	Leu	Leu	Gln
	50					55					60				
Ile	Ser	Ser	Tyr	Leu	Tyr	Leu	Asn	Thr	Ala	Leu	Val	Asp	Leu	Pro	Gly
65					70					75					80
Val	Ala	Ala	Ser	Gln	Ala	Cys	Asp	Ser	Gln	Gln	Val	Thr	Trp	Leu	Leu
				85					90					95	
Tyr	Val	Ala	Asn	Gly	Ala	Tyr	Ser	Ala	Cys	Asn	Arg	Pro	Gly		
			100					105					110		

<210> 440
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 440															
Thr	Ser	Ser	Ser	Gly	Ala	Glu	Val	Thr	Met	Ala	Ala	Ala	Leu	Ala	Arg
1				5					10					15	
Leu	Gly	Leu	Arg	Pro	Val	Lys	Gln	Val	Arg	Val	Gln	Phe	Cys	Pro	Phe
			20					25					30		
Glu	Lys	Asn	Val	Glu	Ser	Thr	Arg	Thr	Phe	Leu	Gln	Thr	Val	Ser	Ser
		35					40					45			
Glu	Lys	Val	Arg	Ser	Thr	Asn	Leu	Asn	Cys	Ser	Val	Ile	Ala	Asp	Val
		50				55					60				
Arg	His	Asp	Gly	Ser	Glu	Pro	Cys	Val	Asp	Val	Leu	Phe	Gly	Asp	Gly
65					70					75					80
His	Arg	Leu	Ile	Met	Arg	Gly	Ala	His	Leu	Thr	Ala	Leu	Glu	Met	Leu
				85					90					95	
Thr	Ala	Phe	Ala	Ser	His	Ile	Arg	Ala	Arg	Asp	Ala	Ala	Gly	Ser	Gly
			100					105					110		
Asp	Lys	Pro	Gly	Ala	Asp	Thr	Gly	Arg							
			115					120							

<210> 441
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 441															
Met	Leu	Ala	Arg	Ala	Thr	Phe	Arg	Ala	Ala	Ser	Ala	Pro	Thr	Leu	Val
1				5					10					15	

Ala Arg Arg Gly Phe Gln Ser Thr Arg Ala Gln Met Ala Ser Pro Tyr
20 25 30
His Tyr Pro Glu Gly Pro Arg Ser Asn Leu Pro Phe Asp Pro Leu Lys
35 40 45
Lys Gly Phe Ala Phe Lys Tyr Trp Gly Phe Met Gly Thr Gly Phe Ala
50 55 60
Leu Pro Phe Leu Leu Ala Val Trp Gln Thr Glu Gln Ala Val Asn Ala
65 70 75 80
Leu Arg His Gly Val Asp Met Arg Ile Gly Ile Pro Gly Asn Thr Ala
85 90 95
Phe Val Asp

<210> 442

<211> 183

<212> PRT

<213> Homo sapiens

<400> 442

Arg Glu Gly Ala Arg Ala Arg Pro Ser Pro Thr Met Ser Asp Glu Ala
1 5 10 15
Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe
20 25 30
Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu
35 40 45
Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys
50 55 60
His Arg Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu
65 70 75 80
Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu
85 90 95
Phe Ser Ser Val Ser Val Gly Asp Gln Asp Asp Cys Tyr Ser Leu Leu
100 105 110
Asp Asp Gln Asp Phe Thr Ser Phe Asp Leu Phe Pro Glu Gly Ser Val
115 120 125
Cys Ser Asp Val Ser Ser Ser Ile Ser Thr Tyr Trp Asp Trp Ser Asp
130 135 140
Ser Glu Phe Glu Trp Gln Leu Pro Gly Ser Asp Ile Ala Ser Gly Ser
145 150 155 160
Asp Val Leu Ser Asp Val Ile Pro Ser Ile Pro Ser Ser Pro Cys Leu
165 170 175
Leu Pro Lys Lys Lys Lys Lys
180

<210> 443

<211> 94

<212> PRT

<213> Homo sapiens

<400> 443

Met Ser Asp Glu Ala Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr
1 5 10 15
Pro Glu Glu Pro Phe Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr
20 25 30
Cys Pro Ser Glu Glu Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys
35 40 45
Gln Leu Ser Ser Cys His Arg Thr Asp Pro Leu His Arg Phe His Thr
50 55 60
Asn Arg Trp Asn Leu Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu

65					70					75			80
Gly	Ser	Glu	Glu	Leu	Phe	Ser	Ser	Val	Cys	Trp	Arg	Ser	Arg
				85					90				

<210> 444
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 444
 Ile Gly Pro Arg Ala Pro Ser Pro Ser Phe Ser Val Arg Asp Val Glu
 1 5 10 15
 Leu Ser Asp Pro Ala Arg Glu Arg Gly Glu Met Pro Val Ala Val Gly
 20 25 30
 Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly
 35 40 45
 Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly
 50 55 60
 Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly
 65 70 75 80
 Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe
 85 90 95
 Met Ala Ile Gly Met Gly Ile Arg Cys
 100 105

<210> 445
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 445
 Met Pro Arg Ser Ser Arg Ser Pro Gly Asp Pro Gly Ala Leu Leu Glu
 1 5 10 15
 Asp Val Ala His Asn Pro Arg Pro Arg Arg Ile Ala Gln Arg Gly Arg
 20 25 30
 Asn Thr Ser Arg Met Ala Glu Asp Thr Ser Pro Asn Met Asn Asp Asn
 35 40 45
 Ile Leu Leu Pro Val Arg Asn Asn Asp Gln Ala Leu Gly Leu Thr Gln
 50 55 60
 Cys Met Leu Gly Cys Val Ser Trp Phe Thr Cys Phe Ala Cys Ser Leu
 65 70 75 80
 Arg Thr Gln Ala Gln Gln Val Leu Phe Asn Thr Cys Arg Cys Lys Leu
 85 90 95
 Leu Cys Gln Lys Leu Met Glu Lys Thr Gly Ile Leu Leu Leu Cys Ala
 100 105 110
 Phe Gly Val Ser Gln Gly Pro Ala Gln Ser Gln Val Glu Val Ser Leu
 115 120 125
 Gly Pro Gly Thr Asp Tyr Arg Thr Leu Gly Lys Thr Leu His Cys His
 130 135 140
 Val Thr Gln Phe Pro His Leu Pro Asp Gly Cys Cys Cys Glu Asn Tyr
 145 150 155 160
 Glu Met Lys

<210> 446
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 446

```
Met Glu Asp Lys Glu Ile Pro Ile Lys Ser Glu Pro Leu Pro Lys Pro
1      5      10      15
Pro Ala Ser Ala Pro Pro Ser Ile Leu Val Lys Pro Glu Asn Ser Arg
20      25      30
Asn Gly Ile Glu Lys Gln Val Lys Thr Val Arg Phe Gln Asn Tyr Ser
35      40      45
Pro Pro Pro Thr Lys His Tyr Thr Ser His Pro Thr Ser Gly Lys Pro
50      55      60
Glu Gln Pro Ala Thr Leu Lys Ala Ser Gln Pro Glu Ala Ala Ser Leu
65      70      75      80
Gly Pro Glu Met Thr Val Leu Phe Ala His Arg Ser Gly Cys His Ser
85      90      95
Gly Gln Gln Thr Asp Leu Arg Arg Lys Ser Ala Leu Ala Lys Ala Thr
100     105     110
Thr Leu Val Ser Thr Ala Ser Gly Thr Gln Thr Val Phe Pro Ser Lys
115     120     125
```

<210> 447

<211> 96

<212> PRT

<213> Homo sapiens

<400> 447

```
Met Leu Thr Arg Val Glu Glu Gln Lys Lys Met Val Lys Ala Cys Arg
1      5      10      15
Tyr Arg Cys Ser Ala Cys His Leu Lys Tyr Ser Pro Gln Arg Gln Lys
20      25      30
Glu Arg Lys Lys Ser Leu Lys Arg Gly Arg Thr Ser Gln Gln Asn Met
35      40      45
Ser Met Phe Trp Leu Lys Lys Leu Leu Glu Ser Gly Leu Phe Cys Ala
50      55      60
Met Cys Ser Pro Arg Ala Ser Thr Lys Lys Gly Phe Trp Cys Arg Pro
65      70      75      80
Lys Thr Thr Ile Ile Ile Asp Tyr Ser Ser Pro Arg Gln Cys Leu
85      90      95
```

<210> 448

<211> 160

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> 114

<223> Xaa = Glu,Val

<220>

<221> UNSURE

<222> 113

<223> Xaa = His,Gln

<220>

<221> UNSURE

<222> 115

<223> Xaa = Ile,Val

<400> 448

Met Gly Lys Ile Ala Leu Gln Leu Lys Ala Thr Leu Glu Asn Ile Thr
 1 5 10 15
 Asn Leu Arg Pro Val Gly Glu Asp Phe Arg Trp Tyr Leu Lys Met Lys
 20 25 30
 Cys Gly Asn Cys Gly Glu Ile Ser Asp Lys Trp Gln Tyr Ile Arg Leu
 35 40 45
 Met Asp Ser Val Ala Leu Lys Gly Gly Arg Gly Ser Ala Ser Met Val
 50 55 60
 Gln Lys Cys Lys Leu Cys Ala Arg Glu Asn Ser Ile Glu Ile Leu Ser
 65 70 75 80
 Ser Thr Ile Lys Pro Tyr Asn Ala Glu Asp Asn Glu Asn Phe Lys Thr
 85 90 95
 Ile Val Glu Phe Glu Cys Arg Gly Leu Glu Pro Val Asp Phe Gln Pro
 100 105 110
 Xaa Xaa Xaa Leu Leu Leu Lys Val Trp Ser Gln Gly Gln Pro Ser Val
 115 120 125
 Thr Leu Ile Cys Arg Arg Arg Thr Gly Thr Asp Tyr Asp Glu Lys Ala
 130 135 140
 Gln Glu Ser Val Gly Ile Tyr Glu Val Thr His Gln Phe Val Lys Cys
 145 150 155 160

<210> 449
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 449
 Met Asp Ser Leu Ala Ala Gly Glu Leu Asn Ala Ser His Gln Pro Trp
 1 5 10 15
 Val Pro Glu Phe Val Ala Tyr Trp Arg Lys Thr His Gln Asp His Leu
 20 25 30
 Cys Ser Leu His Ser Arg Ala Phe Gly Leu Leu Asp Ala Arg Val Thr
 35 40 45
 Trp Ala Leu Arg Arg Ala Pro Glu Pro Val Pro Gly Lys Asp Arg Leu
 50 55 60
 Leu Leu Ala Ala Phe Pro Ala Glu Ala Ser Pro Val Asp Thr Ala Ser
 65 70 75 80
 Val Ser Val Tyr Gly Arg Ala Pro Arg Tyr Met His Lys Gly Val Lys
 85 90 95
 Lys Cys Val Cys Thr Pro Val Ser Lys Asn Ser Thr Ala Trp Leu Leu
 100 105 110
 Leu Gly Gly Ile Ser
 115

<210> 450
 <211> 335
 <212> PRT
 <213> Homo sapiens

<400> 450
 Met Cys Cys Gln Val Cys Glu Ala Val Arg Ser Gly Asn Glu Glu Val
 1 5 10 15
 Leu Ala Asp Val Arg Thr Ile Val Asn Gln Ile Ser Tyr Thr Pro Gln
 20 25 30
 Asp Pro Arg Asp Leu Cys Gly Arg Ile Leu Thr Thr Cys Tyr Met Ala
 35 40 45
 Ser Lys Asn Ser Ser Gln Glu Thr Cys Thr Arg Ala Arg Glu Leu Ala
 50 55 60

Gln	Gln	Ile	Gly	Ser	His	His	Ile	Ser	Leu	Asn	Ile	Asp	Pro	Ala	Val
65					70					75					80
Lys	Ala	Val	Met	Gly	Ile	Phe	Ser	Leu	Val	Thr	Gly	Lys	Ser	Pro	Leu
				85					90					95	
Phe	Ala	Ala	His	Gly	Gly	Ser	Ser	Arg	Glu	Asn	Leu	Ala	Leu	Gln	Asn
			100					105					110		
Val	Gln	Ala	Arg	Ile	Arg	Met	Val	Leu	Ala	Tyr	Leu	Phe	Ala	Gln	Leu
		115					120					125			
Ser	Leu	Trp	Ser	Arg	Gly	Val	His	Gly	Gly	Leu	Leu	Val	Leu	Gly	Ser
	130					135					140				
Ala	Asn	Val	Asp	Glu	Ser	Leu	Leu	Gly	Tyr	Leu	Thr	Lys	Tyr	Asp	Cys
145					150					155					160
Ser	Ser	Ala	Asp	Ile	Asn	Pro	Ile	Gly	Gly	Ile	Ser	Lys	Thr	Asp	Leu
			165					170						175	
Arg	Ala	Phe	Val	Gln	Phe	Cys	Ile	Gln	Arg	Phe	Gln	Leu	Pro	Ala	Leu
			180					185					190		
Gln	Ser	Ile	Leu	Leu	Ala	Pro	Ala	Thr	Ala	Glu	Leu	Glu	Pro	Leu	Ala
		195					200					205			
Asp	Gly	Gln	Val	Ser	Gln	Thr	Asp	Glu	Glu	Asp	Met	Gly	Met	Thr	Tyr
	210					215					220				
Ala	Glu	Leu	Ser	Val	Tyr	Gly	Lys	Leu	Arg	Lys	Val	Ala	Lys	Met	Gly
225					230					235					240
Pro	Tyr	Ser	Met	Phe	Cys	Lys	Leu	Leu	Gly	Met	Trp	Arg	His	Ile	Cys
			245						250					255	
Thr	Pro	Arg	Gln	Val	Ala	Asp	Lys	Val	Lys	Arg	Phe	Phe	Ser	Lys	Tyr
			260					265						270	
Ser	Met	Asn	Arg	His	Lys	Met	Thr	Thr	Leu	Thr	Pro	Ala	Tyr	His	Ala
		275					280					285			
Glu	Asn	Tyr	Ser	Pro	Glu	Asp	Asn	Arg	Phe	Asp	Leu	Arg	Pro	Phe	Leu
	290					295					300				
Tyr	Asn	Thr	Ser	Trp	Pro	Trp	Gln	Phe	Arg	Cys	Ile	Glu	Asn	Gln	Val
305					310					315					320
Leu	Gln	Leu	Glu	Arg	Ala	Glu	Pro	Gln	Ser	Leu	Asp	Gly	Val	Asp	
				325					330					335	

<210> 451

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> 76

<223> Xaa = Lys,Asn

<400> 451

Met	Cys	Trp	Val	Ile	Asn	His	Ala	Ile	Leu	Pro	Arg	Met	Arg	Met	His
1				5					10					15	
Ser	Lys	Arg	Gln	Thr	Ile	Thr	Arg	His	Ser	Ala	Ser	Leu	Ser	Phe	His
			20					25					30		
Ala	Leu	Pro	Arg	Ser	Ala	Phe	Leu	Gln	Leu	Cys	Leu	Leu	Arg	Gln	Ile
		35					40					45			
His	Gln	Ile	Pro	Cys	Leu	Ser	Ile	Phe	Ser	Ser	Thr	Leu	Arg	Ala	Gln
	50					55					60				
Thr	His	Asp	Ser	Gly	Ile	Gly	Cys	Thr	Thr	Ala	Xaa	Pro	Gly	Gly	Arg
65					70					75					80
Arg	Gln	Glu	Gln	Leu	Arg										
				85											

<210> 452
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 452
 Met Lys Ile Ala Leu Cys Gln Arg Glu Leu Pro Ser Pro Arg Ser Cys
 1 5 10 15
 Leu Leu Ser Arg Asp Val Thr Gly Val Ile Cys Thr Arg Met Pro Arg
 20 25 30
 Leu Ala Ile Cys Ser Lys Thr Ala Gln Lys Ala Leu Pro Cys Ile Pro
 35 40 45
 Leu Leu His Thr Ser Pro Leu Cys Leu Gln Leu Leu Ser Ala Gly Leu
 50 55 60
 His Ile Tyr Ala Thr Leu Cys Lys Ser Cys Ala Ser Arg Asn His Lys
 65 70 75 80
 Asn Ile Phe Leu His Leu Leu His Ser Leu Ser Ala Ala
 85 90

<210> 453
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 453
 Met Ala Val Arg Ala Ser Phe Glu Asn Asn Cys Glu Ile Gly Cys Phe
 1 5 10 15
 Ala Lys Leu Thr Asn Thr Tyr Cys Leu Val Ala Ile Gly Gly Ser Glu
 20 25 30
 Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro Val
 35 40 45
 Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys Val
 50 55 60
 Gly Asp Arg Arg Asn Ser Gly Arg Cys Ala Gln Gly Gly Ser Leu Gln
 65 70 75 80
 Thr Asp Ser Gly Arg Pro Gly Ala Ser Arg Lys Leu Leu Cys Leu Gln
 85 90 95
 Gln Ser Gly Arg Ala Gly Ala Ser Gln Asp Phe Asn
 100 105

<210> 454
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 454
 Met Ser Leu Cys Glu Asp Met Leu Leu Cys Asn Tyr Arg Lys Cys Arg
 1 5 10 15
 Ile Lys Leu Ser Gly Tyr Ala Trp Val Thr Ala Cys Ser His Ile Phe
 20 25 30
 Cys Asp Gln His Gly Ser Gly Glu Phe Ser Arg Ser Pro Ala Ile Cys
 35 40 45
 Pro Ala Cys Asn Ser Thr Leu Ser Gly Lys Leu Asp Ile Val Arg Thr
 50 55 60
 Glu Leu Ser Pro Ser Glu Tyr Lys Ala Met Val Leu Ala Gly Leu
 65 70 75 80
 Arg Pro Glu Ile Val Leu Asp Ile Ser Ser Arg Ala Leu Ala Phe Trp

				85					90					95			
Thr	Tyr	Gln	Val	His	Gln	Glu	Arg	Leu	Tyr	Gln	Glu	Tyr	Asn	Phe	Ser		
			100					105					110				
Lys	Ala	Glu	Gly	His	Leu	Lys	Gln	Met	Glu	Lys	Ile	Tyr	Thr	Gln	Gln		
		115					120					125					
Ile	Gln	Ser	Lys	Asp	Val	Glu	Leu	Thr	Ser	Met	Lys	Gly	Glu	Val	Thr		
	130					135					140						
Ser	Met	Lys	Lys	Val	Leu	Glu	Glu	Tyr	Lys	Lys	Lys	Phe	Ser	Asp	Ile		
145					150					155				160			
Ser	Glu	Lys	Leu	Met	Glu	Arg	Asn	Arg	Gln	Tyr	Gln	Lys	Leu	Gln	Gly		
			165					170						175			
Leu	Tyr	Asp	Ser	Leu	Arg	Leu	Arg	Asn	Ile	Thr	Ile	Ala	Asn	His	Glu		
		180						185					190				
Gly	Thr	Leu	Glu	Pro	Ser	Met	Ile	Ala	Gln	Ser	Gly	Val	Leu	Gly	Phe		
	195						200					205					
Pro	Leu	Gly	Asn	Asn	Ser	Lys	Phe	Pro	Leu	Asp	Asn	Thr	Pro	Val	Arg		
	210					215					220						
Asn	Arg	Gly	Asp	Gly	Asp	Gly	Asp	Phe	Gln	Phe	Arg	Pro	Phe	Phe	Ala		
225				230						235					240		
Gly	Ser	Pro	Thr	Ala	Pro	Glu	Pro	Ser	Asn	Ser	Phe	Phe	Ser	Phe	Val		
				245					250						255		
Ser	Pro	Ser	Arg	Glu	Leu	Glu	Gln	Gln	Gln	Val	Ser	Ser	Arg	Ala	Phe		
			260				265							270			
Lys	Val	Lys	Arg	Ile													
		275															

<210> 455

<211> 173

<212> PRT

<213> Homo sapiens

<400> 455

Met	Leu	Val	Met	Tyr	Leu	Leu	Ala	Ala	Leu	Phe	Gly	Tyr	Leu	Thr	Phe		
1				5					10					15			
Tyr	Gly	Glu	Val	Glu	Asp	Glu	Leu	Leu	His	Ala	Tyr	Ser	Lys	Val	Tyr		
		20					25						30				
Thr	Leu	Asp	Ile	Pro	Leu	Leu	Met	Val	Arg	Leu	Ala	Val	Leu	Val	Ala		
	35					40					45						
Val	Thr	Leu	Thr	Val	Pro	Ile	Val	Leu	Phe	Pro	Ile	Arg	Thr	Ser	Val		
	50					55					60						
Ile	Thr	Leu	Leu	Phe	Pro	Lys	Arg	Pro	Phe	Ser	Trp	Ile	Arg	His	Phe		
65				70					75					80			
Leu	Ile	Ala	Ala	Val	Leu	Ile	Ala	Leu	Asn	Asn	Val	Leu	Val	Ile	Leu		
			85						90					95			
Val	Pro	Thr	Ile	Lys	Tyr	Ile	Phe	Gly	Phe	Ile	Gly	Ala	Ser	Ser	Ala		
		100						105					110				
Thr	Met	Leu	Ile	Phe	Ile	Leu	Pro	Ala	Val	Phe	Tyr	Leu	Lys	Leu	Val		
	115					120						125					
Lys	Lys	Glu	Thr	Phe	Arg	Ser	Pro	Gln	Lys	Val	Gly	Ala	Leu	Ile	Phe		
	130					135					140						
Leu	Val	Val	Gly	Ile	Phe	Phe	Met	Ile	Gly	Ser	Met	Ala	Leu	Ile	Ile		
145				150						155				160			
Ile	Asp	Trp	Ile	Tyr	Asp	Pro	Pro	Asn	Ser	Lys	His	His					
			165					170									

<210> 456

<211> 370

<212> PRT

<213> Homo sapiens

<400> 456

Met Ser Ala Ser Ala Ala Thr Gly Val Phe Val Leu Ser Leu Ser Ala
1 5 10 15
Ile Pro Val Thr Tyr Val Phe Asn His Leu Ala Ala Gln His Asp Ser
20 25 30
Trp Thr Ile Val Gly Val Ala Ala Leu Ile Leu Phe Leu Val Ala Leu
35 40 45
Leu Ala Arg Val Leu Val Lys Arg Lys Pro Pro Arg Asp Pro Leu Phe
50 55 60
Tyr Val Tyr Ala Val Phe Gly Phe Thr Ser Val Val Asn Leu Ile Ile
65 70 75 80
Gly Leu Glu Gln Asp Gly Ile Ile Asp Gly Phe Met Thr His Tyr Leu
85 90 95
Arg Glu Gly Glu Pro Tyr Leu Asn Thr Ala Tyr Gly His Met Ile Cys
100 105 110
Tyr Trp Asp Gly Ser Ala His Tyr Leu Met Tyr Leu Val Met Val Ala
115 120 125
Ala Ile Ala Trp Glu Glu Thr Tyr Arg Thr Ile Gly Leu Tyr Trp Val
130 135 140
Gly Ser Ile Ile Met Ser Val Val Val Phe Val Pro Gly Asn Ile Val
145 150 155 160
Gly Lys Tyr Gly Thr Arg Ile Cys Pro Ala Phe Phe Leu Ser Ile Pro
165 170 175
Tyr Thr Cys Leu Pro Val Trp Ala Gly Phe Arg Ile Tyr Asn Gln Pro
180 185 190
Ser Glu Asn Tyr Asn Tyr Pro Ser Lys Val Ile Gln Glu Ala Gln Ala
195 200 205
Lys Asp Leu Leu Arg Arg Pro Phe Asp Leu Met Leu Val Val Cys Leu
210 215 220
Leu Leu Ala Thr Gly Phe Cys Leu Phe Arg Gly Leu Ile Ala Leu Asp
225 230 235 240
Cys Pro Ser Glu Leu Cys Arg Leu Tyr Thr Gln Phe Gln Glu Pro Tyr
245 250 255
Leu Lys Asp Pro Ala Ala Tyr Pro Lys Ile Gln Met Leu Ala Tyr Met
260 265 270
Phe Tyr Ser Val Pro Tyr Phe Val Thr Ala Leu Tyr Gly Leu Val Val
275 280 285
Pro Gly Cys Ser Trp Met Pro Asp Ile Thr Leu Ile His Ala Gly Gly
290 295 300
Leu Ala Gln Ala Gln Phe Ser His Ile Gly Ala Ser Leu His Ala Arg
305 310 315 320
Thr Ala Tyr Val Tyr Arg Val Pro Glu Glu Ala Lys Ile Leu Phe Leu
325 330 335
Ala Leu Asn Ile Ala Tyr Gly Val Leu Pro Gln Leu Leu Ala Tyr Arg
340 345 350
Cys Ile Tyr Lys Pro Glu Phe Phe Ile Lys Thr Lys Ala Glu Glu Lys
355 360 365
Val Glu
370

<210> 457

<211> 393

<212> PRT

<213> Homo sapiens

<400> 457

Met Thr Tyr Arg Trp Gly Thr Leu Leu Met Lys Arg Lys Phe Glu Glu
 1 5 10 15
 Pro Arg Pro Gly Phe His Gly Val Leu Gly Ile Asn Ser Ile Thr Gly
 20 25 30
 Lys Glu Glu Pro Leu Tyr Pro Ser Tyr Lys Arg Gln Leu Arg Ile Tyr
 35 40 45
 Leu Val Ser Leu Pro Phe Val Cys Leu Cys Leu Tyr Phe Ser Leu Tyr
 50 55 60
 Val Met Met Ile Tyr Phe Asp Met Glu Val Trp Ala Leu Gly Leu His
 65 70 75 80
 Glu Asn Ser Gly Ser Glu Trp Thr Ser Val Leu Leu Tyr Val Pro Ser
 85 90 95
 Ile Ile Tyr Ala Ile Val Ile Glu Ile Met Asn Arg Leu Tyr Arg Tyr
 100 105 110
 Ala Ala Glu Phe Leu Thr Ser Trp Glu Asn His Arg Leu Glu Ser Ala
 115 120 125
 Tyr Gln Asn His Leu Ile Leu Lys Val Leu Val Phe Asn Phe Leu Asn
 130 135 140
 Cys Phe Ala Ser Leu Phe Tyr Ile Ala Phe Val Leu Lys Asp Met Lys
 145 150 155 160
 Leu Leu Arg Gln Ser Leu Ala Thr Leu Leu Ile Thr Ser Gln Ile Leu
 165 170 175
 Asn Gln Ile Met Glu Ser Phe Leu Pro Tyr Trp Leu Gln Arg Lys His
 180 185 190
 Gly Val Arg Val Lys Arg Lys Val Gln Ala Leu Lys Ala Asp Ile Asp
 195 200 205
 Ala Thr Leu Tyr Glu Gln Val Ile Leu Glu Lys Glu Met Gly Thr Tyr
 210 215 220
 Leu Gly Thr Phe Asp Asp Tyr Leu Glu Leu Phe Leu Gln Phe Gly Tyr
 225 230 235 240
 Val Ser Leu Phe Ser Cys Val Tyr Pro Leu Ala Ala Ala Phe Ala Val
 245 250 255
 Leu Asn Asn Phe Thr Glu Val Asn Ser Asp Ala Leu Lys Met Cys Arg
 260 265 270
 Val Phe Lys Arg Pro Phe Ser Glu Pro Ser Ala Asn Ile Gly Val Trp
 275 280 285
 Gln Leu Ala Phe Glu Thr Met Ser Val Ile Ser Val Val Thr Asn Cys
 290 295 300
 Ala Leu Ile Gly Met Ser Pro Gln Val Asn Ala Val Phe Pro Glu Ser
 305 310 315 320
 Lys Ala Asp Leu Ile Leu Ile Val Val Ala Val Glu His Ala Leu Leu
 325 330 335
 Ala Leu Lys Phe Ile Leu Ala Phe Ala Ile Pro Asp Lys Pro Arg His
 340 345 350
 Ile Gln Met Lys Leu Ala Arg Leu Glu Phe Glu Ser Leu Glu Ala Leu
 355 360 365
 Lys Gln Gln Gln Met Lys Leu Val Thr Glu Asn Leu Lys Glu Glu Pro
 370 375 380
 Met Glu Ser Gly Lys Glu Lys Ala Thr
 385 390

<210> 458
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 458
 Met Val Gly Gly Glu Ala Ala Ala Ala Val Glu Glu Leu Val Ser Gly

1				5					10					15	
Val	Arg	Gln	Ala	Ala	Asp	Phe	Ala	Glu	Gln	Phe	Arg	Ser	Tyr	Ser	Glu
			20					25					30		
Ser	Glu	Lys	Gln	Trp	Lys	Ala	Arg	Met	Glu	Phe	Ile	Leu	Arg	His	Leu
		35					40					45			
Pro	Asp	Tyr	Arg	Asp	Pro	Pro	Asp	Gly	Ser	Gly	Arg	Leu	Asp	Gln	Leu
	50					55					60				
Leu	Ser	Leu	Ser	Met	Val	Trp	Ala	Asn	His	Leu	Phe	Leu	Gly	Cys	Ser
65				70						75				80	
Tyr	Asn	Lys	Asp	Leu	Leu	Asp	Lys	Val	Met	Glu	Met	Ala	Asp	Gly	Ile
			85					90					95		
Glu	Val	Glu	Asp	Leu	Pro	Gln	Phe	Thr	Arg	Ser	Glu	Leu	Met	Lys	
			100					105				110			
Lys	His	Gln	Ser												
		115													

<210> 459

<211> 163

<212> PRT

<213> Homo sapiens

<400> 459

Met	Glu	His	Tyr	Arg	Lys	Ala	Gly	Ser	Val	Glu	Leu	Pro	Ala	Pro	Ser
1				5					10				15		
Pro	Met	Pro	Gln	Leu	Pro	Pro	Asp	Thr	Leu	Glu	Met	Arg	Val	Arg	Asp
			20				25					30			
Gly	Ser	Lys	Ile	Arg	Asn	Leu	Leu	Gly	Leu	Ala	Leu	Gly	Arg	Leu	Glu
		35				40					45				
Gly	Gly	Ser	Ala	Arg	His	Val	Val	Phe	Ser	Gly	Ser	Gly	Arg	Ala	Ala
	50				55					60					
Gly	Lys	Ala	Val	Ser	Cys	Ala	Glu	Ile	Val	Lys	Arg	Arg	Val	Pro	Gly
65				70					75					80	
Leu	His	Gln	Leu	Thr	Lys	Leu	Arg	Phe	Leu	Gln	Thr	Glu	Asp	Ser	Trp
			85					90				95			
Val	Pro	Ala	Ser	Pro	Asp	Thr	Gly	Leu	Asp	Pro	Leu	Thr	Val	Arg	Arg
		100					105					110			
His	Val	Pro	Ala	Val	Trp	Val	Leu	Ser	Arg	Asp	Pro	Leu	Asp	Pro	
	115					120				125					
Asn	Glu	Cys	Gly	Tyr	Gln	Pro	Pro	Gly	Ala	Pro	Pro	Gly	Leu	Gly	Ser
	130				135				140						
Met	Pro	Ser	Ser	Ser	Cys	Gly	Pro	Arg	Ser	Arg	Arg	Arg	Ala	Arg	Asp
145				150				155						160	
Thr	Arg	Ser													

<210> 460

<211> 230

<212> PRT

<213> Homo sapiens

<400> 460

Met	Val	Val	Phe	Gly	Tyr	Glu	Ala	Gly	Thr	Lys	Pro	Arg	Asp	Ser	Gly
1			5					10					15		
Val	Val	Pro	Val	Gly	Thr	Glu	Glu	Ala	Pro	Lys	Val	Phe	Lys	Met	Ala
		20					25					30			
Ala	Ser	Met	His	Gly	Gln	Pro	Ser	Pro	Ser	Leu	Glu	Asp	Ala	Lys	Leu
	35				40					45					
Arg	Arg	Pro	Met	Val	Ile	Glu	Ile	Ile	Glu	Lys	Asn	Phe	Asp	Tyr	Leu
	50				55				60						

Arg	Lys	Glu	Met	Thr	Gln	Asn	Ile	Tyr	Gln	Met	Ala	Thr	Phe	Gly	Thr
65					70				75						80
Thr	Ala	Gly	Phe	Ser	Gly	Ile	Phe	Ser	Asn	Phe	Leu	Phe	Arg	Arg	Cys
				85					90					95	
Phe	Lys	Val	Lys	His	Asp	Ala	Leu	Lys	Thr	Tyr	Ala	Ser	Leu	Ala	Thr
			100					105					110		
Leu	Pro	Phe	Leu	Ser	Thr	Val	Val	Thr	Asp	Lys	Leu	Phe	Val	Ile	Asp
		115					120					125			
Ala	Leu	Tyr	Ser	Asp	Asn	Ile	Ser	Lys	Glu	Asn	Cys	Val	Phe	Arg	Ser
	130					135				140					
Ser	Leu	Ile	Gly	Ile	Val	Cys	Gly	Val	Phe	Tyr	Pro	Ser	Ser	Leu	Ala
145					150					155					160
Phe	Thr	Lys	Asn	Gly	Arg	Leu	Ala	Thr	Lys	Tyr	His	Thr	Val	Pro	Leu
				165					170					175	
Pro	Pro	Lys	Gly	Arg	Val	Leu	Ile	His	Trp	Met	Thr	Leu	Cys	Gln	Thr
			180					185					190		
Gln	Met	Lys	Leu	Met	Ala	Ile	Pro	Leu	Val	Phe	Gln	Ile	Met	Phe	Gly
		195					200				205				
Ile	Leu	Asn	Gly	Leu	Tyr	His	Tyr	Ala	Val	Phe	Glu	Glu	Thr	Leu	Glu
	210					215					220				
Lys	Thr	Ile	His	Glu	Glu										
225					230										

<210> 461

<211> 101

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> 95

<223> Xaa = Cys,Trp

<400> 461

Met	Glu	Arg	Pro	Asp	Lys	Ala	Ala	Leu	Asn	Ala	Leu	Gln	Pro	Pro	Glu
1				5					10					15	
Phe	Arg	Asn	Glu	Ser	Ser	Leu	Ala	Ser	Thr	Leu	Lys	Thr	Leu	Leu	Phe
		20						25					30		
Phe	Thr	Ala	Leu	Met	Ile	Thr	Val	Pro	Ile	Gly	Leu	Tyr	Phe	Thr	Thr
		35				40						45			
Lys	Ser	Tyr	Ile	Phe	Glu	Gly	Ala	Leu	Gly	Met	Ser	Asn	Arg	Asp	Ser
	50					55				60					
Tyr	Phe	Tyr	Ala	Ala	Ile	Val	Ala	Val	Val	Ala	Val	His	Val	Val	Leu
65					70					75					80
Ala	Leu	Phe	Val	Tyr	Val	Ala	Trp	Asn	Glu	Gly	Ser	Arg	Gln	Xaa	Arg
				85					90					95	
Glu	Gly	Lys	Gln	Asp											
			100												

<210> 462

<211> 93

<212> PRT

<213> Homo sapiens

<400> 462

Met	Asp	Ser	Leu	Arg	Lys	Met	Leu	Ile	Ser	Val	Ala	Met	Leu	Gly	Ala
1				5					10					15	
Gly	Ala	Gly	Val	Gly	Tyr	Ala	Leu	Leu	Val	Ile	Val	Thr	Pro	Gly	Glu

			20					25				30			
Arg	Arg	Lys	Gln	Glu	Met	Leu	Lys	Glu	Met	Pro	Leu	Gln	Asp	Pro	Arg
		35					40					45			
Ser	Arg	Glu	Glu	Ala	Ala	Arg	Thr	Gln	Gln	Leu	Leu	Leu	Ala	Thr	Leu
	50					55					60				
Gln	Glu	Ala	Ala	Thr	Thr	Gln	Glu	Asn	Val	Ala	Trp	Arg	Lys	Asn	Trp
65					70					75					80
Met	Val	Gly	Gly	Glu	Gly	Gly	Ala	Gly	Gly	Arg	Ser	Pro			
			85						90						

<210> 463
 <211> 133
 <212> PRT
 <213> Homo sapiens

Met	Gly	His	Gly	Asp	Glu	Ile	Val	Leu	Ala	Asp	Leu	Asn	Phe	Pro	Ala
1			5						10				15		
Ser	Ser	Ile	Cys	Gln	Cys	Gly	Pro	Met	Glu	Ile	Arg	Ala	Asp	Gly	Leu
		20					25					30			
Gly	Ile	Pro	Gln	Leu	Leu	Glu	Ala	Val	Leu	Lys	Leu	Leu	Pro	Leu	Asp
	35					40					45				
Thr	Tyr	Val	Glu	Ser	Pro	Ala	Ala	Val	Met	Glu	Leu	Val	Pro	Ser	Asp
	50				55					60					
Lys	Glu	Arg	Gly	Leu	Gln	Thr	Pro	Val	Trp	Thr	Glu	Tyr	Glu	Ser	Ile
65					70					75					80
Leu	Arg	Arg	Ala	Gly	Cys	Val	Arg	Ala	Leu	Ala	Lys	Ile	Glu	Arg	Phe
			85					90					95		
Glu	Phe	Tyr	Glu	Arg	Ala	Lys	Lys	Ala	Phe	Ala	Val	Val	Ala	Thr	Gly
		100					105					110			
Glu	Thr	Ala	Leu	Tyr	Gly	Asn	Leu	Ile	Leu	Arg	Lys	Gly	Val	Leu	Ala
		115				120						125			
Leu	Asn	Pro	Leu	Leu											
	130														

<210> 464
 <211> 95
 <212> PRT
 <213> Homo sapiens

Met	Gly	His	Gly	Asp	Glu	Ile	Val	Leu	Ala	Asp	Leu	Asn	Phe	Pro	Ala
1			5						10				15		
Ser	Ser	Ile	Cys	Gln	Cys	Gly	Pro	Met	Glu	Ile	Arg	Ala	Asp	Gly	Leu
		20					25					30			
Gly	Ile	Pro	Gln	Leu	Leu	Glu	Ala	Val	Leu	Ala	Ala	Ala	Pro	Gly	His
	35					40					45				
Leu	Cys	Gly	Glu	Ser	Gly	Cys	Ser	His	Gly	Ala	Gly	Ala	Gln	Arg	Gln
	50				55					60					
Gly	Glu	Gly	Pro	Ala	Asp	Pro	Ser	Val	Asp	Gly	Val	Arg	Val	His	Pro
65					70					75					80
Thr	Gln	Gly	Arg	Leu	Cys	Glu	Ser	Pro	Gly	Lys	Asp	Arg	Glu	Val	
			85					90					95		

<210> 465
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 465

Met	Thr	Pro	Ile	Lys	Leu	Leu	Asn	Leu	Thr	Ser	Arg	Tyr	Asn	Phe	Arg
1				5					10					15	
Arg	Thr	Phe	Gly	Ile	Glu	Leu	Ser	Ser	Asn	Ser	Ser	Tyr	Cys	Lys	Arg
			20					25					30		
Gly	Asn	Gly	Tyr	Arg	Ser	Arg	Val	Pro	Lys	Glu	Cys	Glu	Cys	Asn	Trp
			35				40					45			
Leu	His	Leu	Glu	Ser	Asp	Thr	Leu	Lys	Lys	Leu	Pro	Ile	Ile	Ser	Pro
	50					55					60				
Ser	Trp	Thr	Cys	Arg	Ile	Ile	Leu	Phe	Leu	Tyr	Phe	Ser	Gly	Gln	Leu
65					70					75					80
Leu	Gln	Leu	Ser	Leu	Ser	Cys	Leu	Gln	Leu	Ile	Lys	Leu			
				85					90						

<210> 466

<211> 500

<212> PRT

<213> Homo sapiens

<400> 466

Met	Glu	Val	Ser	Thr	Asn	Pro	Ser	Ser	Asn	Ile	Asp	Pro	Gly	Asn	Tyr
1				5					10					15	
Val	Glu	Met	Asn	Asp	Ser	Ile	Thr	His	Leu	Pro	Ser	Lys	Val	Val	Ile
			20					25				30			
Gln	Asp	Ile	Thr	Met	Glu	Leu	His	Cys	Pro	Leu	Cys	Asn	Asp	Trp	Phe
			35				40					45			
Arg	Asp	Pro	Leu	Met	Leu	Ser	Cys	Gly	His	Asn	Phe	Cys	Glu	Ala	Cys
	50					55				60					
Ile	Gln	Asp	Phe	Trp	Arg	Leu	Gln	Ala	Lys	Glu	Thr	Phe	Cys	Pro	Glu
65					70				75						80
Cys	Lys	Met	Leu	Cys	Gln	Tyr	Asn	Asn	Cys	Thr	Phe	Asn	Pro	Val	Leu
			85						90				95		
Asp	Lys	Leu	Val	Glu	Lys	Ile	Lys	Lys	Leu	Pro	Leu	Leu	Lys	Gly	His
			100					105					110		
Pro	Gln	Cys	Pro	Glu	His	Gly	Glu	Asn	Leu	Lys	Leu	Phe	Ser	Lys	Pro
		115					120					125			
Asp	Gly	Lys	Leu	Ile	Cys	Phe	Gln	Cys	Lys	Asp	Ala	Arg	Leu	Ser	Val
	130					135					140				
Gly	Gln	Ser	Lys	Glu	Phe	Leu	Gln	Ile	Ser	Asp	Ala	Val	His	Phe	Phe
145					150					155					160
Met	Glu	Glu	Leu	Ala	Ile	Gln	Gln	Gly	Gln	Leu	Glu	Thr	Thr	Leu	Lys
			165						170					175	
Glu	Leu	Gln	Thr	Leu	Arg	Asn	Met	Gln	Lys	Glu	Ala	Ile	Ala	Ala	His
			180					185					190		
Lys	Glu	Asn	Lys	Leu	His	Leu	Gln	Gln	His	Val	Ser	Met	Glu	Phe	Leu
		195					200					205			
Lys	Leu	His	Gln	Phe	Leu	His	Ser	Lys	Glu	Lys	Asp	Ile	Leu	Thr	Glu
	210					215					220				
Leu	Arg	Glu	Glu	Gly	Lys	Ala	Leu	Asn	Glu	Glu	Met	Glu	Leu	Asn	Leu
225					230					235					240
Ser	Gln	Leu	Gln	Glu	Gln	Cys	Leu	Leu	Ala	Lys	Asp	Met	Leu	Val	Ser
			245						250					255	
Ile	Gln	Ala	Lys	Thr	Glu	Gln	Gln	Asn	Ser	Phe	Asp	Phe	Leu	Lys	Asp
		260						265					270		
Ile	Thr	Thr	Leu	Leu	His	Ser	Leu	Glu	Gln	Gly	Met	Lys	Val	Leu	Ala
	275						280					285			
Thr	Arg	Glu	Leu	Ile	Ser	Arg	Lys	Leu	Asn	Leu	Gly	Gln	Tyr	Lys	Gly

290	295	300
Pro Ile Gln Tyr Met Val Trp Arg Glu Met Gln Asp Thr Leu Cys Pro		
305	310	315
Gly Leu Ser Pro Leu Thr Leu Asp Pro Lys Thr Ala His Pro Asn Leu		320
	325	330
Val Leu Ser Lys Ser Gln Thr Ser Val Trp His Gly Asp Ile Lys Lys		335
	340	345
Ile Met Pro Asp Asp Pro Glu Arg Phe Asp Ser Ser Val Ala Val Leu		350
	355	360
Gly Ser Arg Gly Phe Thr Ser Gly Lys Trp Tyr Trp Glu Val Glu Val		365
	370	375
Ala Lys Lys Thr Lys Trp Thr Val Gly Val Val Arg Glu Ser Ile Ile		380
385	390	395
Arg Lys Gly Ser Cys Pro Leu Thr Pro Glu Gln Gly Phe Trp Leu Leu		400
	405	410
Arg Leu Arg Asn Gln Thr Asp Leu Lys Ala Leu Asp Leu Pro Ser Phe		415
	420	425
Ser Leu Thr Leu Thr Asn Asn Leu Asp Lys Val Gly Ile Tyr Leu Asp		430
	435	440
Tyr Glu Gly Gly Gln Leu Ser Phe Tyr Asn Ala Lys Thr Met Thr His		445
	450	455
Ile Tyr Thr Phe Ser Asn Thr Phe Met Glu Lys Leu Tyr Pro Tyr Phe		460
465	470	475
Cys Pro Cys Leu Asn Asp Gly Arg Glu Asn Lys Glu Pro Leu His Ile		480
	485	490
Leu His Pro Gln		495
500		

<210> 467

<211> 140

<212> PRT

<213> Homo sapiens

<400> 467

Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly Ser Met Met Ser Phe	
1	5
Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly Pro His Ala His Thr	10
	20
Pro Glu Glu Glu Leu Cys Phe Val Val Thr His Tyr Pro Gln Val Gln	25
	30
Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys Val Leu Thr Gln Pro	35
	40
Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro Arg Thr Val Pro Thr	45
65	50
Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln Gln His Ile Arg Thr Ser	55
	60
Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn Gln His Ser Arg Glu	65
	70
Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile Arg Met Gln His Ile	75
	80
Leu Lys Thr Asp Thr Leu Gln Phe Arg Ile Cys	85
	90
130	95
	100
	105
	110
	115
	120
	125
	130
	135
	140

<210> 468

<211> 100

<212> PRT

<213> Homo sapiens

<400> 468

Met Tyr Met Leu Leu Ser Pro His Arg Leu Arg Glu Gln Ala Gly Val
1 5 10 15
Arg Gly Ser Ile Arg Thr Ala Asn Arg Thr Glu Asp Gly Leu Lys Ile
20 25 30
Arg Glu Ala Glu Ser Leu Pro Gln Ser Asn Thr Ala Asp Phe Lys Cys
35 40 45
Leu His Ser Ala Ser Leu Gln Gln Ala Pro Gly Gly Ile Leu Met Gly
50 55 60
Pro Ala Ser Ser Pro Trp Thr Leu Ala Val Glu Gly Glu Lys Arg Thr
65 70 75 80
Ser Ala Pro Pro Leu Arg Glu Ser Leu Met Pro Thr Lys Gly Leu Gly
85 90 95
Trp Trp Thr Gln
100

<210> 469

<211> 119

<212> PRT

<213> Homo sapiens

<400> 469

Met Ala Ser Tyr Ser Gly Phe Ser Gly Leu Leu Glu Ile Arg Tyr Gly
1 5 10 15
Pro Gly His Arg Ser Cys Leu Pro Gln Phe Ala Phe Phe Pro Gln Pro
20 25 30
Pro Leu Pro Arg Pro Arg Ile Cys Met Trp Val Leu Ala Glu Leu Leu
35 40 45
Glu Leu Gly Cys Pro Glu Gln Ser Leu Arg Asp Ala Ile Thr Leu Asp
50 55 60
Leu Phe Cys His Ala Leu Ile Phe Cys Arg Gln Gln Gly Phe Ser Leu
65 70 75 80
Glu Gln Thr Ser Ala Ala Cys Ala Leu Leu Gln Asp Leu His Lys Ala
85 90 95
Cys Ile Gly Glu Arg Gly Gln Leu Pro Gly Leu Ser Pro Arg Glu Lys
100 105 110
Arg Asn Arg Ala Trp His Lys
115

<210> 470

<211> 140

<212> PRT

<213> Homo sapiens

<400> 470

Met Arg Ser Glu Cys Val Leu Gly Ala Ala Ser Asp Ser Gly Gln Glu
1 5 10 15
Ala Pro Arg Asp Thr Trp Phe Leu Gln Gly Trp Lys Ala Ser Arg Arg
20 25 30
Phe Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr
35 40 45
Asp Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln
50 55 60
Lys Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr
65 70 75 80
Val Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro
85 90 95
Lys Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr

			100					105				110			
Val	Met	Ser	Ala	Leu	Ser	Val	Ala	Pro	Ser	Lys	Ala	Arg	Glu	Tyr	Ser
		115					120					125			
Lys	Glu	Gly	Trp	Glu	Tyr	Val	Lys	Ala	Arg	Thr	Lys				
	130					135					140				

<210> 471
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 471

Met	Phe	His	Leu	Arg	Thr	Cys	Ala	Ala	Lys	Leu	Arg	Pro	Leu	Thr	Ala
1			5						10					15	
Ser	Gln	Thr	Val	Lys	Thr	Phe	Ser	Gln	Asn	Arg	Pro	Ala	Ala	Ala	Arg
			20					25					30		
Thr	Phe	Gln	Gln	Ile	Arg	Cys	Tyr	Ser	Ala	Pro	Val	Ala	Ala	Glu	Pro
		35				40						45			
Phe	Leu	Ser	Gly	Thr	Ser	Ser	Asn	Tyr	Val	Glu	Glu	Met	Tyr	Cys	Ala
	50				55					60					
Trp	Leu	Glu	Asn	Pro	Lys	Ser	Val	His	Lys	Thr	Gly	Ser	His	Cys	Cys
65				70					75					80	
Pro	Gly	Trp	Ser	Ala	Val	Ala	Gly	Ser	Arg	Leu	Ala	Ala	Thr	Ser	Asp
			85					90						95	
Ser	Trp	Val	Gln	Val	Ile	Leu	Met	Pro	Gln	Pro	Pro	Glu			
			100					105							

<210> 472
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 472

Met	Phe	His	Leu	Arg	Thr	Cys	Ala	Ala	Lys	Leu	Arg	Pro	Leu	Thr	Ala
1			5						10					15	
Ser	Gln	Thr	Val	Lys	Thr	Phe	Ser	Gln	Asn	Arg	Pro	Ala	Ala	Ala	Arg
			20					25					30		
Thr	Phe	Gln	Gln	Ile	Arg	Ala	Ile	Leu	His	Leu	Leu	Leu	Leu	Ser	Pro
		35				40						45			
Phe	Ser	Val	Gly	Leu	Val	Arg	Thr	Met	Trp	Arg	Arg	Cys	Thr	Val	Leu
	50				55					60					
Gly	Trp	Lys	Thr	Pro	Lys	Val	Tyr	Ile	Arg	Gln	Gly	Pro	Thr	Val	Val
65				70					75					80	
Gln	Ala	Gly	Val	Gln	Trp	Arg	Asp	Leu	Gly	Leu	Leu	Gln	Pro	Pro	Thr
			85					90						95	
Pro	Gly	Phe	Lys												
			100												

<210> 473
 <211> 141
 <212> PRT
 <213> Homo sapiens

<400> 473

Met	Ala	Pro	Lys	Val	Phe	Arg	Gln	Tyr	Trp	Asp	Ile	Pro	Asp	Gly	Thr
1			5						10					15	
Asp	Cys	His	Arg	Lys	Ala	Tyr	Ser	Thr	Thr	Ser	Ile	Ala	Ser	Val	Ala
			20					25					30		

Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr
 35 40 45
 Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala
 50 55 60
 Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val
 65 70 75 80
 Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu Gly Gly Cys Ala
 85 90 95
 Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr Gly Ile Gly Ala
 100 105 110
 Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu Val Lys Met Gly
 115 120 125
 Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys Val
 130 135 140

<210> 474
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 474
 Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu Gly Pro Leu Ala Ala
 1 5 10 15
 Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr Glu Gly Pro Val Arg
 20 25 30
 Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn Thr Met Ala Ala Ala
 35 40 45
 Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu
 50 55 60
 Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu
 65 70 75 80
 Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg
 85 90 95
 Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val
 100 105 110
 Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg
 115 120 125
 Pro Gly Ile His Leu Cys
 130

<210> 475
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 475
 Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu Gly Pro Leu Ala Ala
 1 5 10 15
 Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr Glu Gly Pro Val Arg
 20 25 30
 Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn Thr Met Ser Ala Ala
 35 40 45
 Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu
 50 55 60
 Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu
 65 70 75 80
 Ser Gly Pro Arg Gly Pro Thr Cys Arg Ser Phe Ala Val His Thr Arg
 85 90 95

Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val
 100 105 110
 Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg
 115 120 125
 Pro Gly Ile His Leu Cys
 130

<210> 476
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 476
 Met Leu Lys Val Glu Ala Thr Gly Ser Pro Glu Glu Gly Trp Ala Gly
 1 5 10 15
 Gly Glu Pro Arg Thr Gly Ala Pro Ala Asn Ser Pro Ser Cys Pro Gln
 20 25 30
 Glu Met Pro Leu Gln Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr
 35 40 45
 Gln Gln Leu Leu Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu
 50 55 60
 Asn Val Ala Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala
 65 70 75 80
 Ser Gly Arg Ser Pro
 85

<210> 477
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 477
 Met Gly Arg Pro Trp Met Val Met Ile Leu Glu Ser Lys Ser Glu Glu
 1 5 10 15
 Lys Met Trp Tyr Gly Val Phe Leu Trp Ala Leu Val Ser Ser Leu Phe
 20 25 30
 Phe His Val Pro Ala Gly Leu Leu Ala Leu Phe Thr Leu Arg His His
 35 40 45
 Lys Tyr Gly Arg Phe Met Ser Val Ser Ile Leu Leu Met Gly Ile Val
 50 55 60
 Gly Pro Ile Thr Ala Gly Ile Leu Thr Ser Ala Ala Ile Ala Gly Val
 65 70 75 80
 Tyr Arg Ala Ala Gly Lys Glu Met Ile Pro Phe Glu Ala Leu Thr Leu
 85 90 95
 Gly Thr Gly Gln Thr Phe Cys Val Leu Val Val Ser Phe Leu Arg Ile
 100 105 110
 Leu Ala Thr Leu
 115

<210> 478
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 478
 Met Asn Arg Tyr Cys Gly Lys Ile Phe Val Ser Val Met Val Lys Leu
 1 5 10 15
 Gln Lys Asn Lys Leu Thr Ser Phe Pro Arg Gln Pro Leu Leu Thr Phe

20 25 30
 Phe Glu Tyr Leu Glu Lys Val Leu Cys Ser Gly Leu Phe Ser His Ser
 35 40 45
 Ala Lys Ser His His Asp Leu Thr Arg His Pro Tyr Glu Thr Ala
 50 55 60
 Ala Pro Leu Leu Ser Ser His Leu Ile Leu Thr Glu Ala Leu Arg Asn
 65 70 75 80
 Gly Leu Gly Lys Cys His Asp Pro His Phe Thr Gly Glu Glu Thr Glu
 85 90 95
 Ala Gln Arg Gly Lys Leu Thr Thr
 100

<210> 479
 <211> 439
 <212> PRT
 <213> Homo sapiens

<400> 479
 Leu Gly Asp His Gly Trp Glu Leu Ser Leu Glu Glu Asp Ala Gln Leu
 1 5 10 15
 Trp Gly Gly Val Val Lys Ser Cys Phe Glu Gly Lys Gly Pro Gln Arg
 20 25 30
 Glu Ala Gln Pro Ala Ser Pro Gln Ala Ala Pro Pro Gly Pro Thr Asn
 35 40 45
 Glu Ala Gln Met Ala Ala Ala Ala Leu Ala Arg Leu Glu Gln Lys
 50 55 60
 Gln Ser Arg Ala Trp Gly Pro Thr Ser Gln Asp Thr Ile Arg Asn Gln
 65 70 75 80
 Val Arg Lys Glu Leu Gln Ala Glu Ala Thr Val Ser Gly Ser Pro Glu
 85 90 95
 Ala Pro Gly Thr Asn Val Val Ser Glu Pro Arg Glu Glu Gly Ser Ala
 100 105 110
 His Leu Ala Val Pro Gly Val Tyr Phe Thr Cys Pro Leu Thr Gly Ala
 115 120 125
 Thr Leu Arg Lys Asp Gln Arg Asp Ala Cys Ile Lys Glu Ala Ile Leu
 130 135 140
 Leu His Phe Ser Thr Asp Pro Val Ala Ala Ser Ile Met Lys Ile Tyr
 145 150 155 160
 Thr Phe Asn Lys Asp Gln Asp Arg Val Lys Leu Gly Val Asp Thr Ile
 165 170 175
 Ala Lys Tyr Leu Asp Asn Ile His Leu His Pro Glu Glu Glu Lys Tyr
 180 185 190
 Arg Lys Ile Lys Leu Gln Asn Lys Val Phe Gln Glu Arg Ile Asn Cys
 195 200 205
 Leu Glu Gly Thr His Glu Phe Phe Glu Ala Ile Gly Phe Gln Lys Val
 210 215 220
 Leu Pro Ala Gln Asp Gln Glu Asp Pro Glu Glu Phe Tyr Val Leu
 225 230 235 240
 Ser Glu Thr ~ Leu Ala Gln Pro Gln Ser Leu Glu Arg His Lys Glu
 250 255
 Gln Leu Leu Ala Ala Pro Val Arg Ala Lys Leu Asp Arg Gln Arg
 260 265 270
 Arg Val Phe Gln Pro Ser ~ Ala Ser Gln Phe Glu Leu Pro Gly
 275 285
 Asp Phe Phe Asn Leu Thr Ala Glu Lys Arg Glu Gln Arg Leu
 290 295 300
 Arg Ser Glu Ala Val Glu Arg Leu Ser Val ~ Thr Lys Ala Met
 305 310 315 320

Gln Leu Leu Gln Gly Glu Arg Asn Pro Arg Leu Glu Asp Ala Ile Arg
 100 105 110
 Thr Asp Leu Asn Arg Thr Phe Pro Asp Asn Val Lys Phe Arg Lys Thr
 115 120 125
 Thr Asp Pro Cys Leu Gln Arg Thr Leu Tyr Asn Val Leu Leu Ala Tyr
 130 135 140
 Gly His His Asn Gln Gly Val Gly Tyr Cys Gln Gly Met Asn Phe Ile
 145 150 155 160
 Ala Gly Tyr Leu Ile Leu Ile Thr Asn Asn Glu
 165 170

<210> 482

<211> 177

<212> PRT

<213> Homo sapiens

<400> 482

Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg Ile Asp Pro Tyr Gly
 1 5 10 15
 Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala Tyr Glu Lys Phe Phe
 20 25 30
 Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala Ile Lys Trp Ser Arg
 35 40 45
 Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg Thr Val Lys Arg Tyr
 50 55 60
 Val Arg Lys Gly Val Pro Leu Glu His Arg Ala Arg Val Trp Met Val
 65 70 75 80
 Leu Ser Gly Ala Gln Ala Gln Met Asp Gln Asn Pro Gly Tyr Tyr His
 85 90 95
 Gln Leu Leu Gln Gly Glu Arg Asn Pro Arg Leu Glu Asp Ala Ile Arg
 100 105 110
 Thr Asp Leu Asn Arg Thr Phe Pro Asp Asn Val Lys Phe Arg Lys Thr
 115 120 125
 Thr Asp Pro Cys Leu Gln Arg Thr Leu Tyr Asn Val Leu Leu Ala Tyr
 130 135 140
 Gly His His Asn Gln Gly Val Gly Tyr Cys Gln Gly Met Asn Phe Ile
 145 150 155 160
 Ala Gly Tyr Leu Ile Leu Ile Thr Asn Asn Asp Lys Asn Leu Phe Gly
 165 170 175

Cys